

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3257	17158	A	3279	404	65	NLVSSPKRSVFFISPSQKIFFFFWNKE SKISLPKEGGPLLLLIRORTPIFFFFF FYFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFL*TAOLF*TFKFTKTK R
3258	17159	A	3280	226	383	GI*KNSMDGCCLGPFVVFETGSHSHPGW SIVWRNLGSLQLLPPKFKRFSCLS
3259	17160	A	3281	91	26	LFFFFFFFFFFFFFFFFWSESS
3260	17161	A	3282	3	321	HTVIYYFGKNEPFGYIGVA*AMISVGS GFMA*AHHIFTGGIDVSPAYLTCATII VAIPTGVKVF*LATLLGSGMKRSAAVL *TLGFIFLFTARGLTGIVLSNS
3261	17162	A	3283	393	112	PPLRVFFPPFPLKNFFSSRRFFFWGGV APFFPPPKKGFFSKI PPGFFPPPLKKK IFFSSPP*FWAPPGFLLKGPFPFFFFF FFFFFFFF
3262	17163	A	3284	360	47	PPLHRWVPPPPP*KFFFSPTKFFGKVF SQNPPPKKSFFPKNPGVFYSPPKKK KFFLPPPIFFPPPRFFFTTPPPFFFFFF FFFFFFFFFLPLFFWSVSF
3263	17164	A	3285	386	157	FFSPNPLIFWGGGPKFPPPKRRFFSKN PPGVFFSPPLKKKKFFFP*NLAPPRD FLKGPPPPFFFFFFFFFFFF
3264	17165	A	3286	3	385	DAWVPCLYLGVFFCFVKISAILILKI LIFNIENKSI*YLLKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKPTPKKKK KDSR
3265	17166	A	3288	81	270	TIKLEKKKKKKKKKKKKKKKK*KGNE KTRGPKKKVHRDVTKKILCYKICPFNG ISLIGHT
3266	17167	A	3289	3	145	LGRRLQENHLNLGG*GCREPKSHHRLA WATEQDSISKKKRIGGPV
3267	17168	A	3290	404	47	GPGGKIIFKKNPEEKIFSTQKKKGFFPP FPPKNFFPPGGFFWGGGGPIFPPPKK GFFPKIPRGVFFTPPKKKKIYFFPPREI WAPPGIF*KGPPLEFFFFFFFFFFFFLV LNDILLA
3268	17169	A	3291	106	362	KKKKKKKKKKKKKKKKKKKKRMRNK KKKKKGRGGKKKKPRGAQIIRGKKKII FFFKKVKF*KGGGDL*KKSFSGENNLE NTHKE
3269	17170	A	3292	3	226	NPLVNLNLGLLFILATSSLA VYSIL*SG GASNSNYALIGALRAVAQKKKKKKKKK KKKKKKKKKKKKGGGVL
3270	17171	A	3293	337	2	FFNRELLKSKNKETEKNDYHKERIWHF DRPYKFYMLFFCFGLIFFLYLPFFIYF FFFFFFFFFFFFFFFFFLNSLNI*F FSINTHKCGNRGQGGGAIGPRLSNGRV
3271	17172	A	3294	327	21	KFFFSPPNKYFFVFPHKFTPTKMF KIPPPPLISPPPKENHQCPPPPHIAPP SHPPFGPPHFFFFFFFFFLFFLWRTGSRY IAQAGLELLGSSYPAS
3272	17173	A	3295	367	101	FFFSFF*KKKNFFPPPLWPPPPNFL*N PPPPFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFLVNSLCRRYRG*SLLY YAWL
3273	17174	A	3296	178	2	KGPPFFFFFFFFFPDSITLFIITKNEK KTRCTSIGE*ITWYTHTEYYSVMKRNE

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						LS
3274	17175	A	3297	147	1	RGPPPPFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFW*FALIFLV*NFAITF
3275	17176	A	3298	3	347	PFGEGETNGRFDLDTKKALVSKKKKKK KKKKKKKKKKKKKKKKKKRGALKKKKN RGGQKKTGEKKKKFFFKKGEEKKTPGNF *KKKKFLGGDNLAQTTPKKKNLWGKKKNFWG
3276	17177	A	3299	405	2	WRPKPENSPSPGGPNPPGQKN*TFPFPK TPKLGRGCGGAPQFPLPVRRAGENPPNP RFLGFN*PKFPFPFPA*\GGNNETFFQ KKKKGPRFWAGVLPTGGAEGESIPHLSP ASGSSRHPWCFMLCRPSRLCLL
3277	17178	A	3300	125	376	DQPVPNSETSSLQKKKKKKKLFPGGGGP PLFPHFLGGWGGGTTRPPG*RKRKSGSV PQQPPPGGRVPPP PHPPKKWGNKGPPPP PGKSFFFFFFFFWRDEVSLFCTGWSQTQT PGLKQSIIHLSLPRWL DYGREPHLAIHF FPTRPRTRG
3278	17179	A	3301	348	1	PQRLLILGGGGPPNSFPKKGFFPKTPR GF*NPPPKGKKKNFPPPRKIGPPQGFF* RAPLEFFFFFFFFGWFFFFFFFFFLFLENG VSLYCPGRSRTPGCLKSSRLLASLRAGITGV
3279	17180	A	3302	2	354	GRVGGRVGSPTTLTT*NPHSHEKTPSCS YPKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKKRKKKKKKKT*GGGAYIKKKG GGS PRTEENQYCFLLGGKKNILRGSCCLKT
3280	17181	A	3303	362	26	SSQAAPTCKKKKKKKKKKKKKKKGGAL KKNFGGGKKNKGGEKKKIFFFKGGGKKNP GGNFKKKNFFGGGKIGENPPKKK*RFRK KKKFLRGKGKKKS
3281	17182	A	3304	371	3	NQKKPPPVFFFFFFFFFKKKKNPPPATPPP GRP*FFPPQKFFFPEGGPPPFKKGAFF PPPKKNDFEPFFPGGVFFF*KKKNIKV PPPKKKKKKKKKKKKKKKPKKQKKGR PARDLEPHAS
3282	17183	A	3305	2	196	DR*LFS TNH KDIGTLYLLFGA*AGVLGT ALS LLIRAE LGQP GNLLGNDHIYNVI TAHA FVIIIF
3283	17184	A	3306	4	339	LFS TNH KDIGTLYLLFGA*AGVLSTALS LLIRAE LGQP GN LVGNDHIYNVIATAHA FVIIIFIVRP IIIGGFN*LNPLIIGAP DRAFPRIINISF*LLPRSILLVRASAIA
3284	17185	A	3307	2	367	KPPAITQYQTPLFV*SGLITGGLLLLFL PDLAGITILLTD RNLT TL FDPAGGGD PILYQH LF*CFGHPEGYIL ILPGFGIIS HIGTYYS GKKEPLGYIGMV*AMRSIGFL GFIE*AHHIL
3285	17186	A	3308	243	370	KGHRFGMVTFCVPNSTLGQGGGWIRRSG I*DQPGQGGVTPSL
3286	17187	A	3309	2	363	LVPLIIGAPDMVFPRINNIGF*LLPPCL LLL IAYAIMEAGAGTG*TAYPPLAGNYS HPGASVDLTIFSLHLAGVSSILGAINFM TTIINI*PPAITQYQTPLFV*SVLITAG LLLLCLPG

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3287	17188	A	3310	1	364	LYITGPTTLALTIALLL*TPLPIPNPLVN LNLGLLFILATSSSLAGYSIL*SGGASNS NYALIGALRAVPQTISYEVTLAIILLST LLIRGSFNLSTLITTQEHL*LLLP*PL AII*FISTL
3288	17189	A	3311	215	2	GMAKLKARFLPKKGGKRSLSPLWGS GF PTSGTGETFFFF*DRVLLCQPGWSAVA QS*LTTASTFWAQAI
3289	17190	A	3312	153	3	MNKCI CMVCVCVCFRSHKHTVCAWVCV Y*V*TYTVCVCVCVCVCVCVCVC
3290	17191	A	3313	149	1	KTEPGFFPGFKGPF*FKGPPLFFFFF ETEDGVLLCRPGWSAVSRDRA
3291	17192	A	3314	282	69	KIGKTAPFFSWPRRVFLLKKKKKK*GL TLSSRLYGGMISLELLGSSDTLASASR VARIIGQCPHAWLT
3292	17193	A	3315	479	60	MMQHSIKHALVEITGWVRWRPVPALW EAEVGEFNSISKTNKRKSNIVKMSILF NLIYRINAPFFKFLIALNKNKSKSISW NLKS**STQ*SSRNVGGITISDF*THQ QATELRQEFLLHTGLVHRSTVSRFRFHA
3293	17194	A	3316	129	3	SFHQKVWPDVAHACSPSTLGG*GGRT GSGDQDHPGQHGE
3294	17195	A	3317	3	156	EFHRVSQDGLDRLTS*STLLGLPKCWDY RCEPPRPASFPSTLTVRISPFLL
3295	17196	A	3318	36	340	TGLVIAEHLFFFFFFKKGFWFCPPGGRAG PQGNLMEFVSGGGKGFPCGPPKSGE*R APPPSRGKFWFFKKKGGLFPWPGGV*TS DPRGTPPPLGPKGGEYR
3296	17197	A	3319	326	2	KAFFLNFKPHPGFA*GLKFKPNSLLEPI* SFIRKT*AFLICL*IQLNRADGKIPLKP GVIPFKKCFNFTPLFFKKNCSSTPNL FFFFFFFPGDGISLCRPGWSAVA
3297	17198	A	3320	175	312	QAGVQWCDLSSPXPSPSGLT*FY*CSLP RTWEYRCPPSRPCNFSIF
3298	17199	A	3321	363	51	RWGPRLPVAWLPSVSRRAEBCSPGRGAH GQGGGGGGQAR*REGPDEWTGGAPVGMG SPSLNRGAGRGPPQPGPSSKSRGRVRC TPHSLIGCGLSFFICKMG
3299	17200	A	3322	344	187	LRQETCFNPGGKNFG*QKLPPCPPAWAT RGWVSKKKKKRKRKEKIRICVLT
3300	17201	A	3323	3	313	TRRRERERERERERERERERERERE REREFFFFFF*KNLSPPPGGKKRGGGG FHSPFWGEKDFLPPRPKGGGERGRPP PVFFFFFFKKEGAPPGGV
3301	17202	A	3324	365	1	SLGWVRVTPPPPLGPRGCSPPRPDKRG SPGRVKFGGVKPPFKVKP*PPKRLDPS GA*FFSPKKICQGPPIPKKKKKEAELS ILCTKFPLQEEVMQVPPPPCTCSSEPG INCICKRHC
3302	17203	A	3325	1	269	ARALSLSLSLSLSLSLEFFFFFFLAPT QILGGGLFYPPKGGGHLNRLGGGRVFF GPPGKKTAPLGGGRVIKKKTPPGTPL*L SPPPGGPPFFQGGQKLSPPFAGLTGGP PPWGGKAPPPKFGSGPKKKKKTLELER ERERERERERELV
3303	17204	A	3326	1	316	ARGERERERERERERERERERERFFV SPPGPDTLQDRGGVSLFASDPTHEIYLP CPLRGPLSERDPEELHGVCFSEPSHRW

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3304	17205	A	3327	2	369	FPEEGVGDICQC*HRGECGSP ARGDVTRESTYQGHHTPPVQKGLRVGTI LFITSEVFFAGIF*AFYHSSLSPTPQL RGHWPPGTITPLNTLEVP LLNTSVLLAS GV*IT*AHHSLIENNRNQIIRALLITII LGLYFTLLQA
3305	17206	A	3328	1	259	GTRKKHSTILIREIDIKFMPRFHISPI RLVKI*ALANIRC*QQCGKVGNNLHC*F SKLVQSTGRAIWHALVLSLARSRLSLS LH
3306	17207	A	3329	2	352	ARGTLLLLCLFFALTIYPRWCDVTRKS TYQGHHTPFVQKEPLVLGKLFITS*VI FFAGFF*AFYHSSLTPTLLGGHWPPTS ISLFNPLKKPLNTSGLLASGVSI*AH HSLIQ
3307	17208	A	3330	3	361	HEEPLGYIRMA*AMISIGFLGLIVRAHH IFTGGIDVDSRTYLTSAITIIAMPTGGK VFR*LATLHGSNMK*SGAGL*ALGFMF FTVGGLTGIVLTNS*LDIGLHDTYYVVA HFHYVLS
3308	17209	A	3331	1	340	GTSGDTRAYFTSATIIIAIPTGVQVFS* LATLHGSNMK*SAAEL*ALRFIFLFTVS GLTGIVLANSSLDIELHDTYYVVAHFHY VLSIGAEFAIRGSIH*FPLL*GYTLDO T
3309	17210	A	3332	2	352	ARGDVTTRAYFTSGTIIIAIPTGVKGFS *LATLHGSNMK*SAAVL*ALGFIFLFTV RGLTGIALANSSLDIVLHDTYYGGAHFH YVLSIGAVFAIIGGFH*FPLFSGYTLD QTYAK
3310	17211	A	3333	85	370	QVSHRVRPCFERERERDRYRHTQRECE AKEIYSGFFLSASEMESCSLAQAGCKE LRMCHCTPAWVTQGDVCS*NKK*HWEKK GLWFLGVNIST
3311	17212	A	3334	362	3	QEVKVSMMNRDTHSLQRGEQKRNSVSKK KKSSQEKLRVHTQHT*IFI AVLFI AKNGKQFKFPSTCEWINNM*YIHTMEYY SATKNQLIHVTT*MNLNNIYTKFLKARQ KMITYSC
3312	17213	A	3335	3	351	HEGTTLHHLFLLTGSNNPLGITFHSDK KTFHPYTIKDAGLLFLLSLMTLTL *PDLLGDPDNYTLAHP LNTPAHIKPE*Y FLFAYTILRSGPNKLGCGPALLLSILIL AIIP
3313	17214	A	3336	17	350	FIFTLTETNRTPFDLAEGESELFSGLKI KYAAGPLALLFITEYTNIIIDTLSTTI VLGTTYDALSPELYATYFVTKTLVTS FL*IRTAYPRLRYEQLIHL*KNFLPL
3314	17215	A	3337	2	349	ARDSLISPILRLHPRPNLRQNAFYHIH RGKSNFLPTTLRPIRNAPTLLGLPRCI HHMKHPIICRLIH*FPLFSGYTLDQTYA KMHFTIIFIGVNLTFPPQHFLGLSGMPR RYSYDPDAYTT*NILSYVGSFISLTA LIIIFMM*EAFASKRKVLIVEEPSINLE* LYGCPPPYHTFE
3315	17216	A	3338	2	386	ARAILNAMAFLILTERKILGYIQLHRGP NVVGPYGLLQPFADAIKLFTEPLKPAT STITLYISGPTLALNIGLL*TPLPIN

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						PLRNLNLGLLFILATSSLDYSIL*SG* ASNSNYALIGALRAV
3316	17217	A	3339	175	16	ILGDLFPFPAWLHPFLFLLLFSRPSLAV TEAAVQWRNLGLLQPLPGY*SSWC
3317	17218	A	3340	1	369	GTSNLSLLFIVATCGLAAN*ML**GGKI N*IYTLRVALAAIHTILYEITLSIILL *TLLISGSFNLSTLITTQEHL*LLFS* PLAII*FISTLAETNRTPFDLAEGESEL F*GLNIEYSAR
3318	17219	A	3341	1	363	GTRGGTILPAMVLMIDLVPISLRILYITN KVNEPSLTIKSNHQWY*TYQYTDYGGI ILNSYILPPLFLQPGDLRILDVDNRVVL PIETPIRIINT*QDGLHS*AGPTLGLKT DAIAGRNVQ
3319	17220	A	3342	181	315	BKSPPTPPPTXXXXXPGGNPPGPTL*G PFYWGGGERGPPF*TGGP
3320	17221	A	3343	3	183	HEVSQSCRELLTSGDPPASASQSAGISG MHRAPVPS*TFHIFNIYCGPGTVLKPY LNL
3321	17222	A	3344	83	354	VLGARCPCAGVSRVSMFPWFLWQQACLL PWWRCCLSTLYANRADRDVP*TSRTGPV MVAHACSPSTLGGQGGWVTRSGV*DQPG QDGETP
3322	17223	A	3345	124	379	GQGICFMVVSGLSHRLAHCRTYGVNN LLCSSSLPFLPLPLPPPEPGWDDIN IIFIIIFRDKVLCCCLGWSAVT*SQLTT A
3323	17224	A	3346	3	368	YEPPI*PLTGALSALLMTCGLAM*IHLH SITLLILGLSNTLTIYQ*WRDVTREST YHGHTPPVQKGLRNGIILLITSEAFF AGVF*AIYHSSLAPTQLGHWPPPTGMT PLNPVQGPLL
3324	17225	A	3347	1	352	GTSAGDVNYG*IIRYLHADGAKIFLRCR FLHSGRGLYGSYVYSKT*NIAINLLIA TIATAFIGYVLA*GQILF*GATVSTNLL SDIPYIGTDLISQRI*GGYSVDRPTLTRF FTFHF
3325	17226	A	3348	2	360	ARAEISPLHSNLGNESETPSQKKKKKKP PGGGGKNWNPYPSTPPNPPKGG*RE EPPPLTKRVF*KKKVFFEGPRVKKNLGG KGKKKRGFPAR*KNPVFKAKGGRNFGP QAFFFKK
3326	17227	A	3349	226	366	PQSFCSVASWPAGDLMEI*AWQKFEYKP GKVPMDPEGCLLPLAKKKEEEEEEE EEEEEEEEEEEEEEEEEEEEEEEEELV
3327	17228	A	3350	2	374	ARGGGYSRPHATLRTVTFHSILFFIIA GLAAIHLFLHETGAYTPL*ITSHSEKT TFHPYTMKDALGVLLFPLSLTTLTLC PNLLGEPHDYTLTNPLNTRPHIKPE*DC LFAYTNMRSGPN
3328	17229	A	3351	1	266	LGLVEHFLTLTKLTSSNISDAQEIQSV *NILTALILNLMVLPRLMLYITNEVFD PSLTIKSIGHQWY*AYEYTDGGLIFNC YILP
3329	17230	A	3352	207	362	ILFLLKQKIYVLFQFSN*GSSIPELAHS DAYQTKEICSSGKVYKYLQCWEKW
3330	17231	A	3353	178	365	NHGIDKGLRYRIYTVQQEDNSVKR*LKD FNQHLKDNIRKADKHKRCPTSLVINI

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						MPKPP
3331	17232	A	3354	359	3	LQVRSIMPLGQFHPP*NFCSFFPKPKI PFFFLFFLKGVFVFFPGWRARGQFWVFG PPPKKFKKFFFTLLRNWGFDFPPSRG KFFFFFFFWYF**RLRFTMLTRLVFN* PQVISC
3332	17233	A	3355	2	354	AREPSP*PLTGALSALLMTCLSM*THL HSITLLILGLLTNTLTIIQ*WRDVTPE TFQGHHTPPVQKGLGYGIIIFITSEVFF FAGFL*AFYHSSLAPTPHLGGDWPTGV TPLNAL
3333	17234	A	3356	1	364	GTREMICCSALSPRIHLSFHRWPDWHC ISKLITRHRTRHVLRWSSLPICPINRS WICHRRRLHSLISPIRLHPKPNLRQNP PHYHIHGRK*SAAVL*ALGFIFLFTVGG LTGIVLANSSLDIGLHDTYYVGAHFHYV LSIGAGFAIIGGFII*FPLFSGYTLNQT YAKIHFTIIFMGVNLTFPQHFLGLSGM PRRYSDYPPDAYTT
3334	17235	A	3357	2	376	ARGGQPEDYILILPSFGIIFHIVTYYS KKEPFGYICMV*AMISIGFLGFIA*AFP IFSVGIDVNTRAYFTSATIIIAIPTGVK VSWLATLHGSNMK*SAAAL*ALRFIFL FTVSGLTGIVLCN
3335	17236	A	3358	357	139	AQPWFFFLFETVFCCHAAQAGLKSIGSSDL PTSASQSVGTGMSHAWPERS*QNTF TYVQSIYSDDIRKSMF
3336	17237	A	3359	277	1	SCQKDISIGFLFVPGFRVKGVAQEHVVG VRMYVLVPTVGGDGKERER*RGIRHTPP PSERVQRERERGRDRDREKERSQRKP EMDRETS
3337	17238	A	3360	261	2	TICSKCAWLCFSKTLTNTCASRSDLAH GP*CPNLCSGIFSSAWTDISRLLLFFCL FVLRQSLTVAQAGVQWNCNLCSPLPPG SC
3338	17239	A	3361	199	354	HLPYWPMMFATFNFFFFETEFHFFPQA GGQWGDGF*LKPPPARLKQFSCLN
3339	17240	A	3362	3	364	HEDRDTPAYFTCANIIIAIPTGVKVFN* LATLHGSNMK*SAAVV*ALRYIFLFTVS GLTGIVLSYSSLDIVLHDTDYVVAHFHY VLSIRAVFAIIGGFII*FPLFSGCTLNQ TYAEIHFT
3340	17241	A	3363	3	360	HEETYIPKQKYSFLHDSQTSFCFSNSI PTPSNMEETQQKSVSGCLRP*AGMGETC GQGSRAAQPLPSLPQLNLKLLRISLLLI EAWLEPERVLKSMFANNLGYDTSDDY HLLKDLE
3341	17242	A	3364	352	27	VYLSSQRNSAASVNRMTVVTDRSLSPYT LGWHRPDRLFHFVFSLFVYTFVERGSQS IAQAGVQWCDHSSL*P*TPGLK**TCSC LP*VAGTTGTHHYTGPIILLNLFN
3342	17243	A	3365	347	99	GGPPLPRGFSPPPGARPLAPPWPPQES PPPPPKTAPQKKKAPSIPAGQWLVEQ NRPQPFKKPPGVGF*NPPPLNMGF
3343	17244	A	3366	3	319	HECLAHTLCFFNLMS*RTTVILHRMFS IVTAI*YLLSSQYVIGYIYVCIHTHTH MYIHTHRHRTFICVCVCVCIYITSIC
3344	17245	A	3367	3	474	YELLLNGPILNARAFLLTERKILGYI

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						QLHKGPNVSPYGLLQPPADATKLFTE PLKPATSTITLYITAPTLALTIDLLL*T RLPFPNPLDNLNLGLLFIATSSLPVYS IL*SG*A*NSNYALIGALRAVAQTI**E VTPTIILLSHYYKWLNR
3345	17246	A	3368	2	348	ARGLQDATFPFIEELITTFHDHALIIIVL ICFLGLYALFLTLTTKLTNTNISHAQEI ETV*TILPAIILVLIALPSLRMLYITDE VNDPSLTIKSIGHQWY*TYQYTDYGGLI FNS
3346	17247	A	3369	64	363	KKWGFVPQQKKGGGRISVNGTPIFKGKG NFPP*PPGEGTKGPGPKPK*IWIFKKR GGLIFWPKQFPTPGPKGTHPPGPPKGGK *RGGPPSPGGFNFRRG
3347	17248	A	3370	34	355	AKGKEYIETVAEKKKKKKKAPPPI*KAP *NPGKKPLALKFPPPSQKAPPPALFCP *KGPPPRVFPKKKKKFPFGRKGFFFTG GKPP
3348	17249	A	3371	1	374	FLHSLHLSLRLLYLP*KFSMFIIILLKAY YTLVCVCVCVCVCVCV*PLNKIHINHF TCSTVGRGRSNPIFFPPLN*RPFYTT
3349	17250	A	3372	429	3	FFFFLKKQKISRVPFRGPEFFGQRKPFW AKGPPRAPQKGGEKGNPSPPPPIIFK KGEKPQGGPLFKKGLGFFSPPKVFFKKG VFKSGPGGP*NFGFRGFSPSPPKKGK KRKPQSPGFFFFFFFFFFEILGCSGRSR T
3350	17251	A	3373	2	404	LGTDLSLIIRADLGQTGDLGNDHIYNA IVTAHAFEIIFFIEIPIIIRGFGN*LIP LIIGAPDMAFPRINNISF*LLPPSILL LASAIVEAGAGTSGTDYPLSGNYSHPG ACVDLTILSLHLAGVSSILGAI
3351	17252	A	3374	2	417	AFV*IAHITRDVYVG*IRYLHAKGARI FFMCLFLHIGRGLYGYTFLYSET*NIGI ILLLATIATAFIGYVLL*GQISF*GATE ITNLLSAIPYIGTDLIQ*I*GGYSVDS P TLTRFFTFHFILPFIAGPNPLHLTT
3352	17253	A	3375	85	1	FWPGAVAYACYPSTLGG*GGWIMRSGVR
3353	17254	A	3376	396	1	KEGYIKGPRGENFF*KNPERKIFSRQRK GGVFSPLPPKFFFPKGLIFLGGGCP IFPPPKRVFSKNPPGVFINPP*KKKIF SPPPENWGPFRVFLKGPPPPPPPPPP FFFFFQTLFLGGCGYNTKLR
3354	17255	A	3377	3	118	LLPPSLLLLLAYAILVAGAGTG*TDYPP LTGNY*KTKA
3355	17256	A	3378	301	82	ERKGPQRGGKKGPKAQKPEKKKPKKRP PPPQN*FFGNPPKKKKGGKDPPSKKRG GKGVPPPRKKKKKKKE
3356	17257	A	3379	2	195	DR*LFSTNHKDIGTLYLLFGA*AGVLST GLSLIRAELEGQGNLLCNDHIYNVIVT AHAFVIF
3357	17258	A	3380	21	411	VFCTNH*DIGTLYLLFGA*AGVLRSA LLIRAELEGQGLLLGNDHIYNVIVTGH FVMNLFVIVPIIVGGSGN*LGPLEIGAP DMAYPRINNIGF*LLPPSLLLLLAYAIV EAGAGTG*TVYPPLAGNY
3358	17259	A	3381	2	421	GRVGGRVGTSTNRDIGTLYLLFGA*TG V LGTALSLIRAELEGQGNLLGNDHMYNV

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						IVTAHALAKIFFILVPIIIGGFGNGLVP LIIGAPDMAFPRISNLS*LLPPSVLLL LESVIAEAEAGTGRTVYPFLAGTYSNPG
3359	17260	A	3382	3	185	VIYSTIFAGTLITALSSH*FFT*VGLBI NMLAFIPVLTCKINPRSTEAATKYFLTQ ATASIIILLAILFNILSGQ*TIINTTN QYSSLIIIMATAIKLGIAPFFHF*VPEVT QGTPLTSGLLLLLT*QKLPSSISSRKQPH P
3360	17261	A	3383	5	398	FFGHPEVYILILPGFGIISHIGAYVSGK KEPFGYLGMA*AMISIGFLGFIA*AHHI FTVGIDVHTRAYFTSATIIIAIPTGVKV FN*LATLHGSNMK*SAAAL*ALGFIFLF TVGGTLGIVLANSSLDIVL
3361	17262	A	3384	1	250	LGNTGETLSLQKNV*KLARCGGTCLRSQ LLRRLK*EHCLTPGGRCSEPRSCHSSP AWATGQDLSQQQQQKYPLRIFSAIKS
3362	17263	A	3385	456	0	IFFFSQVETGIHHIGQAGLQLLTSGDAP CVGLQKSWDYRPEPLHLAWLIHSLLSNF YYC*FGFCKLSVFILINVFCKNCTCNSSM FLFSYS*NPCAQ*KNEGPLLKNKPCRIT DAWADAWAPVF
3363	17264	A	3386	1	225	PSRNFVLVDKILKFT*KYRGPRTAKT TLKKKKKVRLTLLIFKSYKTIIVITIG WYGFQDRQVD*WNRIBSLE
3364	17265	A	3387	3	400	LLILGLLTNTLFTIYP*WGDATESTYQG HHTPPVQKGLRYGIIILFTSQVFFAGF F*AFYHSSLSPPTQLGGHWPPTGITPLN PLEAPLNTSVLLASGVST*AHPLIE NNPNPIFRALLITNILGLYF
3365	17266	A	3388	24	407	IASGRPFFFFFFPKGKFISRGCGPFS PKI*KNWGKGSFFPPQREPCKRGVP KNPSLSFYPPGGKPLGPPPKLVPPSS* PGKKAFFFF*TPPPGFLTPLGGGLSPLK GGYLLAPHFVPTGEP
3366	17267	A	3389	148	413	LNLNNNNNGKNHLLNTVYST*LEEKKKK KKKKKKKKKKKKKKKKKAPGGGFF
3367	17268	A	3390	157	14	RVSACCQVWW*MPVVPATREAEARESLE PGRHRLRSCHCDRDPVSKS
3368	17269	A	3391	2	398	LFSTNHKDITLYLLFGARAGVRGTALS LLIRAELGQPGNLLGNDHIYNVIVTAHA FVINFFIVIPIIIGGFGN*LVPLIIGAP DMAFPRINNISF*LLPPSLLLLVAYAI EAGAGTG*TVYPPLAGNYSH
3369	17270	A	3392	2	395	DQKDITLYLLFGA*AGVLGTAVSLTIG AELGHPGYLIGNDHVYNVIVTAHAFVII FFIVIPIIIGGFGN*LVPLIIGAPDMAF PRINNISW*LLPPSLLLLLACAIVEAGA RTG*TVYPPLAGNYSHPGA
3370	17271	A	3393	396	54	GYPPNLTFTVTSSTSVSPSHPPSHVCS PTPAIPQTPRSPPESTPTPEVSLTPT LSLGAISSLASAGPQASPASPGFWGTS PP*PYS*NRPQTAACGVFSQLFFIRPEV P
3371	17272	A	3394	417	60	KGWVFQRIWPGPGGSPRYSRPPGGPRG LIPLGSGV*TPPGPHWETPFFFNQPI GQGGGGPLIPLGGVKPEKIFYPGNQSF H*PKIPPHPPPLGAKQNFPPKKKKPQKN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						TKGFVW
3372	17273	A	3395	417	3	FFFFFFFFQHFGFEAAA*YWHFVDVW*L FLYVSIY**GSYSFSINS
3373	17274	A	3396	229	1	RSFWTKTMGFSCYKDF*TNKNKDTTYQ NLWDTAKAVLRGKFIALNVPINKLERSQ ISNLISQVKEGQAWWLMPI
3374	17275	A	3397	344	165	ELKSPQPRKRNGCFFLAVDPEDEGF*NLN FCGNGQGLNAPGGYPCPEIPMGFVFNAYG KTF
3375	17276	A	3398	1	409	HKDIGTLYLLFCARTGILGTALSLLIRA ELGQPGNLLGNDHIYNGIGTTQALVRL FIVIPITIGGFGN*LIPLIIGAPNMAVP RINNISF*L*PPSLLLLVAYGIVEAGAR TG*TGYPPLAGNYSHPGACVDLTM
3376	17277	A	3399	3	396	KDIGTLYLSFLS*AGVLGAALRLLRK LGQPRNLLRNDHIYNVIVTAHAFVLIFF IVIPITIGGFGN*LLTLIIGAPDMALPR INNISF*LLPPSLLLLLAYGIVEAGART G*TAYPPLSGNYSHPGASV
3377	17278	A	3400	49	350	KSNSHTEVQAGQEQKSFRRSKHKAGRAG SDPAPYVLACGLCRSISFLFFFSLSLFF FFFFKRDGV*QGYSSGSNTPGVKQSSCL GLPKYWDYRREPLHPA
3378	17279	A	3401	1	398	KPPAITQYQTPFLFV*SVLITAVLLVLSL PGLGAGITILLTDRSLNATFFDPAGGGD PILYQHLLF*FFGHPEAYILILPGFGIIS HIETYYSGKKEPFGYIGMG*AMISIGLL GFIA*AHHLFTG*IDVDTRS
3379	17280	A	3402	388	42	TPLFNPPGAKCVNPPFPKKLKKKNPSRA MGGPPLFPPLWGGKPKGPF*NRKSGAPV THFAPPAPPPGGKREPPPPKKKKKKKRK BEKESNRVQIKKRGKGRPLPVLDPAE ESQ
3380	17281	A	3403	413	2	SPHPLKNFFLPKPPNSGGGLAPFVPPQ K*GSLPKIPRGYKSPPFKEKTNALP GKPGPPRASSKRPPLFFFFRGRVPLCH PG*STVQCVQAQCTLELLGSSNFLTSSS PVTWGHRRQPPRPINFFIFFRGRVP
3381	17282	A	3404	433	274	LGVVAHACNPSTLEG*CGRTAWSPGVQD QPGQHSETPISTNFFWYFRISYFHI
3382	17283	A	3405	131	427	GPPPPQFFFWGKRGGNPPFFFFSEKRD VF*QFFLRRRGPKKFPFFCLQKTS L FSEKKKKKGFPPPLFPQKKKCGGGPHY KKEGFTLNSFLFQGDGVSSVAQAEVQWR NISSLQALPPGFT
3383	17284	A	3406	413	137	SPPPPQGGIFFFFKPR*ETFSPPPNLG FSPSPPLKFFFPKGFIFLGGGPKFP PPKKRFFQNSPGGFFFPF*KNFFFL PPVILGPPRVFF*GPPPPKK
3384	17285	A	3407	319	540	IVFKDQCEESFTTLNVDIRNHQNLDSL EQHGKGDLL*GANAYHCEKCNKKVRAVQ LCLILITFNGFRKNRFFW
3385	17286	A	3408	2	403	SLHLGGGSCIVGAIYFITTIIINIKPAGI TOYQTPFLFV*SGLITGILLLSLPLAA GITILLTDRNLFTTFLNPGGGGDPILYQ HLL*LLSRPEVYILILPGFGIISHIGTY YSGKKEAFVYIGVV*AIISIGC
3386	17287	A	3409	2	142	KKENYRPVSLNRDAKSLNQIQLHI*KII

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						HCNQVGFI PGMQGWFNIL
3387	17288	A	3410	407	48	PPGGKIFFYKNPEKKIFPTQOKKGVFPF FPLKNFFFPFRGKIFGGGGQNA PPPKK GFFPKIPQGVF*SPPKKKKNFFPPGKI WAPQGVFLKGPPPPPPPPPPPPPPPPPP FFFLGVR
3388	17289	A	3411	3	402	SYRLE*QLEDKAAPPQDFTQQLRWPEKQ HRMVWPKEDMHKQLVEASETLKSQAKE L*DAHQQQLALQEFLEFELMAELYSH NHKVWDKEEEMEVAMHKADMMWQEI*RS KKLTKRMLFTQMRRTITPVS
3389	17290	A	3412	1	224	LLFQLLRRLRQENHLNLEGRSCSELKMH HWTTPWGTE*DCL*LKKQSAAYLPNNTI KKLTGSRTIEDICTEYNK
3390	17291	A	3413	202	1	IVMSWPGVVTHA*IPSTLGGQGGWITRS GVRDPLASAFQSAGITSVSHCSQLIFVT VFYLSPLSHLY
3391	17292	A	3414	407	309	PSFKASKDRLTL LLGANAAGDLKFTPMF IYHSENPRLKNYTKSTLPVPVLCIRNI KAWMIAHLFTAWLNEHFKPIVETHCSGK KISFKILLINKAPGHRRAQMERHKMN VFMLANTTPILKLMDQGVF*TFILCLSI
3392	17293	A	3415	404	46	LKKPPFQKFLKILKKKKGGGGGPPF*T PPFGGGRGGVPPRAGVSNPVPQGETLF F'FKNPKFPVGGPAP*FPLLRGVNKKNF FNLGGGGFKKRKFSPPPPRGGKFFFPK KKKKKKE
3393	17294	A	3416	23	404	SVLITGALLLLSMPVLGAGITILLTDRN LKTTFDPAGGGDPILYQHLL*IFGHPE DNILILPGFGIGSHIVYYSGKKEPFGY IGMA*AMKPIGFLGDIAGAHVFTG*ID VNTRSYFTSDTINMG
3394	17295	A	3417	38	469	SGTTHASALFDPAGG*DFILYQHLL*IF GDPEVYILILPGFRIISHIVTDYSGKKE PFGYIGMA*AMRSIGFLGFIG*AHIFT V*IDVDTRAYFTSATIIAIP TGKVFT *LATLHGSNMK*SAAVL*ALRFIFLFTV GGLT
3395	17296	A	3418	1	419	FSTNHKDITGLYLLFGA*AGVLGTGLSL LIRAE LGQPNLLGNDHIYNGIGTAHAF VIIFFIVIPIIIGGFGN*LDPLIIIGAPD MAFPRINNISF*LLPPSLLLLLSAIGE AGAGTG*TVYPPLGGNYSHPGASVDLT
3396	17297	A	3419	397	107	KNSAPPFSPIFLP*GPKFAFFPPGKKVQ KKIF*KFPAPGPQGVYLRGGGSPSPQ TPNWP NKKA AFVLP PPPPFVFGNPKKKK KKAFAFSSENRR
3397	17298	A	3420	3	253	RGCREMRLCHCSSAWAIAGVSEKKKKK KNWQ*CLLGICSYLDLWLPGLFKWLSQI GRIVELQLELKQYLRGITKQTLKILH
3398	17299	A	3421	1	393	RTRTIKTPAITQYQTPPLFVGCALITAAL LLLSLPVLAAGITILLTNRYLNTFFDP VGGGDPILYQHLL*LFYPGDYIVILPG FGIISHMVAYYSGKKEPFGYIRMD*AMI SIDFLRIIV*AHIFTVEN
3399	17300	A	3422	142	377	LSKNCYKPSYVGFVCQCKFFNQLSKFLE VKLLYCMVKLC**EG*MAQPL*KQFVLV ALKLNIVLPYNKAISLPGIYSTD*KTYT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						DTQNLTHTVYSSSLIITKN*KQQRCPVGE*INKCFIYTTEYYSLTKRNKLSHMK A
3400	17301	A	3423	2	435	LILPGFGIISHIVTYYSKGKEPFGYIGMG*AMISIGFLGFIV*AHHIFTVGIDVYTRAYFTSATIIIAIPTGVKVER*LATLHGSNMK*SAAVL*ALRFIFLFTVGGLTGIVLANS*VDIVLHDTYYVGAHLHYVLSIRAVFAI
3401	17302	A	3424	2	436	LNTTFDDPAGGGDPILYQHLF*FFGHPEVYILILPGFGIISHIVTYYSKGKEPFGYIGMG*AMISIGFLGFIV*AHHIFTVGIDVDTRAYFTSATIIIAIPTGVKVS*LATLHGSNMK*SAAVL*ALRFIFLFTVGGLTGIVLS
3402	17303	A	3425	1	193	PTRPPTRPACSELRSRHCPTAWVTE*DSVSKKKKKKFFSPARGAHVCTPTFLGGQRGKKKFCFAP
3403	17304	A	3426	3	446	HKKFLFPKSFNRFPPPTKKKNPRGPGFFFFFLKKIFFFPGGI*SGGFGSLQLFPRVKKFFSPPPEKGGFKAPPPGPGNFFFLKKRGFSFFGGGFLK*NPGFPPPPFFKKWGVPKGGAPPPPPFF
3404	17305	A	3427	202	1	FSPGRMLGNTIKLPYTHSFILMNSQNNLEKYKVGGLPLSNFKNTYKATAIKTMWYWHMNRMYD*WNR
3405	17306	A	3428	159	1	NPPHEKNFCSFFQMESHADQAGVQWCDLSSLQPSLRGFKRFS*VSLVSSWDH
3406	17307	A	3429	22	298	ESYASTAKATERDMSDRMLSASGMPRRYSDYDPDAYTT*NILSSVGSFISLAEGILIFMI*EAFASKRKVLIVEEPSINLE*LYGCPRLRGR
3407	17308	A	3430	267	26	GITFFFFFWLEI*LYYWLFLANKLYFHEQIWFGLVFFGLLLFDFSFYSDYFPLLLCLGSFSNF*CLIHCFFSVIVLLF
3408	17309	A	3431	274	376	NKG*ISCSISPPQHTVRGLTLSPRLECSGVISAHCRLCLPGSSDPPASAS
3409	17310	A	3432	177	47	FYFFFFFFFFFFFFFFFFSLLFFFFFFFFFFFFFFFFFQINRSFIASFYKH*VLIFKKKKN
3410	17311	A	3433	379	83	FKRHFTKEDLRMVTEHIKSCSSSLATRAMQIETMAHCYTFMRLAKIKKYQYTKCC*R*RVGTGLTYCWWECKMTQPFWKTIVRFLKQYIYHVIGYV
3411	17312	A	3434	214	3	AASTFFFFTRSTYYVCIFLKSARMINK*NYIKLKSFCTTTTKINKMKRQPTDWEKMFANHINHHEGLILK
3412	17313	A	3435	1	353	GGQGQPGQ*SETLSQ*KVSWAW*LQLHRMRQDNLLSPGDQG*SEPC*CYTPAWARVRLCQNRSVNEKSLHDICNDKK*QNT*IISVPEGKQRMKGLENLFNEILDENYPSLARDL
3413	17314	A	3436	29	394	VFMEVDFFFFFFFVFGRNFFPPPRGGGGGPF*IFGPPPPRGKGNFPPPPGKGGKKGPPPPPGFFFF*KKGGSPPGGGGFLTPLWDPPWPPQRGFGV*TPWPGPGSDDFLNFFFF
3414	17315	A	3437	108	2	PVAVAHSCNPNTSGGRGGWIS*GHEFQT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SLANTVK
3415	17316	A	3438	215	3	LLLLREFFFLPKHREVFIFVFYFMRQGLT LTEAGVQWRSHGSLWPQTPLK*SSCLS LPSIWEYSAYHHIR
3416	17317	A	3439	1	186	QTSSFSFRRSVITNFFFLKDDV*TH*KE AKNLEKRLDEWLIRIKSVEKTLNDLMEL KTSTRP
3417	17318	A	3440	290	3	PGLGGGPRYSRFSGGGLPKIPLNPEGEG SIKLNPPAPPPGGPN*DSFLPPPPKKK KKKTHVLFAGSGNLLQLPQGAFTTEVN GGLAQQSPKVL
3418	17319	A	3441	163	2	PAGLPVKPPRFQDKLNFPGPFFFFFFF *I*DKVLLCHPGESATVHSSSLGDRA
3419	17320	A	3442	131	1	RPRRPLTIKSIHQWY*TYEYTDYGGLI FNSYILPPLFLEPGS
3420	17321	A	3443	162	2	PGAAHSTGHLPLRFHLRLGAVTHAGNPR TLGGQGRWIT*GQEFKTSIAKRVRP
3421	17322	A	3444	2	130	WEKIFANHVSDKGLIYRIYNELQQLYK* KTINGPIKKRPKSTRP
3422	17323	A	3445	2	117	LALLGLKPLK*ATCLGLPRYWDYRHQP PHPACFSKGI
3423	17324	A	3446	350	101	KAFSSSLGSSRRKKGDSAGFCIHFKTVP FGFFWTLELKKGIPFLNFFFFFFFLRVL KGSKNPF*KRGPPFFFFFFFDNFYIWN
3424	17325	A	3447	106	1	LLQPNQQLGPGTVAHGCNPSTLGG*GER ITTSQVR
3425	17326	A	3448	28	333	GQQEQNSISXKKKKKKKKKTTPFKKGKRR IPGGKKKPLGKSRAPPLGGGEKNPPPG KRAPEKIFKKKPRGNWETFKRMEKGFLK GQ*PGNP*KVKPLWGGKK
3426	17327	A	3449	81	339	PIVSSCPGVAGALKQAMTLEFKVYQHHV VANCRLSEALTELGKIGTGRDTDGVQ QALLVVGLRLAS*PIVSSCPGVAGALKQ AMTLEFKVYQHHVVANCRLSEALTELG YKIGTGRDTDGVQALLVVGLRLASQFV QPGCGPGSAAAAAMM
3427	17328	A	3450	166	322	RDFSTTVLITDRTSRQKIPTDVSQNLNI DIYKTL*PTIGKYTFSSSTYRSLR
3428	17329	A	3451	257	354	KFLSFFRDRVLLCCPGWSAVV*S*FTAA LSSW
3429	17330	A	3452	286	3	TDPPFIKRAKEREMLQITKIRSIRENFI TDQKTKEL*EEQLYAHRVNDNDEMDF LEGYK*PSMTHGKIENLCRPITSKDIES VIKNLLTDEP
3430	17331	A	3453	358	353	R*KLMMPC*IETNKT*NTCTVIKEEK GQPGTVAHACNPSTLGG*GGRIT
3431	17332	A	3454	108	353	THLGGNPVRLYAWLLLHYVASYRIFSVS HCKDQTYLPILL*NFLMELGTVAHTYNP SILGGQGRIT*VQEFETSLANMVKC
3432	17333	A	3455	342	50	GPVTNIPVPPLGGQKELFPKPKKKF* KFWGSPPLFFKKPKNPRETPPEPCPKP KKTPIPVKV*GKKTP*TFSKKKTPPI ELFLLKKKKKLIN
3433	17334	A	3456	343	2	KAPFFFFFFKKFWSQKKRGLFFFFFFKNFF IPGFGPTFFFWGFFFKKGPVF*LKK FFGGPLPLKDPGVPFSPF*FWDPPP PPPPPPPPPPFETVSLCRPGWSAVSRD C

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3434	17335	A	3457	2	259	LTKPTESGTEDEKKGRDSKESEGKTERTE SLRSQNGGENSV*SCPSTSSSTAALNTAA AANPLALNPQVLSLSSCCPISIKGSFV P
3435	17336	A	3458	186	334	AGGNKKMEKRNM*NKEIF*WFKKNWPGA GAHACNPTTLGGRGRRINRSG
3436	17337	A	3459	207	1	YFKPTLKINDKGYNLNETDKFDPDPRDINR TSNLT*EHALFPSTCGIFMRRDYIEGH EVNLTQFQIRITQ
3437	17338	A	3460	268	3	PLNPGPKQSSPPGLPKWPFRGEPLPLG PWFFVFNKRGPR*AFFGTNPLAFFLFFL *DRVLFCHFGWSVVVQSLTVQPPPLRL KQFS
3438	17339	A	3461	350	2	AETAHNINNAFGPGSANKCTVRWWFK*L CKGVKRLDKALGGWPSKVAINQLRAII KGAPLKPTRKVAKELNIEPSAVIQHLKR IGKVKKLHKWVPHELHENKRNRFVWSS LIIP
3439	17340	A	3462	312	1	HIVTYYSGRKEPFYIGMV*AMISIGFL GFIV*AHHIFTVGIDVDTRAYFTSVPII IAIPPGVKVFS*LATLHGSNMK*SAAVL *ALGFIFLLPVGGLTRIVLA
3440	17341	A	3463	181	3	FLPLLAAPFSCLLLFSGFLGVFLFCFFET ELPRLECCGTISAHCSL*LLGSSDSCAS GTH
3441	17342	A	3464	176	263	VGHDAHNPSILGGPGGWIT*GQEFKVDA A
3442	17343	A	3465	239	336	EPGEVAYS CNPSTLGGRSWII*GQEF TSLT
3443	17344	A	3466	88	326	QTSLLNTI**PLH*KNIPLPPPLPPTL TPPFSPPPPPPPKPKKKRKRK
3444	17345	A	3467	4	345	EEERRRRERKKRRKKKEKKKEEREREK ERKKKKKKKEKKRRGRQEKRGKTG*IE RKQ
3445	17346	A	3468	265	335	QMNPDRLHQF*DKVLLCHPGWGTVARF* LTATSRSSCLSPPSGWDCCRVPCLASF
3446	17347	A	3469	115	342	INKQINKIKDPTSYNILLSQSLI*FKAL TLLNSVKAQRGEKATEEKFEKGSIS*FMR FKQINHLVNIKVQGEKPESTD
3447	17348	A	3470	56	328	RTYPTKPKMRDPEDPTSRPRYIPRHL ITDEVNDPSLTIKGIGHQWD*TYEYTDY GGLTFNSYILPPLFLEPSDLRLLDVDR VEPATRA
3448	17349	A	3471	3	329	RIGARDESSLA VTHKPRKIHRKLT LWVF VNDSLVMPRPDKNHQWAFNKNCFPLVDV GIDPYLVYHLRPHQAQGIIFLYECVMGM RMNGRCGAILAD*NGLGKTLQCISL
3449	17350	A	3472	154	2	PNLLYPKSYWKKKDIWTFMFIVALVTIV KIQKQPRCP LMDKSIR*L*YIH
3450	17351	A	3473	132	340	ALKTENITTLCLDF*LIETVR**MCVFK KKKKKKKKKKKKKKKKKKKKKKKKKK IK
3451	17352	A	3474	3	345	VIYSSIFAGTLITALSSH*FFT*VGL EINMLAFIPVLTKKINPRSTEADIKYFLTQ ATASIFLLAILFNILSL*TTTNTTN QYSSLI IMAIAIKLGIAFRRRGREFQ IY
3452	17353	A	3475	1	254	FHHVGQAGFTPDLR*STRGLPKCWDYR

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						REALCLVHLLLYLPMIGPFRIQKLLKAA VFVFLQLHQAFIQSLLLTFYFISFPCNS
3453	17354	A	3476	351	186	SVLSADNTEMGFHHVGGAGLELLSSSDP LAPAS*SAGIRGVRHNTWPVLTITLN
3454	17355	A	3477	330	3	GEKVFEIPLTRDNVSEILRCFLMAYGVE PALCDRLRTQPFQAQPHQQAVALAFLV HELNGSTLIINEMDKTLESMSRYRYEW NVKERLRLRLKTARA*RLGRSQVKK
3455	17356	A	3478	373	248	NRLNPGGGGWSEPRSQHSTPTWVTEYDS VSKK*INKNKNWK
3456	17357	A	3479	3	92	EGQGCSEP*SRYCSPAWVTE*DCVSKNF F
3457	17358	A	3480	380	2	VEVPLLNNTSVFFASGVST*AHHS LIEN NRNQIIQALLITNLGGLYFTLLQASEYL ESPFTISASTYGSTFFVATGFHGLHVI GSTFLTMCFIRQIIHFHTSKHHFGLAA A*CWHFVDVVCIFL
3458	17359	A	3481	225	1	ERAERVVEQVMIALFSPNYIRLSFPISP TPVVRHKFRFHLKGYIWPGTVAHTCNPS TLGSQGGQITRSGD*DHPG
3459	17360	A	3482	332	1	IKYFLTQATASIILLIAILFNNILSQ* TITNTTNQYSSLI IIMAIN*GIAPFH F*VPEVTQGTPLTS
3460	17361	A	3483	277	1	LSMSSFSTISSIPASINS*ALLFSSAES NSLECTFSSSFSPNSESFSSSFPSCSC AS*FSNSQSLIKASSSTEASPLNSSASC FLPLPLVG
3461	17362	A	3484	404	209	ALSVQPLWRPRQENGVNPGGKASR*PRF PCGPAWATKGELVPKKKKKISFLGHD QSLELLLQR
3462	17363	A	3485	31	347	FCILERKAFLYVV*CWKFFFFFFFFFLE KGFFFLPLLVFVWCYHLKGASLP*VFL FFYLHCYSSLFTLFFIFLQSLTPHFELV *TFFYYDPLMFFFLTFLFLV
3463	17364	A	3486	327	161	QKKVRDPVEQL*ANKFKN*EEMPRFLEK HKLPKLTQEEIKNQ
3464	17365	A	3487	311	3	PRRGRFQLTQNFALPFLNGNKTIPFKK KKKKTEPLCPCTCVCAAFVCLCFHLCT* PCDCAHDCDNICVCVNICVYVCVTHLH TGLCSCVDCDHICVGTCC
3465	17366	A	3488	245	1	RPRRLALLLLIIITF*LPQLNGYIEKST PYECGFDPISPARVPLSIKFFLVAITFL LFDLEIALLLPLP*ALQATNLPLIV
3466	17367	A	3489	2	400	AAPILGMLGLRQRGKYKRQRLCLWSA ILLFLYFLNKL*LTKKKKKKKKKKKK KKKKKKKKKKKKGGPRGNPQILKGKIG KPPGGFFKGGGGPKIFFFKNRGALFFK KKPPQKKNLPGPGPLKNFLKEKKA
3467	17368	A	3490	57	366	INVFAGKDQLQPLCACPSPIISVESDR PDYQCGLNHFYILIIYLRWSFALVAQA GV*WHHLGSLHPLPPEPKCFSC
3468	17369	A	3491	25	384	IRGTF*FFWGLGGLSKNNPL*KNFSP PKLGVLPPPLFFPGGGGGGGGAPPGF KKKKPPPKKFFF*KGAPPFFFFFFF FF
3469	17370	A	3492	170	41	AQPDQHGETTFLKIQKLRHGGICL*S QLIGGLSFITQKITC
3470	17371	A	3493	1	240	VLSPADKTNVKAAGKVGGAHAGEYGAEA

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						LERMFLSFPTTPS*FLDFFFFLEKIGFH HVGQSSLGLTSRDPASXNSLIGS
3471	17372	A	3494	359	204	TQWLMPVILAPWEAEVGR*PEVRSRLRPA LNSPFFKRLVIMMYIMNI I ILS
3472	17373	A	3495	1	178	DRLSPGV*GSSEL*LCHCTPGWATEPDH VSRKKKKRKKVGLGKNAKQKHPRGYR AEL
3473	17374	A	3496	361	1	LGPKLLKKPFWISIGIKGVAGLPGFPT PPQ*G*NFGLRGGFFFFFEAKGWENT PGGKQRGPPRSLEPPFRVKLFPPNLP NNWGHKGAPPKPPFFFLRWSFALVAQ AGVQWCDL
3474	17375	A	3497	276	79	AEVYKIKCELGAVAHACNPSTLGGQGR ITRS*VSASF TKKYWQLALMKELLNE
3475	17376	A	3498	3	476	FGTSMSTITLITPRLARGNNLFCFPPT FTFDHLATPLLILTT*LLPLTSMASQRH LREPLSRKKLYLSILNSLQSSLIITFT GTELIIFYIFFETTLIPTLAITR*GNQ PERLNAGTYLLFYTLVGSPLLLIALIYT HNTLGSLNILLTLVSAQE
3476	17377	A	3499	581	2	AHACNLNTLGGGRWIT*GQEFDTSLAN K
3477	17378	A	3500	380	135	RHQSGQIGKTPSLVKIPKLTTPPKGGVL* SHLTKRARQEKGLNPKSKGFN*PKLRPC PPTIVAKKQNPVSKKKKQTRQEPSA
3478	17379	A	3501	1	386	GSR*GNHPERLNAGAYFLFYTL*GSLPL LIRLIYTDNTLCSLNILLTLTGQELSN S*AHNLI*LAYTIAFIVKIPLYRLHL*L PKAHQAQAPIAGSIVLAAVLLKLCGYGII RLTLILNPLKKHIDYP
3479	17380	A	3502	2	389	EKQL*KDKQVYRATHRLVLGAGESGKS TIAKHMRIHVNGFNEGGEEDPHAARS YIDGKATKVQDILNNLKEGIETIGAVM SNLVPPVELANPENQFIVDYILSAMNVP DFDFPSEFYEHAKALWE
3480	17381	A	3503	2	379	PFGYIGMV*AMISIGFLGFIG*AHHIFT VGIDVYTRAYFTCATIIAIP TGKVFVS *LATLHGSNMK*SAEL*ALGFIFLFTV SGLTGIGLTNSSLDIRLHDTYYVVAHFH YVLSIGAVFAIIGG
3481	17382	A	3504	281	68	FKMRFGWGHSTQVSENYKPLLKEIRENP NK*KNIPCSWIGRISIVKMPTLPKVIYR FNAFPIKLESPFFTL
3482	17383	A	3505	139	263	ETGSHYVPQAGL*LLASSDPPATASQNI GITHVSYVQPL*PIFWEAVAGGSLEAR S
3483	17384	A	3506	2	427	LKTSMTMISTTLLT*LRPAWH*AQYQTP FFV*SALITAGLLFLFLPVLAAIGITVLL TDRNLNTTFDPAGGGDPILYQHLF*FF GHPEGYILILPGFGIISHIGTYYSKKKE PFGYIGMV*AMISTGFLGVIG*AHHVFT GG
3484	17385	A	3507	343	3	GWHSRSSGGASSPSSPSHRSRLRVSSGS LGRL*WSKSSKTSVSCGVVARDTEKPPL SKIEASSSDSCSVMAKANAVFTSTTG EKPASSASLSLSVWASGSSPPGAANSSS S
3485	17386	A	3508	3	363	GPGDKAARRIALENLDIT*KWGMRTKHC

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						AKQLLSKQPF*SSRTGDLKLELQIELVR ETKRKC*RVL*IDRALTSHLYSLLQTQD ALGDASADLIQKTS*LQEEFGYYAKTQK LLCRNGET
3486	17387	A	3509	3	434	GPGDHVARGISGKKYDIGQKWGMGTYKC TKELLSQRFGLGSPVLEL*LQIELLR ETKRKYESVLHLGRALTAHLYSLLQTQH ALGDAFADLRQKSPQLQEEFGCYAQTQK LLCKNGETLLGAANLFVSSIYTLGKTMT EDTL
3487	17388	A	3510	1	401	GTRKNSFLHDSQTSFCFSDSIPTPSNME ETQHKSNLELLRISLLIEPWLEPVRFL KSMFANNLVYDTSDDYHLLKDL*EGI PTLMGRLEDGNRRRTGQILKQYTSKFDTN SHNEDALLKNYGLLYCFRKDMN
3488	17389	A	3511	117	2	FKFIFSEMESHSA*AGVQWRNLGSLQP LPLWFKQFSC
3489	17390	A	3512	491	90	KKVKIVLAGFFFKPPPKN*KKKGLK*R KGVGPRGYTVNPHPCGYKPFGGPGVQNP PGQKGETPFFQKKKKPGGGGALIPPP KGGGRGVPLSPEKFGKFPPGPPP*GKK KNRFQKKKKKRQN*PQKSQC
3490	17391	A	3513	2	31	GKGAPTTSLINVAGTKIAKVVEDNKL GAICSLTCGAHIGTPMARDERNLLSF TGSTQGGKQVGLMVHERFGRRLVELGNN NAIIAFEDAHLNLYVPSTLFAAVGTAGP KCTTARRQLIHESIIDEA*NHFP
3491	17392	A	3514	2	390	KEFEKTHPLENITLAPDEGPDGLPFVA YNPWMDIRQREDGQTLNIREPYGPPIVD F*RKIRQSYFASGA*LDTDGRLLSALD DLQLANSTIIAFTSDHGWALGEHGEWA* YNNFDDDDTHDPLIFYDT
3492	17393	A	3515	3	410	RGTGNNWAQGHYTKGAELVDSVLDVVRK ES*SCDCLQGFLTHSLGGGTGFGMGT LITKIREEYPNRMNTRVMPLPKV*DT EGEPYNATLLVHQLVGNDETYSIDNEA LYDICFRTLKLTTPTYGDRHHLVS
3493	17394	A	3516	1	396	GEDAANIYARGHYTIGMENIDLGLDRIR KLADPCTGLQGFLVFHSGGGTSGSFTS LLMERISCDYGKKNKLEVSIIYPAPQVCT AVFEPYNYILSTHTTLEHSD*AFMVDNE AIYDICRINLHIERSTYTNL
3494	17395	A	3517	2	399	EKIGYNPDVAFVPISGWNGDNMLEPNA NMPWFKGWKVTNRKDNASGTTLEALEC ILPPTRSTDKPLRLPLQDVYKNGGIGTV PAGRVETGVLKPGMEVTFAPVNGTTEV* SAERHHEPFREALPGDNVGF
3495	17396	A	3518	1	402	GEDAANNYARGHYTIGTEIIDLLDRIR KLADQRTGLQGFLVFHSGGGTSGSITS LLMERLSIDYGTKSKLEFSIYPAPQVST ACSEPNYSILTHTTLEHSDCAFMVHNE AIYDI*RIINLDIERSTYTNLNR
3496	17397	A	3519	1	408	GSCLGQKLYNSTTKTAT*WSSNHTKKNP FSKFPKLQNVWTHPESHARDWTAPTRL YICGHRPYVKLPNQWAGSCIIGTIKPSFF LLPIKTGELLGFPVYASHAKRSIAIGNW KDNEWPPERIIQYYEPATWAQDGL
3497	17398	A	3520	3	162	ETVLLCCPGWL*TLGLRQSSCLSLPKCS

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						DYRHATVPGQKYRFFENRYVGSYS
3498	17399	A	3521	184	354	ETGSSLLP*GSSELPVSHYPFNTHSLSLSHTHTHTHHTNSSLISNYHCPLYTNMSCQRLVAVYRQKGSFKDQCTDI
3499	17400	A	3522	2	313	YYLSPPMGDQPGQHGETLPLQKLAG*GGARLRSQLLRRLROENCLTPGIQACRELLGWYKSNCAFCQKQPQLLCVNLTYSSLDKARDSVSTKTKREGRGEK
3500	17401	A	3523	13	127	LGLQARTTSMPS*GYRRAPPPCPALLYF*VETGFHHVQGAGLELLTSTRP
3501	17402	A	3524	148	1	VCMFLEESCSVAQAGVQWYNHSSLQP*T PGLKRSF*LSLPSSRDHRLMT
3502	17403	A	3525	1	98	VNPGGEGCSEPRSHHCTTAWVTE*DSISKINK
3503	17404	A	3526	138	3	AASTHDLG*LQPPPPGLTPFSCRLRLSSWDYRPVPLRPANFLYF
3504	17405	A	3527	10	206	PTTSLISFTSYSPCLKCSNVYBQVNRMRVLFYKSKQRLGMVAHAYDPSTLGGRGSKIT*GQRRG
3505	17406	A	3528	345	3	VTELIQSNKAKLKKKSKNKEQSLQKI*DYAKQPNLRISGVLEEEEEKSKSLENIFEKIIEENFPGLTRDLEIQIQAKRPGKFI AKRLSPRHTVIRLSKVKTGRILRAERQK
3506	17407	A	3529	3	90	AVL*ALGFIFLFTVGGLTGIVLANSVDA A
3507	17408	A	3530	3	90	AVL*ALGFIFLFTVGGLTGIVLANSVDA A
3508	17409	A	3531	354	3	AVINSLPTKSPGPDGFTAKSYQRYKEELVLFLLKPFQRIEKEGILPNSFYESSVILIPKPHRGTPKESFRPIISMNLNAKILNKRLAS*NHQHIKKVVIHGGQVGFIPRTQGW FNKQ
3509	17410	A	3532	2	357	FTRPRFSFTFFVLIRKYALSCGKISIQHSY*KKKSKGKLGGL*GINFCFFERKFHSVTQVGGQKHDPG*LKFPPPGFRGFSRLSLPSSWNHKGRTPRLANFCTPNKNGGRRGRKFQIY
3510	17411	A	3533	76	365	KKKKKKKKKKKKKKKKGGAGPEIPKLKMGKSEKPPGVFLRGVGEKIKFFFLKKGGPFF*KKKPLKNKNWAREPSFKKIFKKKKKKAHFFFGPKILKK
3511	17412	A	3534	7	353	FFGFGGVFLVFLFFFF*KYPPFFPPPPPLFFPPFFKWAPRRPPPPFFSFFKNFFFFFPPPPPPFFFPQKNFPLFSPFLFFFFPKFFFFFPLTKKKKKKKKKKTTPKIHPQTQRK
3512	17413	A	3535	354	41	AGGVPPGIPPPWGGRAGGSPKGRGFGPPWPKRGTPPPFF*KKKKKKKPGGPAIPA TREGEGGKSP*PWKPRVQPT*NAPPPSP PGEGAKPPFQKKKSMFHKR
3513	17414	A	3536	174	364	TENSLAFTFFFF*RETGSHFFLEAGVQGNHSSLNP*PPGLRGSSCLTLPC*KDYRREPLPPA
3514	17415	A	3537	38	368	PGRRLRLQEAVNHCTLEPGQOSV*KKKKK KRGGAFFKAKLTLAGWKGEKKKKTGVFF*TLKIRPKAIRNQQGSQQRKKAELGKLQ QTYPVLNFKATFYGEQGDYY*TFFKP

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3515	17416	A	3538	107	349	SVTFPPFFFLKQTGSHFVV*AGGQGGNFD*LEPKPPWLRSSLLTLPSSLDYGPPPTGPSNFGIFFEKRGFCLVPQASFE
3516	17417	A	3539	274	3	PRRWSLPLTQMGLPSRMGPCKTKLCPKKKKKKIPPRKILEPDVFTGQFYLMFKEITSIFLKLFFQQCBEEGTFSNSF*EARIALKTK*DKN
3517	17418	A	3540	1	374	ACALVRNDHIYYVVGPTYALGELFFTETPIII*G*DN*LGPLVIGAHVVALTLINYSIS*L*PPSVLLLLACAIPEARAGTGCTAYDPLAGDYSHRAAYVNLTLISLHLARVSSILWDTDSITT
3518	17419	A	3541	427	76	RGSLSPGV*K*PGGQNQTFPKAPKLRPGAPRCFPAGKGSIKPTPGSPPGGRRGTCSKKKKNFRETPPSFFWGGPPFLKNRGGFMFWASKTKNGLNKTLPNPGPPLGGLRSPFWVG
3519	17420	A	3542	234	88	FFFFFFFFFFFFFFFFFFFFSLFFFFFFFFFFFFFFFFFFFFFFFFFW**ILYFV
3520	17421	A	3543	30	419	TFSFFPFLFFFGFLVLGGEKQGWDPKPPGAEKPPTFSPPKI*KKGAPPPRVNFKKF*KKGPLPFPSPGGKNLSFWGIWSIGNPLWVTPPKNPQKKPPFFKGPKKNFFPKGPKPGGKKTQIFFFLWEKK
3521	17422	A	3544	159	411	VSRDISPVRSLSPSSCFH*PFLHISSSVEGRFSSFAQFLLSCLNCFTFPLLFLLR*DRVSLCHPGWSAVA*SOLTATSTFWVK
3522	17423	A	3545	2	351	CLAHTSGVES*ASLPCGQNSYTHYLLCMEELSFPPYLLIYSISYLY*HTIMVIYFILVL*SILLNLIYLFVTQIFPALASGSFENWLLCLFNTTLAVHVCVCVCVCVCVRVCAC
3523	17424	A	3546	397	1	KPPPPCSYGKKKKIFLLVFFRTLPTKPPGAGRKIFPRGPGFFLKNPKAI*TTFPAPPFIQKKGPFLQQA*IPFPVFFLFKKKPLCSP*GGIGVSLFFFFFFSETESCSVTQAGVQSCDLGSLQPLPPGLKR
3524	17425	A	3547	76	354	FLFNFMGKIFKNFRGGVFFFFFFFWGGYNI FLVFLKIFFFFGGFFLPPFFFLKKFFF FLGFFFGKISQKIFFFVFN*IFLLXXGAPLFFFFFFL
3525	17426	A	3548	197	1	INKMKQQRMD*EKIFAKHVSHKGLISQICK*LIHLNSEKTNSPVRKWAEDLNRHFSKRDTKMVNM
3526	17427	A	3549	175	309	KSTLKVMLISISIFNFYFF*DRVLLCHPGWSAVA*SLLTAASTRP
3527	17428	A	3550	3	196	GFHRVSQDGLDLLTS*SACVSFPKCDWYSHEPPRPAHKTSLKKNKMRVRIIMMTITYPAPVVC
3528	17429	A	3551	3	360	RAVEIFCYDVCVESGCADIQLLLLCPTS IKVCFSSLSLDIVTVIPDIYICIYIYII FFFFFFFKQARS*CQCLNDKE*YCSLWPTPGFKKLSCVSLPSIWDLRCAPSHPPNFCVFGKNGV
3529	17430	A	3552	326	1	KDNHRILKMLAKSGKVRHYVDFGKQISKMSEKNIGVKPPIGKEKTKNPKKPSRTEDPKICTYVL*PDKKWRRLNT*GIQLG*KEIKLSLFADDMIVYLENPIV

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3530	17431	A	3553	186	1	RPRRLPIKLPMTFFTELEKTTFKFI*NO KRVRIAKSILSQKNEVGGITPPDFKL*Y KDTVTN
3531	17432	A	3554	3	366	KTSLGNMVKPYNFFV*TFYI**KKEIKK NSIGVL*PGTEQSKHEFKKILPSKRNI ASKRIKYL*INLT*EGQDMYTENYKTL KEIIEDLNKYKDIPCS*IIRLDLVMAV LTKLIYRFN
3532	17433	A	3555	239	1	GRGKMLPVSLNITRVTFAPCSGSIILV LIALPSLRILYITDEVNDPSLTIKSIGH QWY*TYEYTDYGGILFNYSILPP
3533	17434	A	3556	3	123	QAGLEV*TSSDLPTSVSQAAGITGGSHR ARPANIINSVP
3534	17435	A	3557	237	2	KGFSPTQKFGFLGVFPQKKTKKNPR PPKGLTPVS*KGMLTEPLEPFFFLRQ SRSVAQAGVQWGNLGSQALPP
3535	17436	A	3558	87	379	KKKKKKKFTLQKPVGFNPPNGEAKSQI INELLKIATKKKKNLKRLKKKGKDLF RGNYNPLFKKIKDDPTNGKNFPCS*MGK ISFEKMTLLPKAI
3536	17437	A	3559	390	181	KKKKKNPGGGGPPFPFTRGG*GGGPPQ PGGGGAPKV*ISPPPPPGGKSPQKK KKKKKKKGPFPLPHL
3537	17438	A	3560	2	101	VIVTAHAFVIIFFIVIPIIIGGFN*LV PVDAA
3538	17439	A	3561	2	126	INTLLALLLIITF*LPQLNGYIEKSTP YECGFDPISRRRG
3539	17440	A	3562	16	349	FAFQKITLAMEKATEAQTGGAKKACQGT NNIMKFLKKKCIPTTIFWISFFSFLFFF FETKPHFFNWPEGKGNLG*LKPLPLGL KQFCLTLPRKGNRYHVLPPPVGFFFF
3540	17441	A	3563	6	130	TLRRILEDHFSLSR*GCGEPCLRHCMPA WLTE*DPVSKNIY
3541	17442	A	3564	3	152	GFHCVRQDLDLTS*SAHLSLPKCWDYR RKPPHPAGKGTIFYIDYSTIE
3542	17443	A	3565	241	3	NLVSHVISMRKVINLVEQNVTSNRSNH TWLSFIKLYFIIIIISLVFGEQVFGYVA KFFSDDF*DFGVPIQTQVYTAPN
3543	17444	A	3566	71	256	SVFLLTVFLYPLATSFFFLNRVSLCCPG WL*TPGLKQFSCLSLPKRWNRYHEPLTP GSNFF
3544	17445	A	3567	1	392	AGAGTSGTDYPPLSGNYSHPGACVDLTI FSLHLAGVASMLGAISVMTVMNIEPPA ITQYQTPLFV*SGRNTAGLLLLCVPVLA AGITILLTDRLNLTFFDPAGGGDPILY QHLKGRGIIICSHRDRI
3545	17446	A	3568	334	409	LGTVAHACNPSTLGG*GGHITRSGV
3546	17447	A	3569	3	467	PKNPPGGFFSPL*EKYILPPPP*IWPP PGFF*KAPPPFFFFFFFFFFFFFFFFFTQI YFITE
3547	17448	A	3570	3	420	FFDPAGGGDPILYQHLF*FFGHPEEYML ILPGFGLSHIATYYSKKKEPFYIGMV *AMISIGFLGIIV*AHHIFTG*IDVDTR AYFTSATIIAIP TGVEVFS*LATLHGS NMK*SAAVLSALGFIFLFTRRGLTSIV
3548	17449	A	3571	1	418	NLINHSFIDLPTPSNIFA**NFGSLLGA CLILQITTGFLFLAMHY*PDASTAFSSIG HITRDVHYG*IIRYLHAKGASIFFICLF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LHIGRGLYYGAFLY*ET*NIGITILLLAT IATAFIGYVLPGGQISF*GATVITNLL
3549	17450	A	3572	3	414	SSGLAM*FHPHSITLLILGLLTNTLTIIY Q*WRDVTRESTYQGHHTPPVQKGLRYGI ILFITSEVFFFAGFF*AFYHSSLAPTPQ LGGHWPPTGITPLNPLEVPLLNTSVLLA SGVSIT*AHHSLENNRNQIIQALL
3550	17451	A	3573	2	423	GTLYLLFGA*AGVLGTALILLIRAE LGQ PGNLVGNNDHIYNGIVTAHAFV I IFFIVI PIIIGGFGN*LVPLIIGAPEMAFPRINN ISL*LLPPSLLLLLASAIVEAGAGTG*T VYPPLAGNYSHPGAYVDLTIFCLHLAGV
3551	17452	A	3574	411	117	DGGPFLQLRRARQENCNPRGGGCS*P RLCPCPPAWGAKLNSLSGKKKKKKRHVE KYAQHDY I INVL CVVCVHIKWL SLYMYS ITKSIDKICKKAS
3552	17453	A	3575	2	394	ALANMWEQIRSLHQYAVHRIISLFSLLS KKHDRVLEQATQYLRGSLNTNDVPLPDY AQDLTVIEELIPMMLEIINS*LTNSLHH IPNLVYALLY*RDLEQFRTHPSFQDIM QNIDLVSVNEDIYYDSFLS
3553	17454	A	3576	262	418	GWREWTELIIFYIFFETTIIPTLAIITR *GNQPERLNAGTYFLFYTLVGS LP
3554	17455	A	3577	232	443	PSVQTFPCPLSEEGPWLLCVAMTPSPG VPVPTERALYSMECAFHPLFSLTSGACR LDYRTPDNR*VQLP
3555	17456	A	3578	48	410	GGLLLHRAGCWCGHADRRADQPDSSDPH SLHAACLP PPGAARAAGAPSPA*TPAAA CPAPVPAPCSEHRC*PPGLSQRPCLPGL PDARPPGAAAHGWSLPTRLVLHDRSHP EEAPRRHED
3556	17457	A	3579	422	186	VYSKFL*SQLLRRLRQENRLNPGSRGCR EPRS*HCIPAWVTQQDLSLSSST'SHEI CGSHCSPGYLTVHICDQPVFSL
3557	17458	A	3580	442	3	GSAISSRCTQESTYQGPHTPPVKGLRY GIILFITSEVFFLAGFL*AFSHSTLAPT SQLGGHWPPTGITPLNPLEVPLLNTSVL LASGV SIT*AHHSLENNRNQIIQALLI TILLGLYFTLLQASE*LESPFTISDGMY CGRSRG
3558	17459	A	3581	428	1	IRDIFMASSLGM*FHFTPTILLILGLLT TPLTIYQ*WRDVSRESTYQGHHTPPVQK GLRYGIILFITSEVFFFAGFF*AFYHSS LAPTPQLGGHWPPTGITPLNPLEVPLLN TSALLASGV SIT*AHHSLENNRNRCIAAA LE
3559	17460	A	3582	160	415	RCLSHCLAFPMLSILFIPSQLLSLPFHV KWIFFFFFLNKKFNCVPQAGGQGNLI* LHPPPRGLKKFSCLRITSS*NYGREPQP S
3560	17461	A	3583	399	2	STHLGLPKCWDYRCEPPRPALLAIVKLL CKTIHVRINNVCCLPLLTGAASVIGLSA SLLFSVSPGTS LQLEAR*TFPWPMSST CVWRFIFTSLGRAQPQHS DLQTCPRRDV DLAEPGLLFNGQMLVPPGRS
3561	17462	A	3584	215	1	KSPGLLNAFSGRSQIYQASRAMGA*LNQ RFWPGTVAHACNPSTLGG*GARIMRSGD GDRNSKDGVS PCGRV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3562	17463	A	3585	138	19	LNQRFWPGTVAHACNPRPLGG*GARIMRSGDVYRNSKDEV
3563	17464	A	3586	262	3	GRPEVFKPPPRGEFFFFFFFFFFLFFFFFFF FFFFFFFFVLFLLLLLLLLLLLLLLLLLLLLL*Q VRLYLLEKYELFFFLFYLPQEISLCCPGWS
3564	17465	A	3587	381	1	KKFTPPPPRKMGPPEGFF*RAPPPFFFL GGGGGPLEFLGGPPPPGGGFFFSPPPPV FF*KSPPLFSFF*KKRGPFFFKRGGSPK TPPCFFFKKNPPKKKKKKKKKKKKKKK GRPSSKSDAWVRTRG
3565	17466	A	3588	198	1	PKSPPRPLARGEKPNFFSKKKKKKSI*N LNTNSWLDMAHICNPSTSGGRGG*PHL RSGVRDQPGQ
3566	17467	A	3589	373	1	GIFPPPPKRGGFPPPPPKKFFFPGGFI FGGGGGPFWPPPRKGFFLKKKKGVF*SP P*KGKKFFFPGGGVGPPRGFLKGGDPI IFPPPPPPPPPPPPPPPPPPATIFLITYK DLTCHPGTHFTH
3567	17468	A	3590	506	98	HTSRGPPPPPKKKIPPTRPFFFCFWVV FFPPKKFFFCSPRSFHHSPKKKKKN FFFPKGGGPPPLSPFLTPPPPPLFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFF*LFVSLPSI FVLLIFFLFYNAITTI
3568	17469	A	3591	407	1	LVRGQITNKKNLNLFNLGEELREWRVVF LPQORLFFFKL*LQ*KEIYLF*KMTC SGGAGFKSSLYFFFRSPQVVLFFFFFFF IFFYFF*FFIFFFFFFFFFFFFFFCND FMIYLYISPPPLEKKKKGGRSRSR
3569	17470	A	3592	380	68	FRRGVGPQWPPPPQKKGFQKPPPGGFKRP PLKGGKITFPFPPGKFGPPKGPFKRPPPF FFLEGKTLFLGDDP*NLGWGG*RGHGK *GPANPRVPPVFFFFFEESY
3570	17471	A	3593	394	45	ALMFSTGQEGRQEKHPPPHQKKKASRGE EPRGGVRKNYPPPKKKSFPKKNPPGVTP PKKKKKAKLPRL*GGPQRRPQKTAPP PLNFYPPKEPTKVLSIFSFSSFFFSAND VELY
3571	17472	A	3594	402	62	AMIVLLHSSSLGNKARPCLFKKKWAKDLN KHFSKEDSQMANKYMKCLISLVIRNMQ MKITVRCHEFILTRMAKIKMVNSKCRKE VQKIPTLKHCCWWECKIV*ILWTNLAA RVG
3572	17473	A	3595	220	425	FISGFLNLQEEREIAFFFKVNIRLGAVV HTCNPSTLGGRRRIT*SPGV*DQPGQH GEPCLYLNQKN
3573	17474	A	3596	13	412	AEIAPLRSIHRARNCLKKKGRKGRKNPG GDGNPQIGPAFFGGGNGKTPGQKPHQF QTWGGQRHLKGGGGGPKRKGVPKKKTP TIWGGTPLAFGVEPNWNGHTGNPGGADP KPPGREK*SGGAQITGPHTGP
3574	17475	A	3597	2	293	QQLSP*ELGTPRRERERERERERERER ERERLPPRDLREKRAQDVVFATHPNYEFV CVIRHYRGCVVYTPLTTHAHSIDAHKMCV CVKKRPLYKKKKK
3575	17476	A	3598	243	9	ILLRQEQCWSKGRFQLQDEQVLNT*D RTVEVMWPGAVTHACNPSTLGGRRGRIM

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						RSRDRDSCRHQQGSKPKSPR
3576	17477	A	3599	1	329	PSARRDWKNIPKLPPPRGKNPTGFFFLK PGGPQRGPQKGGKGF*SFQKPF*KGGG PPQFCPPPPRGGFFFFFPGGPPGEKKGG VKGPPPPFFFWPPPPPNLFFPPGA
3577	17478	A	3600	206	1	LRALGIMERAHAHTEVRLVFQILGSPIL* YIF*RQDLSPPSPRLECSGTIAARCSLDL LSASNSPASASQ
3578	17479	A	3601	322	99	KRTGAFGFFFPPLFNKKKKVFLGPEGPK IVKKKKKKKEKKEKQNKNRKQTKKK*KTN NKQNKRETDIFGVEDET
3579	17480	A	3602	410	25	LFFFKKKTGGGGGGPPFFHFGGVNGG VIRVGELSPCPPGGTRFFFKTKNYPG G*GGPFFPPPSGGGLGPKKTLSPRGAS L*PNFGPSLPKKGKGGPPFSKKKKKKK QSRPRDS*SLRRGIRK
3580	17481	A	3603	27	349	RSSIQCGGILLFYFLYFMVFNDIFVVL* GFSAITSLISMLFSCI*YFFKMYCLL FNFRCHWIFILF*MKTIAQIGN*IFFR DAYLGYFFLFLFFFFFSGGKLYL
3581	17482	A	3604	88	435	RAISTCLQNEQYKWLTTTTSVEKSLNDL TELKTMV*ELHDKCTSFSSRFIQLEERI SVTEDQMNMENNPPLIHGFIFYGSSYSW STMVRKQDKLRVKDAGIKHRNQKGFTE EKSA
3582	17483	A	3605	331	428	YGHYQIEATFLPAITTEKETLKTRKLT *SSINLLK*T*NVRPGTVGHACNLSTLG GRGGQIMRSGIRDQPNST
3583	17484	A	3606	3	294	GG*GCSEL*SCHCTPSSLG*NTVRKKER KKGKREKERKREIIPGFGPCAHHKGA VTGLNLFPRVQVSQVLQRRKIIITVIPD RLGEIVLVSQSL
3584	17485	A	3607	263	426	RKLAGTFPFLWKSGPFQTLAAQRMGG NDPKETRVFHAGLSSSLGENK*VWKI
3585	17486	A	3608	213	439	LSWACAAEWTVTPANFPLDYILPFFLL IRESSKF*RHMATQLETAASRPGVVHA CNPITLGGRGGRITRSGVH
3586	17487	A	3609	2	441	MTDLESFPLESELSANSPVQCSGLCKPV LTIFQVISHKHGCHSKYLLNANYNVFL HLSNSVLPRLLSGQRTETQKHFYTAVLS VCLSIYLSRDRVLLCYPGWSAVM*FYSL *PQIHGLKQSSCLSLPKC*DYQHGISPP WCN
3587	17488	A	3610	102	354	EPGAWADRCWLGRVLLTHLLWPCCLYFF YFIIFILNSGDRVSLCCPRWSClk*SSC LSLPECWDYRCQPLHPACAVFIENSKR
3588	17489	A	3611	462	371	GLNFLTTL*SARLGLPKCWDYRHEPPRPA WS
3589	17490	A	3612	463	319	RNSHDGLELLTL*SAHLGLPKCWDYRCE PERPVLC
3590	17491	A	3613	49	476	PRNSITLLILGLLTNTLTLYQGWFVDVTR ESTYQGHHTPPVQKGLRYGIILFITSEV FFFAGLF*SFYHSRLAPTQGLGHWPPPT GITPLNPLEVPLLNTSVLLASGVST*A HHSLENNRNQLMQALLITILLGLYFTL LQ
3591	17492	A	3614	223	467	TPS*PLAII*FISTLAETNRTPFDLAER ESELVSGFNIEYAAGPFALFFIAEYTNI

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						MIINTLTITITIFLGTTYDALSPELYTTYF VTKTLLLTCLFL*IRTAYPRFRYDQLIH LL*ENFLPLTLALLI*YVSIPTITISSIP P
3592	17493	A	3615	2	405	ARGLQEAGAVQNDPVSRLFDHAMLQCHR AHQMAIVTYQEFGETYIPKDQKY*FLHE SQTYFCFLNSIPTSSMEETQHRSSLEL LRISLLLIESWLEPVRFRLSMNANLVY DTSRDDYHLLKDLEEGIQTLN
3593	17494	A	3616	328	63	PSKF*KPCLISPPPLPGPPN*TPGFLK KPKFPPRGGAHP*SPLFRVRPGDPLNP RGQGFP*PKLPPGPTRATKPNFVSQKK KKKE
3594	17495	A	3617	1	379	GTSVGIPITGGQEF*FAALHGSNVK*SA AAL*ALRIMILFTVRGLTGIGLANSSLD IVLHDTDYVEAHFHYVLSIGAVFAIIGG FIH*FPLFLGYTLDQTYAKSHFTIIFIG VSVTLFPQHFLGLC
3595	17496	A	3618	494	17	GSANPRNPRRSGSKTRETSPRNVMSLMS PMSPTLPMRETSPTGTPMHLTNSMGPMQP PNSSRPVNPASSATPVSPASPARPRKPS CFPAPQ**SPPL*SPEPRHGLSCLSWVK KECETWHVVMHIVEDRHSKPYHGPVMV AHACNPSTLGG
3596	17497	A	3619	350	480	LGSWDYVCKPPHLAVLLL*RQSFVLLPR LVTNS*AQVIHLPWP
3597	17498	A	3620	2	400	AAAEPHGCIYAKVLDEFKPLGEEP*NLIK QNCLEFEQLGEYKFQNALLGRTKKVPQ VSTPTLVEVS*NLGKVGSKCKHPEAKR MP*AEDYLSVVLNQLCMHEKTPVSDRV TKLLTESLVNRRPCFSALEVK
3598	17499	A	3621	3	476	LGYSVHPPQPLAQVLSPPPLPGASRAGWL LRMRGPPSPHPPTPAGLQAPHAALVPA RASPSTPPCKLREWAPALASPERGSHSA VGG*RAPQMPPKWEPRQGRCEQARALR TASMLSPLSFTHPVTLNFPSTLPPR NSPSWPVVSVR
3599	17500	A	3622	40	390	MKGALTQPGRAGGLGSQSQMDMASTFKP SPDDQGCSTHILWGFPLVSLPLPSLSPS PPSPPRHSGVTHCAP*VLPRLGALRVP HSSVPRPHAVPVVGTTTRYSRGANPLSL DFRGL
3600	17501	A	3623	52	475	AVEFHLLFLQPLETNNLSVCMCLPILA NSPK*NQICDLFVFFHLA*CF*DLFML EHVSVLHFMAE*FFFFFF*KGVSLESPG WRAGAQFWLTKTPPHSPARLKQFSCLT PGSWNYRRAPPSPANFFVFSGRGFTIL P
3601	17502	A	3624	333	466	SIIGKIRLWKMRPWPQAVQAQCDPGTLR G*GKRITRSGVRDRPG
3602	17503	A	3625	2	138	LRRGNRLNPGGGGCGEP*SRHCTPASST E*DSVSKNQKTKNSQWH
3603	17504	A	3626	3	337	LSLRPPALPPCPPRRLETPGQGHGPGSAG FPGRP*RLPPLPDP*PPSLGLSPGDDP GLAREELKSPCPWGPPLCHLPFP*CWA SSQPSINAYEWRKKKKKKKKKKKKKKK
3604	17505	A	3627	2	393	LGTDLSSLIRFELGQPGNLLGNDHIYNV IVTAHAFVLIFFIVIPLIIGGFN*LFP

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						LIIGAPDMALPRINNISL*LLPPSLLLL IASAIVEAGAGTG*TGYPPLAGNYSHPG ALVDLTIFYLHLARVCSI
3605	17506	A	3628	2	379	QDATYPTIEELITFHEHALIICLICFL ALDALFLTLTKLTNTNISDAQEIVT* TMLPAIILILIALPCLRILYITDEGNDP SLTIK*IGHQWY*TYEYTDYGGILFNSY ILPPLFLKPGDLRL
3606	17507	A	3629	1	400	PTRPPTRPPTRPMTNTLNSIHPPLPR*K KKKKKKKKKKKKKKKKKKKKTAAGGA *KKKNRGAKTHRGSKLNFFFKRNKKN PPVKIEKKTFFLGKKKNKPPQKNNAK KKKNYFEGEGESLLLL
3607	17508	A	3630	416	1	SQLGYSGVRDPLEEATCLFSDLKLHAGR TTPLFQAVRQGHILQRFLOPPA*LCPA PRGGVYRGRQASLSCGGLHPVRASWPLC LPTQFSAMEGAPPLALLPRSSSISDYCA SNEQGSVGIGPSEPCTGYNLLVCHLL
3608	17509	A	3631	275	83	RWGSYVVLQGLQLLGSDDSPALASQSA GITGVSHCTQPKNVI*KISHLTVAGPAA DKTPQTPR
3609	17510	A	3632	186	3	FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFPFFFPFFFLVCQVPLLCNL*HLVYLF YML
3610	17511	A	3633	3	235	GIISFLLIR**YARADANTAAIRAILYN RIGDIGFILALA*FILHSNS*DPQQIAI LPHPSDSKKYLYLSHIQLKA
3611	17512	A	3634	1	428	RTLKTTLFNPDGG*DPILYQHLF*FFGH PEVYIIILPRFR*ISHIVTYYSCKNEPF GYISMV*AMISLGCLGVIA*AHHIFTV* IDVDTRAYLTFATIMIAIPTAVRALS*L APLHRSNIK*SAAKL*ALRLIFLFTVGG QT
3612	17513	A	3635	2	129	PVIYSTIFAGTLITALSSH*FFT*VGLE INMLAFIPVLGFW
3613	17514	A	3636	2	422	DR*LFSTNHKDIGTLYLLYGA*AVVLGT ALNLLIRAELEGQPGNLLGNDHIYNVIVT AHAFGIILFIVIPILIGGFGN*LDPLII GAPDMAFPRINNISC*LLPPSLLLLLAS AIMEAGARTG*TAYPPLAGNYSHPGASV
3614	17515	A	3637	14	479	QNCKINNFPMYFLPHQSEFFRKSCQQN TICFRLSNQNTMKKTENHALLWIRKWQ T*KQCKSNSGYTPSTPSRAKKKKKKKK KKKKKKKKKKKKKKKKKKKKPGGGV LKKL
3615	17516	A	3638	2	449	IIICFVGLCALVLTTLTKLTNANILDA QEVETG*ALPAILMLVIALPCLRILYI TDEVNDPSLTIK*IGHQWY*AYEYTDYG GLMFNAYILPPLFLKPGDLRLDGDNRV VLPNEAPIRIVMTSQDVMHS*AVRTLSL RTDAIPGRL
3616	17517	A	3639	347	98	HFFLGGGKGGGFSPFPQKFFFLRGFF FGGGGPNFPFPKKGFFSKKPQGVF*TP PKKKKKFFFPFGFPGPPGIFFGPPP
3617	17518	A	3640	2	426	DR*LFSTNHKDIVTLYLLFGA*AGGLCT ALSLLIRAELEGQPGNLLGNDHIYNVIVT AHAFVIIFFIGIPIIIGGCGN*LVPLII GAPDMAFPRINNISC*LLPPSLLLLLAF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						AIVEAGAGTG*TVYPPLAGNYSHPGACAD
3618	17519	A	3641	94	294	GRGGGGVAGGRGAMWSKGRQRGRNGPVR GREGGRKSHFRKEG*KEGRKEPPPPPKK KSRGEKNQREG
3619	17520	A	3642	1	405	RTRGFDLERFVLFDAQQMVESGYVCEG DHKTMANAIDRVSLIKRKREQRQLVRE EQEKKKQEESSLKQQVEQSSASQTGIKQ LPFADTGIPASTTSASVSTQVEPEEPE AD*HEQLQYQQPSLSVLSGTV
3620	17521	A	3643	34	405	HLLGRKQNKALFLEAEKKKKKKKKKKKG GPLKKNPGGAKNNRGGEKKIFSP*GGVK KTPLGIFEKPPYFGGGKKWANPPKKIKT LKEKKKF*RGKGGKKPENPWGEKDESS PK
3621	17522	A	3644	430	81	EFAQLSPPQIKGFPSPPNPLPPSLFGF FSPFSP*KFFSLKGFIFVGGFFPFFSP PKKSFFSKNPQLVFISPPFKKKIFLFPF PLNFGPPRVFFKRPPFFFFFFF
3622	17523	A	3645	399	2	AFFFTKKKKEFFPPFPKNFFFSRVFF FLGGFFHFFPPQKKIFFLKIPRGFFLTP PKKKKIFFFP*FLAPPGFFL*APPPF FFFFFFFFFFFFFFFFSPCSWSCHQV FPHASNRIHNPSNSYPLQQY
3623	17524	A	3646	49	326	KKKKKKKKKRGGPFKKTPGGAQKNPGG EKKFFFL*GGHKKPPRGIFKKKPPFGGG KNWTTTPQKNKAFGGKKKFLGGKGEKPP PKPRVKKN
3624	17525	A	3647	327	94	QKKKKKFFPPPPPKNFFFSRGGFFFGG GGPFSPPQKKGFFSKNPGGVFLPPPKK KIFFFPFGGFGAPPGFF*RGPP
3625	17526	A	3648	2	301	TSSVASTFIMSLFPTTFIMCLDQEGIIW N*H*ATTQTTQLYLSFKLDYFSIIFIPV ALFVTWPIIEVSL*YINSDPNINQFFKY LLIFLITILILVTGC
3626	17527	A	3649	2	406	STNHKDITGLYLLFGA*AGILGTALNLL IRAEKGQGNLVGNNDHIYNVIVTAHAFG IIFFIPIIIIGGFGN*LVPLIIGAPDM EFARINNISF*LLPPSLLLLLGCAIVEA GAGTG*TVYPPLAGNYSHPGACV
3627	17528	A	3650	3	418	HAYADAWVHFSITLLILGLLTNTLTIIY Q*WRDVSREPTYQGHHTPPVQKGLRYGI ILFITSEVFFAGFF*AFYHSSLAPTPQ LGHWPPPTGITPLNTLEVPLNLSVLLA SGVSIT*AHHSLENNRNQIIQALLI
3628	17529	A	3651	526	2	WGGGEKGRAGGAGEETPHQESQRQGCAL QPEPPLYPPCPAHPPLPLGGLLFP LPPLP*AAWFPHPGQGRNNGESPTTR BKRLWGPPLPTPLWPPTQPTPLSRRTG CPPCPREVPTPSPPPAEPPPLGPPSEI AHLTTVRRGAALANVNHENISDTDENKL NAFVTA
3629	17530	A	3652	464	297	RNSFHRVSQDDLDLLTL*SPCLGLPKCW DYRCEPLLPASYIDVS
3630	17531	A	3653	162	467	NSKKQQFVLLSEITSYVYWLHKRDLDSH TIIMGDFNTPLSTLDRARQKVNDIQE LN*ALHQADLIDIYRTLHPKSTYTFSS APHCTYNFLFQSYFSSQF

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3631	17532	A	3654	372	1	LMMLSI FSCVHLAFVCF LWRREMSGVSL CCPDYSGAAVHRCNHTALQPOTPLK* SSCLCKRHLQLRPQVYTTMLGYLFLFLF LRQSCSVAQAGVQWHDHSSLQP*TPGLK RSNSPTLV*DLD
3632	17533	A	3655	444	341	VGQDGLLDLLTS*SACLGLPKCWDYRRE PPRLAY
3633	17534	A	3656	466	315	VGHTGLELPTSSELPA*ASESAGITGVS HCTQQSGCAFCYSTMIPTKPYTC
3634	17535	A	3657	40	276	EFDTAHAFVVIFFIVIPITIGGFN*LV PLIIGAPDMAFPRINNISF*LLPPSLLL LLASAIVEKKKNEKKKKTGAPLV
3635	17536	A	3658	351	470	FTTLPVTSASLPLKTLAWPGMVAHACNP STLGG*GGRT
3636	17537	A	3659	40	182	GIRKENHLNLGGRGRIE PGSHHCTPAWA TK*DSVKIKKTRIQKTPLI
3637	17538	A	3660	160	461	INGKDTDTPGMVAHAYNTSTLGGGGGGI A*GQEFQPSLRN
3638	17539	A	3661	145	437	YFSLSLCLLELMNSVILFFFLVLRGFY PPPLVEMQGNFG*LNPPPPGLKQFFCL TLPKSWNNRPPPPRGNFLDF*KKRGFN YVGRVDLKLRTSG
3639	17540	A	3662	255	451	LLSFNPPFFFFFGKGGPPSLPPGGKGG GLNFI*TLGPQGKRNSPPQPPGEPG*RG PTPHPLFF
3640	17541	A	3663	185	66	PLEQPLRK*LYLFRDGVLLCHPDWSAMM QSRLMATSAEF
3641	17542	A	3664	42	193	FQLLTRLRQENHLNAGGTSCSEPRSHHC TPA*VTETQSQKQKVKVLGFSL
3642	17543	A	3665	216	2	KSKGKCSFLHSRVNRGNSKELLFLRDGV WRYCPAWS*TPGLKQSPHFNIPKCWDYR REEFHHPGLVVYEF
3643	17544	A	3666	43	267	GRLWSAMTPGKLTCLCKIDWPALEVWGP LEGSLDRSLVSKVWHKVTYKPRNPDPFP YRDT*LELVLDPPPPPTHSG
3644	17545	A	3667	212	2	SQLLGRAEARGWLEPRSLRKINKTSQVW WYTPVLPSSCDYRHTPPRANFCIFSRD GVSPC*PGWSRTPD
3645	17546	A	3668	104	334	TVLFPPCFLLHIDFCMVLDFFSNFFVLN YF*NYYRRVQKMYEEFPFFLFFLIFSFS FLFFLSTFNFFLCPLCDLWYH
3646	17547	A	3669	369	260	DGLDLLTL*STHLSLPKCWDYRHEPPCP ANMPSEFKN
3647	17548	A	3670	111	342	NGVSFFPPKKGGIWANGNFRFPKPGG* RNFLA*PPQKFGMAGPPPPQPVGIAGP PPHAREILEFFFFFKKGV
3648	17549	A	3671	377	3	FAIIGGFTH*FPVFPGYALAQTYAKIHF TIIFIGVNLAFFPQHFLGLSGMRRRYS YDAFTT*NILSSVGSFISLTAVILIIIF MI*EAFASKRKVLIVEAPSINLE*LYGC PPPSHTLEDPVY
3649	17550	A	3672	39	348	AKIAPLNSSLDERMRVSKKKKKGHLTP KPFLKKKLKGNFPLSQLEGVGKKNQKPF GFKKGLLELAPFNGKNGENPNTRWGW* TMSFFFF*DSHPFIQAGVQWRDLGSLQP RPPRFKRF
3650	17551	A	3673	327	3	SKDPVFFKVFKNPPTPNIGVFFPALPL KRGQFQPLFNPKGFFFFFKPVQLGRGK

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						ISPFQFFFKRFGW*TKSFFFFF*DSHPFIQAGVQWRDLGSLQPRPRFKRF
3651	17552	A	3674	379	267	EPRLSPCTPAWATE*DSISKQNKTKKPKLALNKKKMF
3652	17553	A	3675	2	270	FCRDRVSLYCPVRS*TPGFKGSSCLDLPSWDYRHPGLAKIGGLHVFCCLPCCGSLLCVWSSHCSLAHQELLENKHTDVWMSGWMDR
3653	17554	A	3676	3	54	PVYKNKNKRPDAVAHTCNPSTLGGRGQQITRSGDRDHPG*HL
3654	17555	A	3677	291	30	YSLVLLIFFFYCFISYFISLMNFCHNLYYFLLLDGLVCSYFPSILWHNEIYFIGSMFFIFSVIV*IFFCWEMSCNIYKLHQEMF
3655	17556	A	3678	1	298	RDFSASASQVAGTTGMHRHAQLIFVFRVCVCVCVCVCERERERERDGVLLCRPDCCSVAHT*VQGRDLGSLQPPPPGFKRFFCLKLPSWGHRCVVDAP
3656	17557	A	3679	20	376	VPPPHLANFLNFILLFVDTGSIYVAVAGFKLLAPCNLSASNS*SVGITGVSHHALLLLALKCNQLFQFVIFILLHAVCIYDFIMVRFSLQCFPPQFYDFPFCFILFVSSKAQFCFLRLPY
3657	17558	A	3680	110	334	NTTDYFKLP*ILSGTR*DMYKQPL*HLN TVREYTSKYGWRPGVVAHACNPSTLGGQGERITRSRDQDQCQHGSET
3658	17559	A	3681	326	511	LTMMLQMKISVICCLLRNIFWPALAHACNPSTLGS*GGRIARSRDLENSPSSLGSQPSS
3659	17560	A	3682	448	248	AKDLNTFFTK*E*TPLANKHKMKGSARFTYRNVQIQTT*RCLGTPTRVTGV*MRNSARHR*GCGGLV
3660	17561	A	3683	486	176	PAPINPPQLRSLVQSRGIRFC*AGQVGFKLLVSSDPPTLASQSAGITGVSHQWTP*NYS*NSGMPHPRQASSWRLREQWYHVSLLPCAYYKNGRQNSLLI
3661	17562	A	3684	238	27	NKHILCYVGQEMGMGWSHSHGWKPHFKSFQVCPSAVAHACNPSTLGG*GGQITLVQPGKHGKRRIPALF
3662	17563	A	3685	1	299	LITQTCHVGCLKIKCI*TSKKKKKKKKKKKKKARGPLKKKGPLKTPKPPGGPFFKAPPFWGGPPPRFFFGGGGAPPPVFLKKKKKNSPLWGGGGFFFR
3663	17564	A	3686	494	91	PLGKRFPGGDIALTKLSRPWAWAPPGIPPLGGPGGGVP*VTPFKPTPFRPGEPPLPLKNQTFFGVPGPPPYFPPLGGLGPEIPFTPGGPGSIKLAPPPSPPPGAPKRNFFPKKKKEVMKMLCFHFNLLVQNI
3664	17565	A	3687	17	249	YSRFRHRFHGHDPLGYFQILRRLRWENHLNPGGRGCSKL*SHHCTPAWATE*DPVS*KKNVTTIARWKQLTCPLADG
3665	17566	A	3688	296	461	FWLWVSSVLKHMNWPVGVVTHACNPNTLGGQGE*SA*ARV*DQPG*HGETCSAKEK
3666	17567	A	3689	149	422	ASGRQGPDRGCWGGQAPRHPARGAKPAA DMGMSGQGYTKQAAP*GDPSQRAGVRLPREPTSRKASGGSGGHSRASGGAVPGQRV AQPSPAR
3667	17568	A	3690	1	415	GDPAGGGDPILYQHILF*FFGHPEVYILI

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						LPGFGIISHIVTYYSKGKKEPFGYIGMV*AMISIGFLRFIE*AHHIFTVGIDVDTRA YFTSATIIIIAIPITGVKVF*LATLHGSN MK*SAAVL*AL*FIFLFTVSGLTGIV
3668	17569	A	3691	1	393	GTRKYSFLHDSQTSFCLSNSIPTPSNME ETQOKSNLELLRISLLIESWLEPVRFL KSMFANNLVYDTSDDYHLLKDL*EGI QTLMGRLDGTRRTGHILKQYTSKFDTN SHNHDALVKNYGLLYCFRK
3669	17570	A	3692	402	2	FLTQRWGAPLPPIPPFWEAPFGPSP*APG FKPPPLPPRGNNPPFS*KTIQIPALGARPV IPPSLGGGGGESFLPPGGGFP*PRLFP C PPRGAKPNFFQKKKKCLFCKAPQAQ HRSACLHECLPLGNLLKLCPR
3670	17571	A	3693	3	434	IFYIFFGTTLIPTLAITR*GNQPERLN AGTYFLFYTLGGSLTLLIALIYTHNTLG SLNILLTLTGQELSNS*ANNLI*LAYT IAFIVKIPLYGLHL*LPKAHGEAPIAGS IVLAAVLLKLGGYGIIRLTLILNPLTKH IAYP
3671	17572	A	3694	452	208	INKSARHGSMNL*SQLRRLREVCLSPG VQGCIEPWSHHCTPAWETE*DKTLSQKQ TNKKTQCQLYDHRPSALEATFRLSH
3672	17573	A	3695	464	146	LKQTRATKGNLFLP*KPKLTPPGGFRPP FQPFWKPRPLGPPKSGVLDPPGPQKTP FVLKKPNLLGGVITPLFFPLSGGLGRKI PSPRGGGGAKKRPPRQKKKKK
3673	17574	A	3696	2	465	VTRLRERPALVSSSTWTEDEDFSILLA ALEKFEQLTLDGHNLP SLVCVITGKGPL REYYSRLIHQKHQHIQVCTPWLEAEDY PLLGSAEPGVCLHTSSSGLDLPKVVVD MFGCRLPVCANFKCLHELKHDENGLV FEDS*ELAAHLEKL
3674	17575	A	3697	173	51	TFISVVFGQVVFVFCMEKFFSGDF*DFG APITQG*SFLSI
3675	17576	A	3698	380	26	KQRTNFFLFFFKGTGAFWFFFPFFFNKK KKVFLGPGGPKIVKKKKKEKKENQKN RKQTKK*KTNKQNKKRETDIFGVEDE TWRQRWGLGGGRVANSSAEMGKGNSTTR PSVNS
3676	17577	A	3699	11	414	RLVVTAILIQTP*SFTGAVILIIAHGLT SLLFLCLANSQQKKKKK
3677	17578	A	3700	1	401	SSSLTSLNNKSFLNQVTFNEMWILYD NW**PAQWLDQEAPKHFPKPNLDQKKVM FAVWSAAGLIHYCFLTPGETITSEKYA QQFKEMNRKLQPLQSAMVNRKGPIIHDN A*SHITQLKLQKLN*LGYEVL
3678	17579	A	3701	395	140	TPPKKKKIFPPPPKIFPPPKKYKPPPP PFFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFSIYIDFNLCICDNL*LQKTLVFL E
3679	17580	A	3702	407	371	SFFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFLWYKDIIKKGNEQNV*CS
3680	17581	A	3703	36	409	LLKCEGIWKKEGKKKKRREKKGGPFFR VLLGGPTFRGGAHKSLFRGVFFNLGG FFFEGPFLGGALLGPPPPPIFTPLGKK KIFKGRGPPLIFLFF*IRGPPPPSP PSTKPPPPPPPTP

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3681	17582	A	3704	56	415	QAPWGKKKKKKGKEKKKKKKKKKKKKKKRG GPLKKKNPGGGPTMGGGGEKYFSPWGGEK KNPGGNLGGKKTPLGGGWNAPPPPKKKG AGGKKKI*RGGGGKTPLIGGGKKNGGPP RTSPR
3682	17583	A	3705	108	1	NLAK*IQ**IQTIMHHDQVSFIPGIQGW LNILKSIN
3683	17584	A	3706	425	52	PFPH**L*KVDPIPLPPQNFLHPSNNI YFSPSPKKFFFSLQPPFFFGEIFPIFP PPKKNFFS*NPNLVFISPLKKKIFPSP PPPNFAPPKNLFKSPPPPPPPPPPPPP FSGKNTLYWVDK
3684	17585	A	3707	117	421	VLLVTQAEYLLPEVFGTRSVSDFGFFRF WNICILSG*ASLI*KSEI*NALKNISS FKKKFIFILEPRSHSVTQAGVQWDHGS LQFQTSGLKLFSHLSLP
3685	17586	A	3708	308	3	RSEPPWFFFGFFFLVFFFFVFFQLFES KYNITLYIKKKTETFTENDNGNATCQN LWDTAKAIPREKFIAISTYI*KVGKHQI NNLMKHLKEIBKQKQTK
3686	17587	A	3709	94	420	KKKKKKKKGGGAFKKKPGGAKI*RGKE KKNFFLKGGGKKKVGNGPKKPYFGGGK KREKTPKKN*SLKGGKKFLKGKGKTPP KPWA*KKWSS
3687	17588	A	3710	413	184	LGECISLRSKKLWSPAGGGVCL*FQQV RRRKWEDHLSPIRG*RALSSHR SIPAW TAEQDPVSRGLVWGLPGGSW
3688	17589	A	3711	3	104	GGCSELRSCHCTPAWRQS*TSSQRKKK KKKMY
3689	17590	A	3712	2	393	GLFSTNHKDIGTLYLLFGA*AGVLGTAL SLLRRAELGQPGSLLGNDHIYNVITAH AFVIFFIGIPIIIGCGN*LVPLIIGA PDMAFPRINNISL*LLPPSLLLLASAI VEAGAGTG*TVYPPLAGN
3690	17591	A	3713	424	1	FFFFFFLRRSLTVVQAGVQWRNLGSL*A RPRV
3691	17592	A	3714	2	130	GRVGGRVG*NLKLYSQRLLKKKKKKKKK KKKKKKKKKKGGGP
3692	17593	A	3715	3	197	FHHVQDGLNLLTL*STRLGFPKC*DYR CEPPRPAAFFFFFLKKKTLAPKKFKTL DLTTRERS
3693	17594	A	3716	3	497	RSPPSGFAWPGPAGPWEAGAAAAGQPLG ARPHSPCTGGCRSAGTTP*PAGPAGPPP HAPAAAERKPRGAEQSQRVQETGPPPT RAESNPSGLRGREVPGSAGCWSGSQESD FGAGCPAVT*GTYPYRIAGQVSSRAPHP AESRGCTAGLSIGPDGRQ
3694	17595	A	3717	40	379	AITSPRSPPAVHGSCLARTHPNSPQCLP LSGTLLLPSSSLSLSHPATAGE*IWDA EKKKKKKKKKKKKKKKKKKKKKKKKKK SPGGALKKKNPGGPNPPGGGKNISSPPR G
3695	17596	A	3718	445	286	KKKK*METRSCYVGQSGLELLASSDPAT LASQSVGITGVSHQAQPVNKLPRVQ
3696	17597	A	3719	15	383	GYFLEASCLLHPLLHPMYQNCGHVACLA AKENGKFMQAACGQLNSPALSLKNGRLS AAYGGSDCVYLFPMKMLVLTQ*ALNKY TLNGPGAVAHACNPSTLGG*GGRNLRSG

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						VGDQPGQHGET
3697	17598	A	3720	14	472	RSCARNPGLTHASAQYQTPLFV*SVLIT AVLLLLLSLPALAAGITILLTDRNLNTTF FDPAGGGDPILYQHLP*FFGHPEAYILI LPGCAII IHIVTYYSKGKEPFYIGRV* AMISIGYLGFI VRAHHIFTVGIDRDTRA YFTSATIIIAIPT
3698	17599	A	3721	3	298	EAAIKYFLTQATASILLIAILFNNILS GQ*TI TNTNTNQYSSLLIIMAIKLGIA PFHF*VPEVTQGTPLTSGLLLLT*QKLA PISIIYQISPSLVN
3699	17600	A	3722	86	505	AGAVTYIVTYYSL*KKDSFWIHSVWC*A MRVNWES*GLSV*AHHIFTVGIDVDTRA YFTSATIIIAIPTGVKVS*LATLHGSN MK*SAAVL*ALGFI FLTAGGLTGIVLA NSSLDIVLHDTYYVVAHFHYVLSIGAVL
3700	17601	A	3723	432	48	FKTSFLPFLPSFCPSFSPSFLPFSFS CFLSCPSSLSFLFFFLSFHPPFFPTLL ISF*VFLF
3701	17602	A	3724	2	406	HHIFTERIDVDTRAYFTSATIIIAIPTG VKVS*LATLHGSNMK*SAAL*ALGII FLFTVSGLTGIVLANSSLDIGLHDTHYV VAHLHYVLSIGAFAIIGGFH*FPLFS SYTLDQTYAIIHFTMIFGVNLT
3702	17603	A	3725	174	158	KFFGGGFPHPFPQKGGFFPKNPPRGFF TPPLLGKNFFPPPPVNLGPPRGFF*GP
3703	17604	A	3726	2	392	LFSTNHNDMGTLYLFGA*AGGLGTALS LLIRAE LGQPGSLLGNDHMYNVTGHA FGIIFIVIPIIIGGFNRLGPLIIGAP DMARPRINNISC*VLPPSILLLLASAIA EGGAGTG*TAYPPLAGNY
3704	17605	A	3727	48	474	KKKKKKKKKKKKKKKKKKKKKKRGP KKTPAGPPPPPPPREKNPPPEGGQKKPP PAH*KKPPPPRGQQPPPPPPQKNPPPE KQKTWGAEGGTPPPKPPRKNKGSQQIAD PPSNAAKNRHPTQEP PPQSQCIPPPPTP PP
3705	17606	A	3728	387	53	PPPKGVLPSPPNFYTPPK*GVFSPLPP *KFFFS PKGLIFWGGGPNFPKPKKFF SKKPRGGFFFP*KKKILISPPREKLGP PRIFLKGPPPPPPPPPPPPPPPPPP
3706	17607	A	3729	1	397	PTRPLQPLSPEFKRFSRSTSPDVAW*VS LPSPPPSGRSFFVFL*VESFCVWIKKRF TMLARLVDS*PSDPPAWASQSAGITGA SLRASLLYIY*CF SIQLGLLPEFLIQYV QLLIVYPRIHHLVLSVPHLH
3707	17608	A	3730	407	0	TLKHTKKKKKKKKKKRGGLLKKT LGGPK *NGGRKKKIFFLKGGKKKQTGEILKKKL ILGGEKKGNPPKKKKPLGEKKNFKEK GKKNLKMFVVIKLTSSKKIIF
3708	17609	A	3731	3	200	GGCSELRSCRCTLAWVTE*DSVSLKKKK KKKGPFKVLRGKPSGNKREGAKKKIQG KPCPFWESF
3709	17610	A	3732	3	380	TNHKDIGTLFLLFGA*AGVLGTALSLLI RAELGQPGNLLGNDHIYNGIVTAHAFVI IFFIVIPIIIGGFN*LVPLIIGAPDMA FPRINNISF*LLPPSILLLLASAIVEAG AGTG*TSYPPLAGN

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3710	17611	A	3733	6	394	AMISIGFLGVIG*AHHIFTV*IDVNARA YCTSATIIIIAIPITGGKVFS*LATLHGSN MK*SAAVL*ALRFIFLFTVSGLTGIVLA NSSLDIVLHDTYYVRAHFHYVLSIGAGF AIIIGGFH*FPLFSGYT
3711	17612	A	3734	27	238	GIPGSSHASAHIG*IIAVLPHYLNITIL NLTIDIILTTAFLLLNLNSSTTTLLLS RT*NKKKKKRGGPF
3712	17613	A	3735	402	249	ASAHASAPLV*SVLITAVLLLSLPVL AAGITILLTDRNINTTFFDP
3713	17614	A	3736	100	430	VTWPKSDSYBEVKIKLEPRQTDLRALGF CLSFTGKKKK*KKKKKKKKKKKKKKKD KRGG
3714	17615	A	3737	158	306	FLSSVFSVLVQGVLFSSSLCDRLNLPDMMQ LWSEIFNK*LYLOELSILGVY
3715	17616	A	3738	279	3	PGHCFYNFNLNFYFQIFFQNVLANSGSL LFLYQTLILSFNIFYILYLI IQISIVFQ SVIL*FIFSNSYSWWYGLVCLMTFEGK KQTCAHV
3716	17617	A	3739	268	388	HFFFFEMEADSVAKAGV*WYDVGLQQPP PPGVKRY*LSL
3717	17618	A	3740	395	153	GWLRFKERCGLQNIKV*GEAASADAEA AAS*PEDLAKIADEGSYT*QWIFYVGET AFYWKMPSTRTFIAREKSMPPGFKL
3718	17619	A	3741	271	386	TCPPPLKLWVYELGLL*RKNMRQGAHAH ACNPSTLKG*GGRI SRSGDR
3719	17620	A	3742	406	190	QLLKLRLQENPWRWGG*GCSKPRSPRP QAWVTERDFVSKSKTKTNQPKQNGERKV FFWFFFLRKPQVQFEI
3720	17621	A	3743	272	408	MGLQACANSP*YVDIATPCNNKGAHSV GLMWWMLAREVLRMRGT
3721	17622	A	3744	211	407	KGKRNILFGPVKNIFCDTQFTSCVNFFR EEVSLDCPGWSQTPALK*SSCLGLPTCW D*RREQPRL
3722	17623	A	3745	405	189	CVSQDGLDLLTS*STRGLPKCWDYRKC WTNQLFVNGQKSLNSFCVYSFMVLDITG FKEIVMLVHLVPLF
3723	17624	A	3746	120	362	LKA*EISWLNGTIOTHQEKPEVQNVIL EENIVFLGPQDRI FECQAVTAELEPEKK AIVAGCSDSHLYPSTLGGQDGWIT
3724	17625	A	3747	401	233	NSGGRGCSEPRSLPCTPAWVTDTRDPISK NKNKTNHQ*QKKCKR*TKVIFMTRSIL
3725	17626	A	3748	353	109	LGLANFCIFSRDGVFPWPGWSRTPDLR *SAHLSLPKCWEYRA*ATMPGLLMCFLLI KALDFQGCVRWGGGSWTDIKLCQM
3726	17627	A	3749	412	221	HGLKECLVYPKWCQNSISLQGIHFSEV AM*QRAHNHGIHWFYHDSFPRKIWINWA RRGGSCL
3727	17628	A	3750	1	355	FHHVSQDGLDLLTS*SPRLGLPKCWDYR REPLRPAENTVYVHFSSWSFTNHSGKIN *TLDQWKEQLPGWL*ILRGVFFFNPSIW NS*QKKASIYVFPWCWKRDIFLYHFPVS GTFRGF
3728	17629	A	3751	423	125	QVCEKVLISLITEMQIKTTVRYHLTPVK MAFRQKTDNKNKWRGYGEKGTVPHCWWK CKVVQPL*RTAWRFFK*RKIELPYDPAT PLIGI*PKERKSGQV
3729	17630	A	3752	3	171	FQPIAFLYANSEQSGKEESTSIYSSVEE

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						YLGINLTKEMKDL*KENYKTLMEKIELD
3730	17631	A	3753	2	247	FHHVS*DGLNLLTS*SAACGLPKCWDY RHEPRPALTRFLFVFLYLQRLDHLIRI NSFFIMSVNGMFTFVVLKLFNLIIHA
3731	17632	A	3754	3	197	GLELLTL*SAACGLPKCWDYRHDPLCPA QYLSFLYAINKLFSSTYLEIHNRLVCCI VTLLIYKP
3732	17633	A	3755	2	103	VSQDGLHLLTL*STLLSLPKCWDYSCEP PRPAW
3733	17634	A	3756	103	2	FRPGMVAHACNLSTLGG*GGGITRSGVQ DWPGQ
3734	17635	A	3757	394	244	ASTHPANFFCRNGVLLCCPGWSQMPGLK QSS*LSLPKC*DYRCEPPHSAS
3735	17636	A	3758	341	2	AETAPLHSSLGMRDVSVKKELKKLNK QKPNPLKK*AKDMNRHFAKGIQGANEH KIKCSTSTNLREMQIKTTVRSLLI*VRM AIIKKSTNISCW*ARREKGILITYTWEC K
3736	17637	A	3759	2	322	PPRPTRPLNNTINQMETICMYTKCYLII AE*TLFPSAHGTLIKIGHILGHKASLNK FKRIKIIQSAFFKHNGIKLENDKRKITG KHPNTWKLKHTSKPMSQBMFF
3737	17638	A	3760	444	422	VRLPHRPSPPPDPVRVRFHHVGOACLKLL TSSDPPTSASQSAGITVPSLQ*QP*SVR LP
3738	17639	A	3761	266	1	GGGVPLGFPVIPPRLRPPQVRGFOALAPQ GPQSKIF*IFFGPQFKNRVFFKGRNLVF FPLFLSLLPFFFFFF*DGVS LCHPGWSLE CSGM
3739	17640	A	3762	70	381	HSTSYI*AFIWGFFLFCFVFLIKEME SHYVAQADHELPAWAPPTSASQYAGIS GGSHTQHYFIYWFYFTVFCGGGFLR RSLAPSFFAQAGAQRDLGS
3740	17641	A	3763	229	390	DIPYSFCFFFFFFWKGFSFVFPQAGGKGR KLG*LKPPPPGLRGFSCLTLPGSWEN
3741	17642	A	3764	119	1	QTSCRPGAVAHTYNPSTLGG*GVDHLRS GVRNQPDQHG
3742	17643	A	3765	400	200	ITAYCSLDLLQPHFLFFSRDKVSLCCPV WSRTPELK*SPCLSLPECWD*S*ATASG LKHFIKSLPL
3743	17644	A	3766	376	44	TQPIFLGPGFQAPPGPMG*PNFLF*EKK LVFFPKPKPTAPAGGGGPKFPLPRKPKQ KKGPHPGSQNFQKPRPKFPPRPPTWGKK REFFSQKKKKKRERDVKITDLNTST
3744	17645	A	3767	403	3	DHFFFKGPPSQKGEFFFLKTFPSPLGG FG*ISLFPFPPINFPFPPPKRIFPGPLSF FFFKKKKTPAGKGLLFFFPKPKPGGGF KRWPGPBKFFFPFPGWACSPFFFFFF FFGAKVSLVAQAGARSRSRTS
3745	17646	A	3768	407	177	FHHVSQDGLDLTS*SARLSLPKC*DYR HDPRLARCIKNFCRGWRCNLRKSPLS LPPSAGELRAPFLDFLEDAQ
3746	17647	A	3769	292	391	RPGVVAHTCNPSTLGG*GGQITRSGVQD QTQGY
3747	17648	A	3770	395	198	LDMGFHHVGQAGPELLTSSDLPASASQS AAITGMSHRAQPY*VISMCCQCYKHFIR IPFNLHNNV
3748	17649	A	3771	1	241	RTRGRTRGRGLLSAHTGRYQKHPRIR

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						TPQIFSTGTTKAEAGELLEPPGGGACSEL RSCCHSPARATRVKLHVKKFKKIK*KHP RIRTPQIFSTGTTKAEAGELLEPPGGGAC SELRSCCHSPARATRVKLHVKKFKKIK
3749	17650	A	3772	112	406	FFFFFFFFFFFFFFFFQGEVPPPI*KPPPP K*FMFPKKKLPPPPPPALKLFFFSPPPP FFFFF
3750	17651	A	3773	24	197	IFSVMGFCHVGQCDLDDLSSNPPASV S*SAGVIGVSHHAWPLVKLFVKRNKLSY V
3751	17652	A	3774	85	201	VNFFHLI*FVNKRIKLEKKKKKKKKKKK KKKKINWKKKKK
3752	17653	A	3775	1	382	WENHLSPGSRGSSEP*SHYCTPA*VTE* DSVSKKKKPNLQEAERLTLLLIKKAIF KNRGSPCFSLKWAGFKKIKQGWFVATR MGDRSRGTPNLGENFLKSFLSFSIKIQR FYVLGLKNSPSRNIY
3753	17654	A	3776	1	181	IKMATVTKATYRFCVIPSCLPMLLFTKL ETKILKLIWNLER*IPKAILS*KNKMGL SNS
3754	17655	A	3777	70	385	LNKMQTKTFDSDTHTSICFTLHFINTKL QFIFLLAIYLLFVNFPPIFINFFEEPGF CFDDLSSCFLFY*CIP*FYFFSAFFRL HLFFFYRFLSLTLDLFSFLI
3755	17656	A	3778	2	406	KDDRNTHEQVHPNASDQDEAFDPYENF FEDSDSPTKSSSTEPSPIHPVDIQTMI FHCADNFARQYILAKLAKKKKKKKKKK KKKKKDSSSPGGGPKKGAPPPPRGEKN FFFGPPLIFSGGGF*NGGGGGP
3756	17657	A	3779	403	176	FLFPILFFFLRQSFTLVTQTGGQQRD LG SMQPPPPRFK*FNEGKGRKLWGGGA
3757	17658	A	3780	3	248	GLNQTLRKILAYSSTITHIG*IIAVLPY NPNTILNLTIYIILLTTACKKKKKKKK KKKKKKKKKKKKKKKKKKGGGGA
3758	17659	A	3781	3	330	VDRRLRTGVQDHPGKHSESPSLPKKKKKR *KILPKRGVYLNPHFFERLRGENNLTP GGEGQRETESPPCLPAGGKNKIFV*KIQ KKKRGGPFGKNKFFPRGGGKKIFF
3759	17660	A	3782	399	187	FPPPAKGFLEPSHLFGLPFGFSPPPVFK PRPRNLILGPP*KKFYLPFPPRP*TWFL* NGPPPPFFFFFLLDF
3760	17661	A	3783	392	11	KKLKVNLPDHPAVPPLGIFPKEMKAGI* RAICTLMFIAALLTIEK*WKQPNWLLVD K
3761	17662	A	3784	324	80	PGPFFFFPPPAKRGFFPPPPFLVPPGFF PPPLF*TPPDFFFFLAPLKKFFFFSPPPA LNFFFFKGPPPPPPPPPPPPPPPPPP
3762	17663	A	3785	354	24	PPNKIFFSPPQKKYFPYKTPPPFFFL SSFFFFFFFFFFFFFFFFFLC*MVH FIVKYRKCKRGTRIIILHTPLRQLVLC LSDVLLGCCIFIYVTMCDLCAPKLG
3763	17664	A	3786	3	369	SCRGLVWVYGELLLHPCRGNQISRVMQK KKKKKFGASPPREGAPPGEPP*RGF*TQ KEPPPLKK*APPPGPGGRPPPMGLGGG PAPPPFFWPKAFFKKGFSGQEFGFPLK GLFFWKFPF
3764	17665	A	3787	1	125	FRHFRSRDGLDLIF*SARLGLPKCWDY RREPPRPAHSIII

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3765	17666	A	3788	427	251	LTPKGRGCSEPR*CHCTPAWVTEGDSVS KKQAKNRCSLRMKYERNEFTSSPC
3766	17667	A	3789	250	2	GFPPVEKIKKNPFFIF*KKPGFFFFPNP FF*ISGGKGKIFFLGPPPFSSFFSPFF* DRVLLCHSGRSAVAQSQLTATSTFRR
3767	17668	A	3790	412	3	GSTPITTPFWGVGGALPPGGVPPPPAP PGGTPTFFFKKKKKKKFQNFPRPCSRYN GGLGRKNFFLEAKGSINPNFSPAPPPG GQNKTPFPKKKKKSR*MTLQSFPRPGTA PGAAM*PVSPPEPCGPPAPALSTK
3768	17669	A	3791	10	187	GCESEL*LIHCTPAWVHSETLSQKKGRG KGGFKNGIPCFCGKNKGKRFSGFHF STG
3769	17670	A	3792	1	331	FRVPLGRLSRGEHQQQ*QQQPPPPPPPP GPLRPLAGPSRKGSFKIRLSRLFRKSC NGSGGGDGTGKRPSGELAASAASLTDM GGSAGRELDAGR*DRPGAGRQTSFSW
3770	17671	A	3793	1	431	FRKGSARCRAPKAGADGVHWHHRASP QTAQAPPVTCARGSWMDFSHASGPQDR DLHSPSPVCPRGWAPGTHSPGASGA*G RTPVGGGK*VAGVQQRHPLAPG*LVL PGIAVHITKKPGSKGTTTPTGTVAHACNP NTLG
3771	17672	A	3794	342	48	KRENMPGVAYNPSTLGGCNPSIVGGFCN RVCNPSALGGCNPSFLGGFCNHVCNPSP LGG*GGRISRSAAQDHPROHGEKMSPOK IQKISQACFARVG
3772	17673	A	3795	2	189	LNPGGRGCSEPRSCHCTQAWATE*DSVS KKKKKKGSRFQNTIPSALPGFPVSGELI LGGPNL
3773	17674	A	3796	1	401	LNPGCKGCSEPRSCHCTPVWVSE*DPIS QKKKKKKKKK
3774	17675	A	3797	279	3	ILAKVYPMVNSFLEKIHYFLLVLCCL QHVLYYLTFTTETGSRVSAQAGVQWHD RSSL*PLPHGLKRSFFLSLPRSWDMHT PPCLATE
3775	17676	A	3798	229	394	VFVKSLLCQPGMVAHACNPSTLGG*GGR ITMSGD*DHPGKHGEVSTYNTKKKGG
3776	17677	A	3799	380	206	AGHM*S*LLRRLRQEDPLSPGVGCSEP *S*PCPPAQVTVRISLKKRLHERDKSS AS
3777	17678	A	3800	450	3	IYLLRGRHSLHYSRPSFYFSNYRGACSY MRPPQATLLGRLNQGITREGPAIAHSP AVRPRLSLAHAHVRLCLPRPGAAPFP AFFLPCLLVAQAGVRWRDLGSLQPPPPR FKRFSCLSLPSSWDDRRPPLSS*FAFL VEMGFRRV
3778	17679	A	3801	301	10	KKQPPKKKKRCFPPLFPFPKGFKGSPPF FFLTTPPLKNLPTLKPQIFLRTFFF FFFERGSPTSQTQAGVLWHDLSLQP*TP GFKHMPSCPVLLC
3779	17680	A	3802	420	51	SASSPPASFFFFPPPKKIFSHPPFFFF PPFFFFPPFF*PPPPFFFFPPKKKIF PPPPQKIFFFLKPPPPPPPPPPPPPP FFFCGFVNCQFSVLI
3780	17681	A	3803	253	73	QTTPSKRYSYVLNCCNN*ITTCKRIKLD PFLTLDLKIN*KSFADLNVRAKTIDTIK KVKG

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3781	17682	A	3804	385	55	AGTRPVFAALAAAAPAPRLPLAPHGSA ATGFPFPPPCPHGEGLRGAPAASSSPPLA HRSQTPNWVDCGESPIPDQFPLL*NGP PALCLPQGLETVNVESLALCFTSHGN
3782	17683	A	3805	191	2	QKHLKALNLFPRCVCVCVCVCVCVCVNV TF*ACKICTCSDFPGSPRKKYLEFGTKI INIVDFN
3783	17684	A	3806	1	367	KLRQVIYLEDLPTIIDEGSYTKQWIFNV N*TAFYWKMKPLKTSVTREKSMGPFKA SKDRLTVFLGANVVSDFKLKPMPIYNSE NPKAIQNDAKSTLPMLYKRNNKACIAAH LFTAWFTEYF
3784	17685	A	3807	3	145	LGGPGGGGCSEPRSCHCTFAWATRGKLC LQEKKKKR*RLDPEAEVAVSRGRAIALQP GQQEGNSVSRKKKKKGRDKVSLCCPAGF
3785	17686	A	3808	362	86	NPPFICSPFPFPLWGPQVVPWCEG* TPGPGPCEIPLPPKKKSKSPGVWGPFF FPPPWGGGAPKFFLPKWFPPQTQICPL PFGLGEKN
3786	17687	A	3809	245	377	FGYMPSFFETQSRSVTQAGVQWHDLGSL QPLPPGFK*FSCILGLP
3787	17688	A	3810	3	268	KRNFLNLIKRRYEKPIANFVFNSTVNT FHLRSSTS*GYPLLPLLNILKVLNPEI RQQKEIKGRKNKGKKTISVYSIMLSANT EKPK
3788	17689	A	3811	2	388	SAENCLNPGGRGCGDLRWCHCTPAWVTE RDCVSKTNKKETEKYMRN*TGNMLTIIID AGRRYMRCHQTIITFFFWRGSLIFLAP PPSQGEGIFLPHPPPEKWKKKVRITTPTY FCFLRTDGFLECGPGGF
3789	17690	A	3812	292	136	PPTVIARKGKPRPKLSSEPWQFSAEQLG LPSFLCFFVCVRCCCLLFLLLFCRDEV SICCPGWS*TPGLKQSSHLSFPNCWDCR CEPLCRAIF*FFCLCTLLFAFVSAAVL
3790	17691	A	3813	359	52	KKGRFFFEKPNPFGDLVPKKKKKKTFFP PNPKKKKRGAPPPPPPPFFFRH*VPLCC LGWFRTPGLKGSSCVGLPKPWDYRHKPL PLTKDDYVYGLPFVSLQ
3791	17692	A	3814	382	1	GGPGMEAPLGYHIKTPFLPKPKNNEGG GAKPVVPPPPGG*AGKMGLPPRQRFLPT QKGPPPPPLGGKREPPPKKKKKRVAM GDP*NSECR*GCHLRVQKEMRLPGLRNS PPHYIPNRNTDMCSC
3792	17693	A	3815	472	340	TGFHRVSDGLDLLNS*SACGLPKCWD YRRGLFIIIFNMGEWS
3793	17694	A	3816	247	378	PPPPGGGXGNLGLLKLPLPG*REIPPP PPRGGNPGGAPPPPG
3794	17695	A	3817	25	465	TPPLGG*GKRFPGRGPFSPPPPKGNPP FF*KFKKKPRPGGGAP*FPPPGGRPKN PLPPGPKGSH*PKFPPPPPPGETKRKPP PPKKKKKKRKKKEKKKEI*AYKAYICFDC PLTGPGLKSDKTLAFPSVIGLPRPCTC LSPR
3795	17696	A	3818	475	147	PPKG*RHPPGPPRRRGPGNPPPHRFFF VLRTPGYSFPF*KKRGPPPTFFFTLPGP PGFLKGPPSPGGGQKIPFPRGGGGLK *IPPPPPPGKKKDFFLTKKKKKP
3796	17697	A	3819	461	57	TNQKKAAPPPLKKKFFFFFKKHTGAP

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						PGEKKRRGGGEEKKKRGVYRKGPAPSRG CAPPLYRGLLFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFHVKNILVF*DYIVIIADL IQSLRHKDFQELLRR
3797	17698	A	3820	1	418	HAYHI*KPSP*PLAGALSTLRMTSALAM *PHFHSITLLILGLLTTLTIYQ*WCDG TPESTYQGHHTPPVQKGLRYGIILFTS QAFFFFAGFF*AFYHSSSLAPTQGLGHWP STGITPLNPLEVPLLNTSVLLASGVSI
3798	17699	A	3821	385	1	LQFPFSPPLLFQVQRPFFSSFPSCPWWG PVPSKLLPLQLGRGFYQKSLLVSLG FFFFFFFFLIKKHRNEVLCCPGWSRTPE LK*SSHLGTPKCSDYRCEPPHPPDPWDI CSYVPFLQSTHFGNLN
3799	17700	A	3822	72	424	KKKKKKKKKFFPRKKGAPPAPPLFGKAG GEKLFPPRGLIFKKPKKAPGEKKKNLFFK KKKKRGGP*KKKKLKAGGGEKKIFFKGA QKKNPGAGFKKGGRGKNRGAPQKKGEG SSS
3800	17701	A	3823	154	2	GHHTQHTEPQRLNNSYRAELKHLNNTK NNPI*KWAKDMNRHFSKEDIQM
3801	17702	A	3824	422	212	MGSSNPSPPTASWVDEPTGICQHT*FYVE MGFCHVSKAGLGLLGLRDPSPASQSAG VAGVSHCTRLWILL
3802	17703	A	3825	2	417	KRVNTRGFPPPPFFKTPPPKIFMGPQKK KNFSPPPPIKIFFF*KAPPSP
3803	17704	A	3826	423	65	ACGRGKYFKSGGRVVKPFCAVDFFPSGKK ANQPTPKNPRKKQKPSGRGMSPMGKPPG CPCMPKASPGPVSNKGGVAPATKDFC PIGKTA*IPSKKKKKSDPG*VKKGKPN LYSIYNK
3804	17705	A	3827	285	136	FFFLFFXFLFFFFFFFFFFFFFFFFFFFF FFFFFFFFFSGA*KIFIATIH
3805	17706	A	3828	425	316	QDGLDLLTS*SARLSLPKSWDYRHEPPH PAQTFFKQ
3806	17707	A	3829	3	169	LSNS*ANNLI*LAYTIAFIVKIPLYGLH L*LPKAHVEAPIAGSIVLAALLKLGG
3807	17708	A	3830	6	452	IGFCQGFADFCSSKKFQNRVVRVSPRGGE GRKFLFLFKGGGFQKFPPLPPGWAKTPF LKPPPKKKKKKERKEKEKEKKRNPGRP VSPSSWSPVP*APSEQRSGPQLPPSRGD *VVRLPSPPRPFRDCVRRSATRGNSPPC RGSQGP
3808	17709	A	3831	45	387	NFGVKVFS*LATLHGSNMK*SAAVL*AL RYIFVFTVGKKKKKKKKKKKKKKRGGT PPGGEKRKFSPKKKKKKGLKNPQPKK NFFWKGPKKKGGKTPFWGGGKKAPKKT P
3809	17710	A	3832	463	288	DGLDLLTS*SVRLGLPKCWDYRHEPPRP APCILMATFFQFEVLFSEFLETIVKSVL LH
3810	17711	A	3833	294	90	FFFLFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFF*AGIYFI TCAPPPAYPRS
3811	17712	A	3834	427	37	SYHFGRLRRADHEVRRRL*NRKGRPGAVT HACNPITLGG*GGRIMRSED*DH
3812	17713	A	3835	499	53	AKLMYFQSRENVAKRSYRRNQKASMVHP

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						NQEPAVIAGQGTTALEVLNQVK*LSSYH CRLLVGMVYHGCLLVSSVTPFCNIFSGLK VH
3813	17714	A	3836	304	3	RLKITKTNNNQTEINS*YIKDLNARAET IRLLEENIGGKPHDIRFAMIFWI*HLKK TKNIYKLDYTKILDFCISKDTINKVKR* PLEWEKIFANHISDKG
3814	17715	A	3837	475	135	MEGLFCPAPMVHPFIPPLPGG*GGGSPG PGIQTTPPGYPGEPPFFFTLKKLPRRGAV FFFPPLGLGPKNVFTPGAGASLEPGW APSPPPGGPP*NPFPKKKKKKRLKIGWH F
3815	17716	A	3838	415	245	ETGFHHVGDGLDLLTS*SACLSLPKCW DHRREPPHPDPQVSFIRALFFMRAPLS
3816	17717	A	3839	460	413	WDYIKLTGFTAKETRVKROPTWDKTS AKYISDKGLKTRLHKEQ*KMTNLI*NWV K*LGRYSH
3817	17718	A	3840	2	470	GGDAPHFPDGVAAARRRGSSLLRWGGCQA QGLLTSQTGWPGRDAPHLDPGVTAGPRR SPHLRRWAAGQTRSSLPKCDGGREEALL TS*VGWRPGRDAPHFPDWAARQGGSSHP RRWAARQRRSSLPKRGSGRAEAAISNSA SLQRVSKVSVSCRPGG
3818	17719	A	3841	54	332	QFGFHHVDQAPELLTSDHLPSSASQSA GITGVSHRARPSLAHSTHSLAL*PTPA HSLIHWLTHSLTHSLSFCSFSSPPSHT HSLARPLGV
3819	17720	A	3842	208	468	ENPTPPPLWCFALGVL*EDGFSLYLSA HVCEIVFLYCPVLESARPLMFLWNLAHV CYEWHLFVSLSLEFHTVS
3820	17721	A	3843	406	2	PSSSSSSSSSPPAFFLGCPCGVFPSPFF LKPAPGFFFWGPKKKNFSPPRGVKFFF FKGAPPLFFFFFFFFF*DGVLCHPGW SAAHAS
3821	17722	A	3844	370	253	VGLLEPRGQGCSELRSHHSTPAWATE*D PILKQNETEQK
3822	17723	A	3845	369	73	LRQDNGMNPGRACSEPRSHHCTPAWAT E*DSISKRRKSQNSVFTESYFASEHCYS LTGGGVAILMEGPTGPDGAIIFMCHLRNL CRCSPILPLALQCDH
3823	17724	A	3846	198	388	FRKSINVRYHVNRLNKHNTIIPIDAQK P*EKLQQLTMKYSIIMNSRKLSPALR NLF*KPS
3824	17725	A	3847	391	20	GFPPPRVF*HGPANFFLGPPKKKFIPLP PR**TWFLKGPPLFFFTFFF*DGVSLC RPGWSAVSKN*QTNKKSIIILPIRGKINL FVHSMILKGFTCDLLIFKNRKVKESTKT IDHIFSRQLMA
3825	17726	A	3848	227	2	KRRNPFHKAIAIDSSDGPR*SKLKNFW RGFSIADAIKIFRDSWEVKISILTGFWK KWILTLMDDFEGFNRTGR
3826	17727	A	3849	373	2	SSPQKYVGGGPGFFPPPGFKTPPPPPFFW APTCKKIFFGAGRENFFFLRGPPPIIF FFFFFFFFFFFFFFFFFFFFF*YNSF I*DIKTHVFLHLSVGFRVLVYKTRLYFT LYHSFLKNELG
3827	17728	A	3850	394	2	EACSVTQAGVQWRNLGSLQAPRRQSFC RGSLLSPQH*EDRT*HIGGTQQTSMNE*

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						MNLYLQWLCPLLYQLCSTSYT*EVIQLN IAPCVCLVGFFCFVFLFFETASQSF* AGVQWCHHHSLOPQLPKL
3828	17729	A	3851	3	164	NHLNLKGRGCSDLRLCHHTLAWATEGDS ISKTKTVQ*RLQNNIPHEHTCKNL
3829	17730	A	3852	35	390	NFVSNSFFFFFNGAPRGPRGGQGP LG*GEPPPPG*KQFSFLTQPRGNNGGG PPPRVNFGLRKNGVPPGGPGGPDDL GTGPPPPPEGSPPPGPQFSKTKRTAPGQ PKGGPF
3830	17731	A	3853	6	437	PNK*KTPGLPPPPFFYFFPPPPFLSFL KPFSFPPPPPLFFFLPPP
3831	17732	A	3854	1	236	PTRPLRWLRQENRLNPEQGCGEPRSCY YTPAWATE*DSISKKKGGRLKGPFLT SGGGQGLFLLRGPKSTSGAAF
3832	17733	A	3855	52	351	TVGIMEPQTTDVYVKLHKCTDFLLPDYI FNKQHYPKKKKKKKKKKKKKKKKKKK KKKKKKKRTKQKKKKREKKKKRGGGAPQ *LTLSPPPPLYFFFF
3833	17734	A	3856	72	420	NTYGKKKKKGKKKKKKRGGREKEKLW EAGGGGTTRGL*KENSGGNMGKPRIKKK GGKARGAPLGVSSSTQLL*RGEKEKCLSP GGGGCSEHKTTPLAYPGLGKKKETQSGK EKK
3834	17735	A	3857	410	107	SSSSSPLARYFLGVAPGFPLPTLFKTGP RIFFLGGP*KTFSLPTGR*T*SP*KGP PFFFFCRRDRLW*PGWSEMGGLKQSSC LCLQKCWRVRYKPPQLA
3835	17736	A	3858	419	239	TTRSQLLLFLVEMGFHHAGQAGLKLLTL R*SACLPCWDYRRESLYLADA*GFYNL EDPL
3836	17737	A	3859	262	1	TAAQEFNFGGPIKKIFRCQPGVEKLDFF KRPPPPPPFLFFFLFF*RRVLPCCP GWS*TPEFK*STCLGLPK*WDYRHEPPN PAS
3837	17738	A	3860	357	133	NTPPPGAGRKNENPLFPKKKPRGVGLF PPRKAQTEEWLYPGPK*FFFFPPPPG GKNTKKKPPQKKKKKSL
3838	17739	A	3861	253	375	TLSPQG*GGPPPPPPRGGLEAPPPPPG LFFVFWGKRGVSP
3839	17740	A	3862	3	482	YITDEVNDPSLTIKSIGHQWY*TYEYTD YGGLI FNSYILPPLFLEPGDVRFL
3840	17741	A	3863	1	129	LANSNYERTHSRIIILSQGLQTLPLIA F**LLASLANLAKEG
3841	17742	A	3864	289	372	NHLVKKWAKDLNRHFS*EDIQIAHRHMR
3842	17743	A	3865	266	31	KICFIFSPQKKSVPFKVRFPQKRKPP PALLFSAYFFFEAESSVTQAGVVQ*CN LGSPQPPPPGFKRFSCLSTLGG
3843	17744	A	3866	1	395	NTSDFCIKPRAYNESEHHWDMVRRHL*G KEDNLTLDISKLKEQIFETSKAQLNLVS ETAMVKAVDSLTNLNPVTWKTIGNST IANFVLILGCLASLLVYRYIQQLRRDS DQREGAMMTMAVL SKRKG
3844	17745	A	3867	137	2	APLIKKEHCLRAVAPACNFSTLGGRGGE ITR*GV*DQPDQHGETP
3845	17746	A	3868	1	108	ENRLNPGGRRRCSEPRSCYCTPAWATERD SMS*INN
3846	17747	A	3869	198	302	LLNINHNYYGV*GCSEL*SHHCTLAWAA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						ASLHPKKKKKKRKKSVKSQGAIFYSHYA MAILNYIREKKLFLKWK*LLNINHNVGG VLEKKKP*SYTYNLKKSQNLPLQLL
3847	17748	A	3870	237	419	KEIQSKQGLRAICIPMFIAASLMIDKG* RQPKCPWREE*INKLWYKHL MAYHSALK RNEIL
3848	17749	A	3871	239	232	KAFHLTRVKGRIQPGAVAHACNP SALGG RGGRITRSGDRDNPA*HGF SWGKCLGIE LVGHMFNFLRNCQTVFQSGYIIYILPMP LDS
3849	17750	A	3872	417	219	CHVAQADLKLSSSDPPASASQSTGIAG ISHRAWPRGTNP IHKGSTLMT*LPPQRP HLLT LSPRGF
3850	17751	A	3873	45	414	NILFFFFFWKSNLVPQGEQGQSLG*W NPPPRGLRGFFNLTPPR TGNKGGDPPPQ ENFGF*RKGGVTQGGGGSKTPALGGPP GLTPQRGNNQDPRPPAKKFGLGKKKK NRQLPFLGFFR
3851	17752	A	3874	278	2	LISIVSIIYLYHSGFQLSKISPPQQL AYLSIYLSVCHFLIYEIGVITMPASKID K*DLIKIKSFCTAKETIIRANR*PTEWE KIFAIYSS
3852	17753	A	3875	233	379	QCDYFNELLRMEILPGGAVAHACNPNTL GGRSG*ITRSGV*DQPGQHGE
3853	17754	A	3876	6	247	MLITSASYPEDLAKIIDEGGYNKSQIFN VDETALN*KKTPSKTFTARDKSMGPKA SKDRLTLLLGANFKLKPMDLILI
3854	17755	A	3877	411	3	AKIPPLTSSQGHRTVCQKKREREREKE KEEGRKERERERKKGRKKERKEERKGS* VRMLFLDKVDFRSQKIITDKEGHYIMIR E*MHQ*DIILNMYISNNRALKYMKQKLT ELIGRVGRPGRSGTVPGRRNGVQ
3855	17756	A	3878	174	375	SFQQ*TAELEIKNTTSFTLTPPKLYLG INLT KYVQDLYK
3856	17757	A	3879	1	106	FHRVSRDGLNLLTS*SARLGLPKCWDR REPPSPA
3857	17758	A	3880	383	24	FALNNFPQGGAFSGPLTSPQVGLFFAP GPPPPGGGFSCPLAQSFRIFPQKSGPP ALSFSPLFKKNPVVFLRTQPLLPFPQ PRVFFFPFPPFFFF*DRVSLCCPG*SAVA QYGS LQP
3858	17759	A	3881	400	71	RIRQENRLNPGGGCYSEPRSRPRTTAVV TG*DSISKNNKNK*NLSFIYFYFFLR WSLTLS PKL
3859	17760	A	3882	282	3	IFNFCGYIVSVYIYEQEIF*YKHAMCN NHIVENGVSIPSSIYSLCYKQSNVILLV ILKYAGWAQWLTPVIPALWEAEAGGSRS QEMETILA
3860	17761	A	3883	1	175	LYKNFFKLAHGGVYQILRRLRQEDCLS PGG*GCSEFKSCHCTPAWVTQQDPVSKK FF
3861	17762	A	3884	415	233	SQDGLDLLTP*SARLGLPKCWHYRHEPP CPAANFFLKARYFWLMVARYFWLWCNYS ALPS
3862	17763	A	3885	237	367	GPVLGPGMVARTCNPRILGGRGRWIT*G REFETNLANMAKPCL
3863	17764	A	3886	359	108	TGQGGGGPPPPPLGRLKKKNGVNPEGKN SNKPKLAPSPPPGGKRKPPSKKKKKKKG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						G*HLPMLPRLGNSWAHDMILPPYPKK
3864	17765	A	3887	245	377	QFIKNISWPGAVAYACNPPTTLRG*GGWIKRSRV*DHPDMVKPHL
3865	17766	A	3888	406	2	SLNIFFFFFFFFFFFFFFFFFFKPGRVFFLKNFFFFFFFFFKGCRIFPPIFPLWLKVFFGPTPL*NPRG*KEGFCCPPFFFFFFFF*GRVLLCRPGWNAVAQSRLTATSAHAS
3866	17767	A	3889	3	114	EFHCVSQDGLDLPTS*SAHLGLPKCWDYRRKPPCPA
3867	17768	A	3890	395	1	MVLIS*PCDPPTSASQSAETTGISHRARQFPMLLSQ*LVCHSVTEVFLIFLLKLFYIYDILLYIINYILLIYYLFLFLFFETGSCSVIQTGVSSSTITAHYSLKSHPSGLKRSSHLSLPSSQDYRCAPT
3868	17769	A	3891	2	189	GRVGERGGTLL*SQLLRR*ENHLNLGGKGCSEPRLLHCTPSWATEQDSISKKKRSFIKALHM
3869	17770	A	3892	410	258	GC*GCSEI*SRPCTPAWATE*EPVAQKEKRKKRKEKKHVLATLAISSLICL
3870	17771	A	3893	244	412	GIEEACGNFRVIVLKSSLALEGEEPSGRDSS*EASGGRARWLTPVIALWEAEAGG
3871	17772	A	3894	208	2	RISPPITPFPWPVTKKTG*PGFFFQKN*KSFFFLRWSLALVPQAGAQ*LDLGSLLPPPPGYKPFSC
3872	17773	A	3895	407	18	PLLGHPPKKAGAPLIFNLPRRPK*KDEFPPPPPLSPTQPPPPPPPPICPAWLPPPGVPSSFFKG*MGGPP*RDEV*GPINDFWAPSLPVWPQNPIPPPKKKKKGEBIHCMVCPLSFNETFSFFKMESLRDGK
3873	17774	A	3896	82	401	KGFLKNSPKGEGLEFLFSFPFFFLFLATWLWPRCLKSGAIIARCSL*LLGSSNPSDPTSTTFGEAGITAAGHAQFPDPSPPKTRAHHVTQPGLKLPS*SSPPASA
3874	17775	A	3897	263	396	VWVPGGLG*Y*TPPLLGGQGGRITRSGDQDHPG*RGKPVSTKNT
3875	17776	A	3898	2	386	KTGLELLGLSNPPASASQSAIGIMSHCAWPNLFLYWNHHLYPHKK*VWPGTVAHAYNPSTLGG*GRRIA*AQEFKTSL
3876	17777	A	3899	140	33	IFFFHL*GEIGFTMNMLDIGGGFTGTETFQLEBVFNSVNDINKIIAFVTV*GVDV*SRIFTMAKTKPYNISLKLCS*KTF
3877	17778	A	3900	377	2	TPPKENGGLPKIKVPYFRGNKFKKFPFLCFSKVPPISTMWVLKNQFPPIPFLLKKNFKTPKKGVSHYNFPQPKS*GVFFFSKKKNFYPPFFWEEQKKQGRGPNALFFLLKKKRAAARPTRPPTRP
3878	17779	A	3901	2	123	RVSQDGLNLLTS*STCLGLLKCWDYRHEPPCPALRCVFG
3879	17780	A	3902	188	3	LRCVCPGTDCWVSHLAHL*FKKGRPGAHAHACSPSILRGQGSWISRSQVQNLGQHVETP
3880	17781	A	3903	422	238	ILHVQLPSSWDSKRKPFFFFFL*R*GFTMLPKLLLNS*GSSDPLASACQRLGITGMSHYTWP
3881	17782	A	3904	414	1	STHLGLPKCWDYRHEPLHPASMSYL**IFFYILFTHWSVSLTARMQFAEDRDLIFLHCYISSDSNSTSVVL*YILVFVHSPWLVTTIALILGFYVVFVFLFFETGSRSV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						AQAGVQW*GLSSLQPSIPPGFK*FSC
3882	17783	A	3905	396	236	DRVSLSPRLLECNGTISAHCNLCILGSS NSPGL*NRGHQIFSIEGQIFLQAMSLSQ LLCSALVVQKQPYTMYKGMEMAVCL
3883	17784	A	3906	377	57	RGLVFFFQNPQA*KNLGRGRVFFPSGAQ KNPQKGGWAFGRPPPRFGRPRGPGAR CPLNLTGGGPKGKALGPPPWGWSKFKQ GVPLQWVGNSGLFFSKKKHKL
3884	17785	A	3907	341	3	TRFFFFSPLGKKGFFSKGFKLGTTPRVFP LPFFLNPGPGIYFWGPIKKKKTFPPPGV KFGSFKRAPPPFFFLMFTAALFMVVKTW KQPRRPSVSE**NKLSYL*TTEYFSSIK
3885	17786	A	3908	3	162	MMRKAIRGHL*NNPALEKLLPHIRGNVG FVFTKEDMAPFQKPALLOHHSQYI
3886	17787	A	3909	1	421	PTRPPTTRTRWGFTMLVRLLLN*KHSQAG AVAHACNPSTLGGQGRQITRTGVQEOPD QHGETPSRTRGRTRG
3887	17788	A	3910	2	424	PRVRTSPGLALSGLTGLKFSKNQKKKGK KPQTTKTQKKKSPKKKTPKKKKGAP LKKKNFNARGGENFFFF*GPKKKNPGAR FKKGGGKTRGTPKKKAVGKTPFFRGGE KKKESPSQFYKKIKKKVFGKKIFP
3888	17789	A	3911	3	236	GFCHVGQADLELLATDDLPAAPQSAGI SGLSHCAWPV*PHVMSSLSLLATRPSL HRVKLQKNLGRKTRRELYMKNS
3889	17790	A	3912	304	2	VAKKGKSKPGGLKKNPPIGLGYPQGGP QNQIWEKFFFLTPKNRWGAPL*GGGGPP SLPKKRGPPPPGWSNPPPPFFFLRQ SCSVTQTGVQWRDLEL
3890	17791	A	3913	91	344	HAAPVCGRRTLKVHPPHAPSWPPSSWAHP PPTWPEPSGTTWAPEGTVVTLGPPQELS LRRGVSYHCPPP*PLIWRKWPPLPLCL
3891	17792	A	3914	328	402	KSWGWPXAVAHVCHPSTLGG*GGR
3892	17793	A	3915	16	179	GGCCSEL*RHCTSAWVTRARLSQKKEK KKKGPRKGEVATGSVWTRGELKSWAL
3893	17794	A	3916	229	46	AGPELLASSDPLTSASQSSRITGIPFLT GLYSKDHIIETANISYTN*AL*ITLRT RGSTR
3894	17795	A	3917	42	383	AFPCFVIGRVISKGKECTLYFFLFLFFF FFFEKKFFFSQGGKKGGEFGSMFPFPS GLKETPLPHLLEEGKFWAPPPPVYFFV F**KRDFTLVARVVSRLPSREKGLDYR P
3895	17796	A	3918	402	286	PPPPF*TPPPPKIFGAKKKKNSPPPPG ESFSF*KRPPP
3896	17797	A	3919	349	380	KKSPFPQ*RNFGSLQPPFGLKPSSPLS FPSSWVPR*TPPNPANLFFFKMRISHV AQ
3897	17798	A	3920	28	327	KTTLLNQATIIQAKAGTWGHPPLSPRE NKQNQKKKKKKKKKKKKKKKKKKKKK KKKKKKKKKNGGGGP*KKKNFSGGGEK FFFFWGAKNFGGGGF
3898	17799	A	3921	414	1	NFPKVSGPKLMSPSPHFFFPKSFPPP PLFLEKKNGRFSPPFPEKKV*F*KKPPF FFSPKKKPRFPKVLKVGKKRVI.KNLG PGLLSKKGRGTPPPPLFFFFF*DGVS LCLPGWSAVVRSQTLVTSASQVQVE
3899	17800	A	3922	1	169	LRSCHCTPSWATE*DSVSKKKKKKTLKN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LSPQKLNRRAGKIFLRVFPLEKKGQTQLL *NRAGKIFLRVFPLEKKGQTQLL
3900	17801	A	3923	263	74	LLSVWRIPCAQKKERKKRYECECLIVF VFDLSEENSSYISFKPILCVVCVCVCV CVCVW*VKNFRKS*SSDRSKTKTIKKH SHSYLFFLSFFCAQGILQTERSHELLPHL EVSLEFKE
3901	17802	A	3924	3	129	TGFHHIGQAGLKLTLT*SACLGLPKWWD YRHEPPHPAPFCD
3902	17803	A	3925	281	10	NLEPLPGATDYPASGGGGCNEMRSCHTP AWVTGAKPHLRKK*KKKRQMLKTISKEM GNENMVYILDKITK*FLYFKQLILSPLM GELGVK
3903	17804	A	3926	110	1	QLGAVAHACNPST*GGQGQAEHLRSGIQ DQPGKHGK
3904	17805	A	3927	180	368	EINFITNYIILFFNRQGLALSPL*SG GAIITHGTLKHLDSSEPPTS*VAGTS GTYYHA
3905	17806	A	3928	92	2	VRPGAVAHACNPSTLGGGEG*ITRSGDR DH
3906	17807	A	3929	2	146	HLNLGGGSCNELRLHCCTPAWATE*DPA SKKKKSFKITSFTCCQIVML
3907	17808	A	3930	221	3	KBRAIWGTENLMVSKIFPI*LKQRKNL* PENIKCYNNLLRP*LGPGTVAHACNPST LGSRGGRITRSGDQDH
3908	17809	A	3931	1	102	GGRGCSEPSHNCPTA*VTKRDSISKNI NNKIVK
3909	17810	A	3932	351	69	GQGGGFRFIQPPSSRGKRFPPPPPIW G*RIGPPPRANFFFLFF*KRGFLLFGRE LFFPPPPGVPPWPPQNFQGGAPPPP PPPPPPPP
3910	17811	A	3933	401	94	RGEPPPLNPLWEKNHAGPPKVG*KKPP PTKKKPLFS*KTKIFPPGPPPLPPPR GGKPKKFLYPPKFRFRPKKGFPPPPRG TKKKTPPPKKKKKKKVS
3911	17812	A	3934	184	2	LKEFFPSRNSRSLHTSNF*HLFI*LI YFFEIESVSVTLAGVQWSDLSSLQPRPP GLKQ
3912	17813	A	3935	2	393	KILIKVEIEGTYRKITNAICEKPTANIV PNRKKLKAFLRNGTR*GCPVSPVLFNI TLEVLARVIYSEK*IKGTIKIISATME NSKKFPQKTENKTTICSSNSTTGCISKR KEMHISKRHLHSPVYCN
3913	17814	A	3936	291	2	FPPPPQTRGPKSSSRAHSPGPGPGSTT GAR*PFRPLLLVRASLRPLGLPTPTGP TGGMQRPEA*RTPATDKPQNSRRGP*GA WGRPGCRGGA
3914	17815	A	3937	382	1	QWTAQTWSVQNELLFLCKPHPPPSLLP PSSCPGPHLGTPTWPAFSPHTSTLKAH PIGSGPSSPLLLLTSRMPPEIQTATG* PASSLTPTVCSQHGNRFFKKGVRAGRS SHLESQHFEAGPEAG
3915	17816	A	3938	398	2	PPPLLLNKIGAKKKAFFCPSFPGPRKIP CGQKTKKSVFPRVP*DKSTFDCFLCPI VYVKQIWLAPLHCVFSGRVAQGSKKSP LCLSLPFFFFEMESHVPTQAGVQWRDFR SPQPPPPGPKPFSCLGLPSS
3916	17817	A	3939	240	385	KLLFLFLFIYFF*DGVSLLCCPGWSAVVQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						TLLETPSAIPGAGGTPVSPFI
3917	17818	A	3940	230	381	LISSSYREYLAKDLRFSSKQS*WLCSKE FRGLGAVAHVCNPSTLGGQGRW
3918	17819	A	3941	1	107	CWVPVWS*TPDLKQSTCLGLPKCWDYRQA QPHRNLL
3919	17820	A	3942	2	95	DLTTS*SACLGLPKCWDYRRKPPRPALF AFS
3920	17821	A	3943	163	404	CRHKAQWLPQLPGHLLSEKTLKYSSPK GLRSQH*KLLFLFCFG*TESRSVTQAGV QWRNLGSLQPLAAGSKRFSCLSL
3921	17822	A	3944	3	200	GLDLTTS*SAHLGLPKCWDYRREPRLA YFTFIKKKKKDGCELLNLPNSCMDTAH VHPAHLTGG
3922	17823	A	3945	423	2	LFFFFSEV*SHSVAQAGVQWYNLGLSLHS S
3923	17824	A	3946	209	413	TTCIEQCCKTRRLGAVAYACNPSTLRG* GRWITRSGVDRPDQHGGETTKNTNISTT KKSTKNTKISQA
3924	17825	A	3947	425	3	SPSQGLRDKTPISLGQSTWGKGQMWQR QQT*TSWPDGSESSRSPTFEQQISER SSSAKGQTNSSSGSLNSVSPDWETPPSR SQQTTPHTGELQLASGRCSGMNLPPEGT DSNLCCSATHAS
3925	17826	A	3948	299	3	ASQTTTFREGCFLFFSFFISVCLFVCLFE MEFHSCRPGWMECNGDRARLHLKTTITT TIEIVKDDTNKWKHIH*RLPNIKMSILP KVIDILFNAIPIKI
3926	17827	A	3949	331	374	NAPKSERASKAF*ATLEENKEKLPDIN PVVHPHGHIFKCVAPPHCLGWDLSAVPA SHALGFPPQONSAWHVARSKSAASCLGT AVTSAGSGVLGTPNKMPPQKVRERARLFW R
3927	17828	A	3950	439	69	TNQKVWVPPKEKGLFKKKQLRPRVGGPA FHSPPLEGQGS*FP*GQRFKPRPPWVK PLFSKNPKNYPGGGAPFFPPSPGG*GG KFPPTPKAKVPFIQISPPPAQAGPTQV PFPKKKKKSH
3928	17829	A	3951	422	3	CFPALGIGPPHPPKRVG*KGGTPPPGLF FGKFLKEKNFGKNPGPGQGGPFFPPKKQ RGPFNNGRPGKVKKKGAPGPGVPKKKPP RVPPPPGFFGNPPGAPPKFFFSRGGED QKRKNFFFFFLRWSFTNEAQAGVQWR
3929	17830	A	3952	223	3	ALFFWGRGTLPRVKGLNPKGGGGKFFFF FFF*ETESHVAQAGLQWHDLG*LQPPP SRFKPFSCRLRPGSSLS
3930	17831	A	3953	1	388	EKGVSPGGRTCSEQRWCHCTPVWATERD SVSKKKGMSNNFSLILRSWNNKGQGGTY FQQKFIYPCFLKIKGHSYINCKIFKK** NLSLHVHVTDVNVRIILQKLDQCIIHWVD FNFELNILQCQGLGGCK
3931	17832	A	3954	1	396	KLRPKDQDTWPTQQSAIVVEFVPPSVYF VKSISEILFFFLKKNFFLGPQLKGRGQ ILVKGNPCPGGKKKFPAPPQQRGGKKG PPPPQFI FVLKKTGV*KIGPGGV*TPA LGIAPPPFPKGGE*RGGPPP
3932	17833	A	3955	2	199	PGGGGCGEPKTRGCTPAWATERDSVSKI NK*KLKLKNSWLYAKSLASSPTGR*EE WGCFTNEHI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3933	17834	A	3956	393	2	KEFPLFPFGAPPWPLSGPFSVLEKPKCG GGVVPGLINTPPGGGGFPQGSILWAGDFP* PLFSPQIPFFKKQKFFFLPRGGLWAPF FPPFGGGLFSQNF*KTGF*GGFFFFFFG DGVSLCYPGWSAVAPHAS
3934	17835	A	3957	278	390	LVYIFKIRTCWPGAVAHACNPGTLGG*G GRVTRSGDQ
3935	17836	A	3958	385	311	GPKNPPASASQEGETTEV*HHAWLIFFL FFVELWSSSHVAQAGLKLPASSDQS*TLY I
3936	17837	A	3959	410	119	SPPPRFKTPPPEFI FGAPKKKFFSPPPR PLNLILLKGPPLFFFFLPKAFKPHINPV FPPQKKKNV*INLYFPPPKKENESS*GK HFALHCNPSCISK
3937	17838	A	3960	77	400	TALPLKPKKKKKKKKKKKRGGPLKKKK FKAPGEEKKNFFKGAPKKKFRGRV*KTG ERKKPGGNKKKTFGKKPPFRGEKKKKP QA
3938	17839	A	3961	2	194	CL*SQLLGRLRWEDHLSSGN*GCSEP*S PHCTPAWVTE*DPVSRKRKKYPVVNQT RGFLSPA
3939	17840	A	3962	52	409	NSKTSSQEKRRVIRLSLRVRGDDTKV NTRRWGVFGWHLKNLPTTLVLKMEKIL ETYFMTPLDHPHTTSYFNGCQLQAIKV GGTITDLIVF*IVSKPNAAGLSLNNVN AKFNDLI
3940	17841	A	3963	382	96	LSSQLLREAGERNE*TGWLQOPLQMQIH KNPCIEPRSRCTPAWATEQDPVSKNQ TNKQTKNSLHL
3941	17842	A	3965	3	169	DAWELRSHRCPPAW*QSETPSQKKKRG KKKIFRFYLFNKRKKFLNGGNLGVIP
3942	17843	A	3966	1	121	AGFHRVSSDGLDLTS*SARLGLPKCWD YWCEPPHLAENS
3943	17844	A	3967	200	2	PPFRIYWGEVLTPLFLRVKPKFFKPWGF PFCLFFFFFFEMESRSVAQA*MQWRDL SLHPPPPAFK
3944	17845	A	3968	471	440	MELRFYHVGQTGLKLLTS*APPVMASQS AGILGVSHSTW*EAPNSLAITFLSSHLS PROP*THLGC
3945	17846	A	3969	214	2	EGQPECQLQAGDWVSLWNLVCSGLEVRA WREAPRLEWSFCLFFVSEM*SHSVI*DR VQWHNIGSLQPLPP
3946	17847	A	3970	53	398	GDLPKKQQQKPLNFCFQLLLYARLFGP IFLV*HLATYNNKHLLCVCVKVMINCOA DILNKMEISKVGAQKKKKKKKKKKRGG PLKKKKFI PRGGEENFFFLGAPKKKTGG GFK
3947	17848	A	3971	396	160	KRERI KEKEDNKEEKDKKASGKKERK KEKEIRDRESKEESSNLLQEELSLCCP SPGHPPNSSL*DPYFATGNSLRC
3948	17849	A	3972	416	3	FPFPRVPEGVPGGEGVFPPGFFGKSGVP FPRPRGGGAPI*KPPPFEGGPPNFF*K KTGPFFSPPGAPPAKRAPPFFGGGGG KIFTPLKKGLFFFGPPKKGVFFGPKKT LFFFQKKKKKKGRPPRSHASAHAS
3949	17850	A	3973	232	381	YKTFSLIF*LFFFRDRVSFCHPDRSAVV LS*FTVASISWAQGI LLAQPLE
3950	17851	A	3974	396	141	CFFPPPPKRGFFPTPIFGGPPGFFPPF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						F*NPPPKIFFGAPKKKKIFPPPGGKNNFF FLKGPPPPFFFFFFFFFFFEDG
3951	17852	A	3975	286	422	RKQLISPHSQDNSKQKEQSWRHATCLQ TILQGYNSQNS**APIAKTILSKKNKAG GITLPVFKLYYKATVTKTAWYWDQK
3952	17853	A	3976	3	116	GFHRVGQNGFDLLTS*SACLGPKCWDY RHEPPRPAR
3953	17854	A	3977	223	399	EGPRTQSFDFTEVHSVTDQGVRRRLNLS LLPPPPGIK*FFYLSLPSNWDYRRLPPR PVN
3954	17855	A	3978	227	422	SFPSPCIFISSLVDLGVSLYCLGWSQTL LKGSSLSFSPKCDYRQ*ATTPGLPVYF FFFPVFTFF
3955	17856	A	3979	519	313	KKNLLNPGDGGCREIKSSHCAPAVTEK DCLKKKKKKTSVCVCVCVCVCV*NHL SSLGLFPEPVGLN
3956	17857	A	3980	217	414	IYIFCGDGVSLCCPGWLKQSFCLSLPKC *DYRHVPPTSFHLLTNIGVLQFLKLQ ATLSFTLFL
3957	17858	A	3981	2	409	KLTFVAV*DY*EKLLLSLASLTSQAALF PEHPYTVISNPCSPANYIFTLSSGTFH QFYAKS*CVTYE*KKKNLLSPPTGDKPN *GRSQTKKIQTKY*SEICFFVHLFETGS HHVAQAGLELLSSRDPPPTSASQST
3958	17859	A	3982	234	416	SVLPSTPLLNKL*KSKKKKKKKKKKKK KKKKKKKKKKKKKKKSRGGAPKKK
3959	17860	A	3983	414	291	GGRACSEPRSCPCTPAWATERDSV*KNK QPNKQKNKKDLL
3960	17861	A	3984	192	415	TNANKLDNLDEMDFLETQNLRLNNEE TEYQNRPVTRREEIE*VIKNLLTEKKNPG PDGFTGEFYQTKEKLI
3961	17862	A	3985	403	145	AFFFFFFFFPGEKGFSPVTLFGGPPGFS PPPVFKTRPNFFLGPPKKKYSFPPGPG KNWFP*KGPPPPPPPPPPPPFWKLGI EVI
3962	17863	A	3986	255	425	GGRFKGSNFTSAGLQGFXXXXGPPKFIS RPGV*QRGEWKNPVGNLFAIISTSPFGR W
3963	17864	A	3987	247	2	EEAVRVSNLYTKLDEEQ*VVKKQLNYVE RLKK*ELFLQDLYRKVPLKI*IF*VKNL NSFWPDAVAHACNPSTLGGRGGWIT
3964	17865	A	3988	1	394	HHHTWIIKFFFCKDGVSLCCLSWARTPG LKRSSCFRLTKCDYRHEQLCPAFKHFF LY*HNFMSTEKMQE*HKNS*YPSPTVPK GVTFYIYISYICFIILILSAITYKFVHTY IVSLNHVCYSNEAPLSLNI
3965	17866	A	3989	208	402	ETDRRLKSGGSLSKTLIKMTCFVVFRD GVSLCCPGWIQTPGLK*SSCISLPSSWD YRHMPPCPA
3966	17867	A	3990	2	408	THRPYHATPTYLPHYTNMLIKGGKKKKK KGGKKKKKGPPPKKKHFSPPGGEKNFF FYGPQKKKSRGRV*KRGEKKNPGAPQNK PLGKNPLFPGEKKKKKPRFAS*PPPPPF SFGKKRAPPTKYPGAGLHP
3967	17868	A	3991	81	406	KGGLFLLPRGKGKGIWVKNLGLKNKK NPPA*PSEEGEKKGGPHQAGKILKFGGK RGLNKGKGTGQKLKPGGIPPPPG*KVGE KKEKPPAPGQKLFKKRKGQKKNF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3968	17869	A	3992	396	64	YSSPPPTKKTTDDSDASRGPPFFPPPEKRGFFPNDFWVPPGFFPPPGF*TPPVPFFWAP*KKIFFPPPRE*KFFFLKGPFFFFFFFFFFFHLQVLLIC
3969	17870	A	3993	367	193	KLWEKKKILWKKG*GEIKSCHCTPAWATRVKLCCLTKKKKKKKKKGGEGEIKKKKSFSLGKQKKKRGPAFF
3970	17871	A	3994	188	2	KRANTLPDFKTYKATVLKTLWYWRKDKHRSMKQN*ESNEVELLYHNIHRNKLKMDHRLKCCQ
3971	17872	A	3995	2	147	QENHLNPGG*GCSELS*HYIPAWATE*DSVSKKNYI**TSHIFSGDF
3972	17873	A	3996	23	329	RNSFIRSAFNVLNKVLFLTSEKKKKKKKKKKKKGGGRKREYLTRGAGENNKYFYK*KKKNTCG*KKKGWGRKREREKRLGGKKKFPPEEGKKKPG
3973	17874	A	3997	164	392	KPLGRAGLVPCLCSSFTGFLM*KTEPCS VVQAGVQRGHLCSLQPSMPFKRPSLLSLPSSWDYRVLLRHPWSAVV
3974	17875	A	3998	396	3	FFFFFFPPGGKWGISDPSQLFFSGVKNFSPPPPVNWGLRVWPPQKNFFFFFF*KKVFSFFWGPPNPFFFSLLGGPPPPPIFSGEKIPPSLFFFFFFFEMESCSVAQAGVR*RHPGGLQPPPPWLKQF
3975	17876	A	3999	383	2	VPSPEKVGIIKKIQPLDPFF*FLGDCQRKKKSPS*RPPEPPGKKLN*IRLGPFFNSKEKFF*KF*AFKPPFFPPKGEI*GFFSRAHSFPNQALFWFFFEMESHITQASMQWHDLRSLQPPPL
3976	17877	A	4000	213	1	RGRQNKTLFLTKPNQTKPNQTKPNQTKPTTFL*SVIEIRVKKYKTRKTTKNPTTSLTRSLGRYKSPTRP
3977	17878	A	4001	412	129	GSLSSPRLECSGTIPAHCSLNLPGSSSPCTSAPRVAGPE*MGQACMPCLPVNFFFWGGGGILVETRSC*VAQADLELLSFSDPPASASKVLEL
3978	17879	A	4002	411	293	RDTRCLPP*LDNFVFLVEMGFHHVQGAGLELLTSSEIA
3979	17880	A	4003	46	392	QDFFFFFFFLGKGAPPPEPKKGGTFFPKKKTGGGPRGPPLEPPPLGGPGPEPGGGDLKKPWPPQGTPL*KKPKMGGGGGGP*TPGTGGGGEKNPLTPGGGPKNGPPPPPGG
3980	17881	A	4004	360	1	KCLGFQFFFRFWNICIIFISQLSIASQVQKSEIQNAPMSIFFEHVSVFKQFQILEHFGFWIFILGMLSTYKTLILLKLN*RFNAMPINIPVVIFMEIDKLILKFTWKYKEPRRVKAILRN
3981	17882	A	4005	152	408	NKFVSEFYWMGNVLSRYPQFT*QFSFCHVRLPSVF*YLTRNKLIFFAHKAFFLD AKYVCVCVCVCVCVCVCVYFGIGEGNLP S
3982	17883	A	4006	411	67	YLPPSSSPTPGVFFFPKKEFFPNPFILGTPREFFPFF*KKPKFFFLGPKKKK*FSPPRGKKIFFFKRAPPFFFFFFF FFFFLGGSLSFMYFIKTYK
3983	17884	A	4007	217	2	PLFFFFKHLKAYYSDVIHISFAILRYLLF*DRVSLCHSGWSAVARSWLPVAGQNTF

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						ITRQEAPYLLAIPRV
3984	17885	A	4008	235	406	GRHRVSSNPISIT*RRRGLSLLPKLECSG VSIACHCSFDLP*SDPSASARLLGLRLR Q
3985	17886	A	4009	833	237	SLDNRRARPCLVSFIFKKGRSTAERCGAP GTTSPFPRLSERGHPIIPS*RGWERKS QLCSHLQSSRDPSGLGRAGCGGGDLRE SPGTTPGNGGSDLPVPTAPIPIEPQIC QATCAVMKLSFDEEYRRAMNELGECPRS SGKPSSSPRTGGSSAAKGTQAGSSELG LGIGARRGTDLSLHSTSHWTVTLGPL SP
3986	17887	A	4010	276	2	VEVKGNNSESEGSITLIPNPKQPKETT DQPLMSTYAKIESPGKNPSHDG*LI FDK GAKIIQ*VKNSIFNKWCWDNDFHVKT MNPHTLI
3987	17888	A	4011	188	27	REKFOIYTIKNDKGSITTDTER*KIIR DYEHLYAHKLENLEEMKLGIP
3988	17889	A	4012	1	202	CLHQKVIISN*L*ATTQTQLSLSFKLD YFSIIIPVALVVTWAIKFSL*YINSP PKKKEAEKDLN
3989	17890	A	4013	1	403	CLDQEVIIISN*H*ATTQTQLSLSFKLD YFSIIFIPVALFVTWSIIEFSL*YINSP PKKKKKKKKKKKKKRGAPLKNRGGP NFWGGGKNIFFFFGGDKPPRAFWK LFLGGGNLGPFPQKFTPWGK
3990	17891	A	4014	67	439	TELIIFYIFFETTLIPTLAITR*GNQP ERLNAGTYFLFYTLVGSLLIALIYTH NTLGSLNILLTLTAQELSNS*ANNLI* LAYTIAFMRKTKKKKGGGLLKDPWGGQ ILAGREKIKFFP
3991	17892	A	4015	3	260	LIVPTIILLPLT*LSKKHII*IINTTTHS LIISIIPLLFFNQINNLFSCSPTFSSD HLSHPILLKKKKKKKKKKKKKKGGGA F
3992	17893	A	4016	258	3	LKKIFSPPTINLFFPPFLKFFFPPLSL *FFLGVSFPFPPPKGFPKIPPGVFF SPPFKKKKFFPPPFYFAPPRVFFKGPP
3993	17894	A	4017	287	2	KKQKNFIFFFKNLSFFGRGAFFPPLFPP ILRGKGGDFYPRGLKPALGNQ*NPFSR F*IFFFFFFLRRSLAPVTQARVQWHD P GSLQSPSPGFK
3994	17895	A	4018	228	487	SYDVQKEKPNGI*ASKYWAYVFHSFFLS FFFFFFKKKNFFFCPQGGGQGNLSLRE PSPPGVKKLFGLNLSKSWE*QNCPPPI IF
3995	17896	A	4019	35	228	EELNHLNQGGEGCSEQRSHHCTPAWATE *DSSQKKNKFWYIHCNRIVTTTNTPMT ESPKHYAE
3996	17897	A	4020	2	402	ARGNLNTTFFDPAGGGDPILYQHLF*FF GHPEVYILILPGFGIISHIGTYCGKKE PFGYIGMG*AMISIGFLGFI*AHHIFT VGIDVDTRAYFTSATIIIAIPTGV*VFS *LATLHGSNMK*SAAVL*ALG
3997	17898	A	4021	1	420	TRGATELIILDLVETTLIPTLAITR* GGQP*RLNAGTYFLFYTLVGSLLMGL IYTHKTG*VNILLTLTAQEL*NS*AN NLI*LAYTIAFIGKIPFYGLQL*LPKAH

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3998	17899	A	4022	409	3	VEAPIAGSSIGLAAGLLKLSGYGIIRLTL LEMASCLIIICNNNNPFFYQIVTCDEKWI LYENW*LPAQWLH*EEASKHSPRPNLHE KKIMVPVW*SADGLIHYSFLNPCETITS E*YAQQINVMH*KLQGLQLTFINRKGPI FLHNNTKLHVAQPMQLKLNELA
3999	17900	A	4023	464	374	HLPPWEDKARRHLPDARTFILAFSLARN VRNKKFSLQATQFLVLYASSTKITKPLK TNQKKRLKKSEQLSRNMWTPIKRTNICI VGIIEGKEGEKGAERIFBEIVPQT*NL VKDIK*KVQ
4000	17901	A	4024	58	323	RHKLLCEHVKKCSAVLIIREMQTKTLK YHFLLVTAIKIFNLIHF*RSVGETLICQ WAGRNAKS*PFWRRIISQYLTKLYVCVCM YTHS
4001	17902	A	4025	480	150	RNSLLRRLRQEDGMSFGCQCSEL*LHH CTPAWVTEQDPVSKKKKKKAYPDPK KTDKSNKKGPDPFSRKNPKNPPPPWQ RSTAFRGRAAKSCPTH
4002	17903	A	4026	204	1	KKKFGALFFFFMQGLTLLPRLEYR*WCD HGSL*P*PPGSSDPPTSVSQIAGTMGVH HEFLRSGVVLK
4003	17904	A	4027	116	472	MPPLPKPVSGPRPHSCSPPLGCPQLSTPL TGPRPASLSLPISEIGICGCTAILWAVW YLVQLMLGLSLFMA*RGAGSSCSAHKKW WLGLASPSC*TFFKNRTKGRARWLPVI PALWEAE
4004	17905	A	4028	355	444	VSYKKK*SRPGAVAHACNPSTLGG*GGR IT
4005	17906	A	4029	410	181	ASIIILLIAVFFNNILSGQ*TITNTTNQY SSLIIIMAIKLGIAPIHF*VPEVTQG TPLTSGLLLLT*QKLAPCF
4006	17907	A	4030	49	474	PXRXFXCHIVTYYSKGKEPFGYIGMV*G MISIGFLGFIV*AHHIFTVGIDVDTRAY FTSATIIIAIPTGVKVS*LATLHGSNM K*SAAVL*ALGFIFLFTVGGLTGIVLXN SSLDIVLHDTYYVXAHFHYVLSIGAVFA II
4007	17908	A	4031	274	427	FFF*EMESHVSQTQAGLLGRNHSLLVPQT PGLKRSSLLSLLSNQYYRSGPHT
4008	17909	A	4032	205	393	TWGGFKNPSPGEG*IKKMHDFNEMFLQN CWKILFFGGGFFTQGIFFRAAPPINKNI LVWGGGK
4009	17910	A	4033	2	386	SEPLSRKKLYLSILISLQISLIITFTAT ELIIFYIFFETTLIPTLAITR*GNQPE RLNAGTYFLFYTLVGSLLPLIALIYTHN TLGSLNILLTLTAQELKKKKKKKKKK KNIGGPPLRAPSGAPN
4010	17911	A	4034	3	169	GLFLAMHYS PDASTAFSSIAHITRDVNY G*IIRYLHANGASIFFICLFLHIGRGL
4011	17912	A	4035	3	317	HASADAWAFIGYVLP*GQISF*GATVIT NLLSAIPYIGTDLVQ*I*GGYSVDSPTL TRFFTFHFILPFIIALAALHLLFLHET GSNNPLGITSQKKKKKGGPF
4012	17913	A	4036	446	194	KKKNQPGGPPPPPAFPVGGLIKRRFPPT PGKKFKFR*KFFPPKGGFFVRDPPPKPG CWEREKKKPLNNTDKWVILEGSEAGLF
4013	17914	A	4037	213	1	GMAKVKARFLPQKRQVRVLPNPPWVGKGF

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						PNSGKTETPFFFF*DRVLLCQPGWSAVAOS*LTASTFWAQAI
4014	17915	A	4038	307	36	RKGFFFSKCGEFKKLPGPPLGGWYLKLI FCQKFFHFKFPFGPG*IFLPPPKIFFI FSFEMEFCSCCPGWSAMGRPLTATSAC WAQANS
4015	17916	A	4039	2	372	NDTSLTVKSIGHQWE*TYEYTDYRGLVF NCYILPPLFLEPGDLRLLDVDNRVILPI EAPIRIINTSQDVLHS*AVPTLC*KTDA IPGRLNQTTFTGTRPEVYVYGQCSEICGA HRRSMLIVLELI
4016	17917	A	4040	107	279	LLLLFFFFWRKSLALAPRWECRGKI*GH CKLRLPSPCHSPA*ASPEAGTTGWTYGC F
4017	17918	A	4041	3	351	GSHYIAQAGLKNPGSSHLPASAAHSAGI TGVSHHAWLKIFFKESVSDYSPHLNSRK NAVYVSFFFWKKS FVFVPQAGGKGLNL GSLKFSPLRLKQFSCLTLPRS*EYGLAP PPPV
4018	17919	A	4042	1	385	RPRRPDIE*QERRTQEVLOAVAKKVKKE SQLPGTGGPKNVLPVPRAKAERPCKQA EASGLKKETDVLKVDQAQAKTEPFTQG KGGGQTTPESEKAPQVTESI*SSELVT TCQAETLAGVKSQEMV
4019	17920	A	4043	3	282	TAILIQT*P*SFTGAVILITIAHGLTSSLL FCLANSNYERTHSRIILSQGLQTLPL IAF**LLASLANLALPPTINLLGELSVL VTTFVSDAA
4020	17921	A	4044	2	407	GTRLEIMSRNHGIFPFTLEIFKDNEFEE PYREALPTLKLRLDSLYFGIEPEEHVSG* ESLEESCFATPTSKIDEVLKYYLIRDG* VSDDSVKQYTSRDHLAKHFQVPDFKFEG KDHKEVILH*RDLCVGVMDERSR
4021	17922	A	4045	4	380	ENWLTIIRQAWHEADRNLTTFDPAAGG GDPILYQHLF*FLGHPEGYILILPGFGI ISHIVTYYSKGKEPFGYIGMG*AMISIG FLGFIV*AHHIFTVGIDVDTRAYFTSAT IIIAIPTGVKVFS*LATLHGSNMK*SAT IIIAIPTGVKVFS
4022	17923	A	4046	2	94	ADRNLTNTFFYPAGGGDPILYQHLF*FF GHPEGYILILPGFGIISHIATYYSKKKE PFGYIGMV*AMISIGFLGLIV*AHHIFT VGIDVDTRAYFTSATINIAIPTGVKVFS *LATLHGSNMK*SIPTEILIFRPP
4023	17924	A	4047	376	138	LLARQRQENGVNPGGACGEPRSRHCTP AWATE*DSVFLWREALLTQTAPFNRLQ LLALPSEFFHFRILIVLQPHHSQ
4024	17925	A	4048	145	226	EPIQACSSRRVCEPIQACSSRRVCVCT PSRHALPGVCV*EPIQACSSRRVCV RAHPGMLFPACV*EPIQACSSRYVCV RAHPGMLFPACV*AHPGMLFPACVCD PIQACSSRLCVCV*ERAHPRLLF*ACVC VCESPSRHALPGVCVRAHPGMLFPVC VCESPSRHALPGVCVSPSRHALPGVCV V
4025	17926	A	4049	2	414	ADRNLTNTFFDPA*GVDPIYQHL*FF GHPEVYILILPGLGIISHIVTYYSKKKE PFGYIGMV*AMISIGFLRVIV*AHHIFT

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						VGIDVDTRAYFTSATIIIAIPTGVKVFS *LATLHGSNMK*SAAVL*TLGFIFL
4026	17927	A	4050	472	228	LTRDGGACPFPSKLFRRVRQKNPLVLGE* SCSEPKLCPCPAKKTKDYPVSKKKKKF IWIINRTKIPRKRKKKNKAYHKVKYF
4027	17928	A	4051	238	3	RRHGSFAPLPPGLPLCISYIWLFIITILC NILYLYFETGSRVVAQVGLKLLCSSEPP PSTS*STEITGMSHGARPHNIP
4028	17929	A	4052	225	172	IARYPFHIQSCNTMPPSPNKSITSKEEDN GPGAVAHACNPSTLGGQGGQITKSGVRD HPG*HGLV
4029	17930	A	4053	471	30	GPGGIKISGALFPLNKVKRVPVVFPRPP LIFFPQKGVFNQNGGDPGGGFWPGETPGR VPPPPGVFFVKSPFLSLFPFPPPV*KTA VKTGFPYRPGVPPRGLVFPKKKKSILN RPDLMSGPQPE*SLPLPGEPSVSHAGCL PQAWRG
4030	17931	A	4054	425	41	NWGSGLCPQKLGVFPPPPPPGEGGVPGA PPPARLFFFF*KKGFSVGRGGFKFLP PKNPPPLPPQKVGIEGGPRAGPIFSPP QLFFFFLTWSLTPSPRLCSGAILAHCT PAWETEQDSISKQTKK
4031	17932	A	4055	312	1	IKNARAHLLPQGSPPPLIPVVIETIS LLIQPIALTVRLANITAGHLIMHLTGS AALAISTIIILP*TRIMFTIIERTILEI AVALIQAYVFTLVVSLYLHA
4032	17933	A	4056	648	123	DDDPVPSARGCVPSGAPGRGAQLKKA WALALA*LPPCLCAQELPSLSLTGGPAVG LSVNSERDGRLEVSINAEFTVAFLKG TQSRRINGMPLPQREPSRYCLGLGGE SSAQGTSGLTGQRV*QNSDLPELASGDD KGQRSSQGGAVSQSSPRGRQIPSSPPA ALFNFL
4033	17934	A	4057	135	464	QHNSRLMQAKKGVTVLARVIDLDYDE ISLLHNGGKEE*AWNTEPLGCLLVLP CPVINVGKLQRHNPGRITNGPDTSGMK VWVTPAGTKPQPAEVLAEKGKENKECG
4034	17935	A	4058	3	575	LRSRPLHIIILSCGLLVTPRSLSPPPPPQ RLRLCRPSRGAAEFFFLRTKLHFATLP LRIEGSKTL*NCC*LYHGC*IS*IHHGG LFDVAAKNIIEHEVEKYDKQYRGKELLG FATYKTFEIIVHQYIQ*LVEPALSMLOK AMETIQAFINVANKHFGFFNLNQTVQ STIEDIKVKHTAQAEYMIQLQVR
4035	17936	A	4059	389	3	TFKGPKVFRYPTFFLCPPPRGFFSKNIW TPPPPPFFGVFPEREKIFFFLKGALPLF SFRVTPFFGLKRGFFLSPTPPFFPPPPF WPPPPPPPPPPPPPLRRSFALVTQAGVQ WRDLG*LQPLPPGFKR
4036	17937	A	4060	397	1	KRRGNFFFKKGISLFI*TPPRGPLWVFF F*KAPKGFCAKFPFFFPPLPKENGKTH RQKTPFPHFQIFKNGFWVLHAFSLGDF PARVWGPPFKRFFKGIFKEFPYPGSPPP KGPKKKKRTAARDLELADAW
4037	17938	A	4061	38	410	AWISI*ERPFTLVRVFNFLAISGLLFS YFRINFLYVQIHIHTFRKLFVLSYVFR FTDVKFFFYILPFFPPHFLFGWICSYAA L*FFIYFCFLPFFFNPGTSP*IGLFLLI

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						FFFKKPTFGFGG
4038	17939	A	4062	405	81	GGANVFPPQKSPFFGNKKGGHFFSYKILN NPGHPPFLKKKKKNAPGGWGNPWFSPPWK GAL*PKKKNPKKKKKSPPKGGKKKNP FPPKKKKKKKA*GDNFDMGTGN
4039	17940	A	4063	415	239	RPSFFFFPPPKSCFSTFFFLSPGFFF PPPPFFTPPPPPPPPPKKKKYFFPPPG KKFFFF*PPPSLFFFFFFFVFFFFF FFFFFFFFFFFF*GLTSPHKQIGLVLA FLALSKITHASIPVPVSSPSKKKKKKK KKKKKKKKKK
4040	17941	A	4064	95	241	SPCRSPHRWVNS*ANNLI*LAYTIAFTV KIPLYGLHL*LPKAHVEAPIAGSIVLAA VLLKLGGYGIIRLTILNPLTKHIAYPF LVLSL
4041	17942	A	4065	28	288	YFDIFVEARSPYVFQVGLLELLGSSNPPA SASQSVGITGGSHCAQP*VTILFTTCTL HVNG*I*CIKFLIHNIPILVISLQYIFG FFL
4042	17943	A	4066	338	134	PGGGCSEPRSGHYSHCTPAWQ*SETPSK KNKKKKITYFSVKNWGI R V F I E I I L N S F T T V R P
4043	17944	A	4067	26	365	WVSLMTSALAMRVDFYFTLLILGLLTS TLTIYQ*WRDVTRESTYQGHHTPPVQKG LRVGIIILFITSNDCEFFAGFF*AFYHSSL APTPQLGGHWPPGTITPLNPLEVPLLNT S
4044	17945	A	4068	491	174	TQLKTH*GSTTDNRTEVRVEPRVRTNYK DLLKFL*SKGYDFESETETETIAKLVKY MYDNRESQDTSFTTLVERVIQQLVLSHI FKDNYANINAEKLSGN
4045	17946	A	4069	210	402	NVSKGLRKVPSTQ*VINISCRPGVVARA CGPSTLGG*GG*ITRSGVRDQPGQGET PSLGPGAV
4046	17947	A	4070	202	1	DSAIALQPRQ*EQNSVSKKKIYRTIDLR SEYFARWSFTLAARAGVQWRNLGSLQPP PPGFKRFSHAS
4047	17948	A	4071	412	143	FLGAGV*PRLGPKG*TPPLLNQKLIGH GGGALYSQYFGGWGRNSFNPGGKGFTN QNFPPSLQTWGKKGVSFSSKKKKKTR KWGGE
4048	17949	A	4072	2	324	RRGNFCMF*SDRVSSCCPSWS*SPGLKR SSCLSLPKCWDYRFEPLYLARLVLMRCY STHNTYIMYQMQRLFQGHRYLSVSTSS ATRPYLDNFFFCCKNKVMPCCQG
4049	17950	A	4073	2	326	RRGRMLPRTPRPGNDAQQPQKHS�VD* LFIYLFYFLWTGSHSVAAGGQWRNHGS LQP*PPSLKGSSRQSAGRVKGVSHCAWL LLDFLSFGKPYTYKKVDKVSFEA
4050	17951	A	4074	422	116	EIKQEKNPFPFFPPPAKRGFFPTPLI WGPPGFPSPFLKRRQGFFLGPL*KGN PVVFPKVFVFWAGPPFFFSFKKKEFF LVFQSTFIHFIFHICYLL
4051	17952	A	4075	3	294	VFCHVGQAGLELLDSSNLFVSASQSAGI TDTSHLT*PDLSFCCKTKFD
4052	17953	A	4076	60	389	PSAQLGSTKHIHMAVQP*PPSPPELLHL PKMLLCPHSAHTPRPPNPNGTVCTYSPR SSPAFPQEGPSSGEGGLVLSLFSPPN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						HVHPAPTSPESGRGRGVRPREGAYV
4053	17954	A	4077	93	385	KPLFAPGVLFGGPGEPKREKKGGAQGGP KKFSPPPPPFSFPPPKTLWVAPLFQETQ GLRLCPPFFF*RGKGALF*KRGGRFRKP PPPPGLLGPPTP
4054	17955	A	4078	2	365	RKVEGRVS*DEDLKLTLLRYMLNIEA AKDLLYRRTKALIDYDNSNKALDKARFK SKDLKSDCAHPRDC*RA*APYFLFAKNE LVVPTGEQRHFLQDVPLIVQRTLTLP DHTSLPLSL
4055	17956	A	4079	6	298	PLAIMGGFFTLAETNRTFPDLAEGESEL VSGFNIEYAGGPFALFFIAEYTNIIIN TLTTTIFLGTTYDAPPR*LSPSLFYEE PPSPYPTPWSTST
4056	17957	A	4080	414	154	PIPATREGKAGNSLNPEGEGCNKRSRH CTPAWQEGKTPSQKNKKVLLALKV*SI FHLMES*KYLPKPGFSLDLITVIPTYFDL FRC
4057	17958	A	4081	347	1	VLKPRPGNIIFSPKKKKNLPPPPGRNYF FFFPPLPFLFFFFFFFFFFFFFFFFFFFF FFFFFFFF*RGGLLLFRLKIQLPPTPHP YLSNTLRGWNPGEGSCWRSEGGRGEDCL QDH
4058	17959	A	4082	1	354	STFIISLFPTTIFMCLDQEVIIISN*H*A TTQTQLSLSFKLDYFSIIKKKKKKKKK KKKKKKKKRGGGGLKKKFNGGGGKKF FFWGGKKKNWGGGVKKPGGKKRGGKKK KGGGEK
4059	17960	A	4083	384	85	FFFPKEFFGCPFFFSPPGFLTTPPLQV LEFPICKKLSPPPPPLKNFFFTTPPPFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFLLM*AKKFISWR
4060	17961	A	4084	1	122	FHRFGRDGLDLTS*SARLGLPKCWDYR REPPRPAFLPOP
4061	17962	A	4085	223	401	NGKLVSVFFGFCFCFFEM*SRCVAQARV QWRIFSSLHFLPPGFERISCLSLLSRW YRC
4062	17963	A	4086	160	408	ALPFRGGGGAPSFNFCLLPGP*GKKG GYGDAPSCRSGLGQHGETAAPLKAQKSF GHGGRGYQVRRRVGPPGPGRRQKLN EGAPPPRLGGKAAP
4063	17964	A	4087	261	81	YDIDGRIFCQKLESSHYSPGAVAHACNP SPLGG*GGQITRSGVQAIHPSWPPEVWG LQA
4064	17965	A	4088	428	140	QPLKNPPLGGRAPPFLRGKKLPPPPQ EPPPF*KKKKKRGGGPPFFPPPPRGE PKKSL*PQGGGKKKKSPPPPPQKKK NPPPKKKKKK
4065	17966	A	4089	1	205	FRLRQENCLNPGGGGCSELRSHYCTPAW VTEQETLSQKKNFN*KTFKAKSTGNF HMPNTSIQQLPI
4066	17967	A	4090	154	410	ITGCSIIKYFYRAMREREKSEVGYFPSS SINTPLRHLSDGVLSRITSLSTHSPA PFIKSKNRPGTVAHACNPSTLGG*GRL TK
4067	17968	A	4091	428	67	LPHPPPPPPPLSSSSSSSSSSSSSFP PPPLPGQRTLTPLPAPAGQLGSRES CGAPPSSLGASLHVA*NADGRQ*RAALS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4068	17969	A	4092	431	3	TPHGPLTGSPAARWRGRREQDLLLLCS APTSNKGSTIPILQIRKLRAATPCSSIGP SPSTLPVKLEL*SVLLPGQWLNFSFCHF FPRPKCSNRPRYTLPVKLPSSGLPPRP SPSQQVTAFFPLTSRKEFPSSPTPASDA FFFPAPVSARRQEVLCESIPSVTMHE
4069	17970	A	4093	151	1	SIMPMWMDAVAHACNPCTLGG*GGWIIK SGVRDPPDQHGETSSPPKTKL
4070	17971	A	4094	35	363	LQSKIYCTFFFFLERGFFFSRVRGPGA HPGLGAKTTGVKGNPPP*PPKGGDPGGV PPPPGCFWFFLLGKGGFLLPGGG*NFG KKKKPLVWPPKGGELKGGTPGPPPY
4071	17972	A	4095	376	1	LGKSPFFLGAPFFLLKGSLLGLLKGKF TPP*LGGPHPLEKGPPLGQWNPQKVVW KRGFPQKGGENPPFFFFFRRDGASLC CPGWPTPGLKQSSNLSLSSWDYRCLS KSLFKENTETLAS
4072	17973	A	4096	65	446	PFFLFFLNKGPLFTPKRQGGKPRNFPT*T PCPRGKKNPPPPP*GGEKRGPPPPGK FFFFFGERGFFGGGVLFLLDGLTPLLGPL KGGEKGRPPGPGPKPFL*KRKKNSP TGGERGRGKKHCLP
4073	17974	A	4097	34	387	IKEADEYVLTIRLACVFGDMEPLSSPHR LHTRIGSSPSTTCTPACPCSSW*HGAS VIPSQYAYEDWFITLYNVLYTSLPVLLM GLLDQVGASHKQGHFWTDENALEKSQAN VSMHSSGVYFFLIKPYNSVVRHQGSWL CFLFCNKERGF
4074	17975	A	4098	80	422	ILHVLYTCIILCFVLQS*ILWFLVQNYI LHVLYTCIILCLHVLYTCIIMCYIHV* FCILALFAGLS*DSPYHESL**SFFMEA DISLCRCVITDQLNFI CSLQH*ELRMF QF
4075	17976	A	4099	74	402	IYLLSTHLHYQFSWISITFDISFFFFF LKKESSLFPQGGGGNGLLKP PPPGE SPFPPIFRGGGKKGPPPPWVIFFF* KKGGSPIYPGGG*IFGPGDPPPPP
4076	17977	A	4100	3	335	DAWASAWTEYDSVSKKKKKRGGGKK KQFPKKIGRGSFLFKPRGGEKPLSLKTP PPFF*F*KPPFKKGAEPWEPFLKPPF CLKDRGGAPKIYFFPNPPGAPRGAFFIK RGGGK*GPPGGLL
4077	17978	A	4101	406	1	RFPKFPKPKMSKWLK*KGFFPRE LLIGPPPPPKKKKFPTLFFAKVLPPR FF*NFNQVSKKRPTPLKVGQ*PPMLV QKKPTRGFPAFLKKKKRSSLVIREIKRK PTMRYHLTPIRMAVFHKSNNRC
4078	17979	A	4102	2	183	VNPGGGACSEPR*CLCTPAWVTERDSVS KKRADNDKQALRSFPLGFPPFLPLHPT SFAF
4079	17980	A	4103	119	391	DNLCQFFFFWKRGLLFLPRGGGFKSTG PFSFGVPGTPPPPPGEGGLTPKPPPPG *ILFFLEKGDFFLLARVV*NRQKKKNPP PSPPKGG
4080	17981	A	4104	413	64	GFKPPPKDPPPPPPQKGGFMGWRPPPR PFAPLFSPPPPRGGGGIFP*GGGGGAKK FHIWPGF*KKPPPGG*NSGGQKNPPG GGGNPPQKKKKKQPTTANIWFLCLEI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4081	17982	A	4105	2	196	LSGM RGRVGKVLISLFTNTDLLWLLCILICFHK TQ*LCNG*CHSRMKVCVCVCARVCVCV CVCERERD
4082	17983	A	4106	1	335	FLVET*FHPVGLAGLELLTLGDPPR*ST LGDPKCWDYRCEPLDPASVSFFLCLKLF IFVLLKLLFFFKPPLYSKLTRGRDNNYN YFPPPNPGPLPHWRADKSIIGNRRLL
4083	17984	A	4107	1	148	GERGCSELRSCHCTATWAAE*DSIYKKK KKKEPPKFFLAGFSGGGKTP
4084	17985	A	4108	331	41	GLNFLAQKFSGRFSPPPGRVPLGPKPF FFLGKPPILEGFPGP*KVFFSPILPPKE VLTFSPGGEKIGPPFSGGACSGFPKPG AKKKKKRPSN
4085	17986	A	4109	137	3	TKKERNINRGP GAVAHTCNPSTLGG*SG RITRSGDRDHGQHG
4086	17987	A	4110	3	269	GFHRVSQDGLYLLTS*SACLRLPKCWDY RHEPPHPGFLGFFCFFFRDSVQPGQQ SENPSHKKKDEGPFWKAGKIFLFPKN SSAL
4087	17988	A	4111	196	330	GAIARGRSNCDCI*GSVGHVL*NDPTLN CILDDQDTLYGSIMINEYERASDAWALL PDEEQLPEGDQTVIA**A*DMSGGQQHR VSLARAVYSGADVLLDDP
4088	17989	A	4112	426	241	LLKRVREHILFTIRGKGFSEPRSPCTP AWATERISVSHKEKKRVLVRP*VDLSN SSLSVL
4089	17990	A	4113	394	1	GPGVFPSPGCLYHARAQYFWPHKKKKYF PHPGQKNSVFLKGRPLFGFGFLLIFFFF LVEMGSCCIAQAGLELPTSNNPLTSASQ RAEIKDVSHRSQ*FFVFLFETGSCSVTQ A*VQWCNHSPTPTGLKQF
4090	17991	A	4114	328	2	KKRAHPDWDTGTIEVPSNPSNIRFLGA PESFFFKRNLPQGDPLEKPNPCYFFFG VTTPPPLFPFPKIFFFFF*DGVSICR PGWSAVARSQLTATTHLPSSSDSP
4091	17992	A	4115	220	3	FKKGEPGDEPPVWVFLGWVWVWVGGFFF ERHSFTLVTVQGVQWCNFSLLQPPRGL KSFHLSLPSS*NYRH
4092	17993	A	4116	342	2	PINFLYLSFNPNQV*RSNFSKILHFCF KILSFFYTALFLPFSSQLIRQSFFRVYL INTICFLQDLYLYILNLYLILFLFHL ASRLDFCLFFVFETVLLCHPGWSTVAQ S
4093	17994	A	4117	124	352	TSGFT*TRMKSKIPT*RSFIIDLEAKM KEKFLKAARETQLITYRGTSIQMPVDFS WRKTEAKAQWNLMFEVLKEKNCETRSLH PATMSFRNEGKTKMFSDERKL RDSVILP LKD
4094	17995	A	4118	11	387	KTGKLLATSAPGDGIMVMVETFCVLVVSF FLSVSKKKKNPLPQIKNPLPKPCNVFK RAPTPNH*KAFPGPKTPP*KQPKQIP CRPPKKGPFCI*PNPBNPSPLFEKKN KGKAPPFKNSKQK
4095	17996	A	4119	2	407	NTFODQSGSSSNREPLLRCDARRDLEL AIGGVLRAEQQIKDNLREVKAQIHSCIS RHLECLRSREVWLYEQVDLIYQLKEETL QQQAQQLYSLLGQFN*LTHQLECTQNKD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						IANQVSVCLERLGLSLTLKPEDST
4096	17997	A	4120	157	2	LTGSHSVT*AGVQWCKHGSLLPRPLGSK RSSSLNFLYSWDHRCGPPhSANF
4097	17998	A	4121	3	168	IALKSGRKVDIRELGHVVC PGWS*TPEL NQSTCLGLPRCWDYRREPPWALANMF
4098	17999	A	4122	2	376	ETGFHCVSQDGLCLLTS*STRGLPKCW DYKMREPPRPADGFINIRDFNPLRLTST CCCHVKKDI FASPFTMIVSFLRPPQPCR TDPIQNTLPLVIMSPVALLGCD SFSAFP VLMNLPFSSDCTK
4099	18000	A	4123	11	221	GTQLLLRLRGEDLLNLGRGGCTEPRLHH CAPFWETE PDPV*EKKQAAKAKNSLLTA ALLKTQVKKDSVAW
4100	18001	A	4124	2	125	AIKKTKSNRWW*GCR*RGMLVHCFWKC KL VQPL*KAAWRL
4101	18002	A	4125	425	152	TPVILALWEAKAGRSLEPRS*RSAWATW QNPISTKKYKK*GGRTSAWGG*GCNGL *WCRSTPASATETPSQRKKK*EKNLFT LILKVIK
4102	18003	A	4126	3	99	CQAGLELLTL*SDSLRLPKCWDYRCEPP RPA
4103	18004	A	4127	396	58	ENCNPLSWSGGIISGLLLVSGYSNKFPS FLVCLLPVIGPPENTAGPSLVPGTKWHD HSTL*TSQTPGPSLVPGTKWHDHSA L*T SQTGPKLSSRLSLPSSWDYRHKTPYPA H
4104	18005	A	4128	51	549	LGQSYLLLLLRKCF SFNFQVGDLDISYIN IBGITATTSPESRGCTLWPQSSKHTLPT ETSPSVYPLSENVEGTAPP*AHQSFMS P PSWGGSPNLNFFGGGGFEKEQSPLKKKS FTLYPLGPPSEGEHF*PSPLCFPPGFQ SPPKTGIPSGDELGFF*TPGPDKKK
4105	18006	A	4129	97	362	RK*SACLSLPKRWDYRHEPPRPACSC
4106	18007	A	4130	376	279	DQDDL DLTLS*STHLGISKWDYRHEPP HRAS
4107	18008	A	4131	133	344	I I F F F F * N F V L Q A G G Q G N L G S L K P P P P GLKQFLGITFGRSWDHGPTSFTRANFCI FRKKRVLLCCPGWS
4108	18009	A	4132	164	3	MNEMSYESSLLDHLLKRQ*NQCCLGSSE PSPRLKQFSHLSPSSWNYRKT SK
4109	18010	A	4133	355	2	GKKQNRKTGNFKTHSASPPPPPKERSSS RATEQSWMENDFDEMREGFRRSNYPEL REDIQTGKEVANFEKNLEECITRIPNT EKCLKELMELKTKARELREECRLRS*C DQLEE
4110	18011	A	4134	193	357	HHCNPSLCQNDLFWHLVLSPTGVQWYN HGSLQP*PPGLE*SSCLSLPGS*EYRH
4111	18012	A	4135	357	104	LRRL*YENHLNPEGGGCSEPNNLRCTPA WATEQDSISKIIII*CNFLH*QNMQKI KQNPKTNSKILTEIKISLKGNLRELRE
4112	18013	A	4136	179	381	DTSLHIQNRLSISKKL*TLFYIY*DR VPLCCPGWSAVVQS*FTAALTSLKRSSC LSLLSNWDCRC
4113	18014	A	4137	89	318	CLEISCTKIGQDLYTENYKTLGKVKC PNK*NTTFMDQAEVSIKISFLPRLIYR LRIIPVRIPAGIFVEILKFG
4114	18015	A	4138	315	60	KKLPAETHAPLAEATD*AELKPAGETH AEVQAPTEQTPAAEAATTIAEASVKVQP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4115	18016	A	4139	377	51	PPAEASLAKFPAEIQQPADQERGSEDI GFTSPFPED*RIPGLFSCIGWTIQSFHF RNIGSVFPSPPGFFFFPQEMRVLLCCPG WSQTLGLKPSSCLSLNSWVYRCAPLVP GMPIF*LSCFLAIGFLEFVIYIGY
4116	18017	A	4140	413	175	NFGIFCRDGVLLCCPGWS*TPRLKPSSC LPKCWDYRREPRTVPGLPFLFLNLRKDG NSVLEIYLEYKITQIIVQRLLVL
4117	18018	A	4141	1	394	EIFVTKRWSGLGVAHASNPSTLGG*GG QITRSGV*EQPDQHGSPPERGLKERRGL MVMKATFLGLRHHLEHTVGHRELRLHN NSKKKISSHPLSTPHVPGTVLKPCLRLIL CFKHQKPVKPPNSPSYR
4118	18019	A	4142	22	376	LVNKGKTIFFFLKRGVVLPPKGKGRGIN TVNGSLNFRGQGNPLA*PPKKPGTKGGG HNPGEI**FFGKKEA*QCGPGSGIPGP RRPSGLTLQKGGTYGREPSPLPGPTKEN PRLTKT
4119	18020	A	4143	161	1	PIPAKYEHFCFFVSLF*DRVSLCHPG*S AVV*SQLTTASTFQGSDDLTSATP
4120	18021	A	4144	18	159	KHLDPGGGGCREPRSCHCTPAWVTAKL HLKK*K*VELKSPSVIHT
4121	18022	A	4145	383	109	LFFYKIQNYTGHGGPCLLTPFLQRVKQK NCFNPGGGGCR*PKLVFCPTWGKKQGF VFQKRLKKPKPKPKPNWRGLFLPPFS KRPKPKI
4122	18023	A	4146	374	164	QCQLLRSLRWEDCLSWG*GCSEP*SCP CIPAWVTARSCLQINKSLPAEIVIPSLY NQIARG
4123	18024	A	4147	25	375	RKKKALFFCQGGSQPPPSNLMDDPPPPGE KKISWLNLFPKKEKKF*KKKKF*KVK KNPFLKPKGRPPPGKKKKGKKKPTPO KGKGFLLFAPPPKKPIKKSPHFKIPKKQK NFWQR
4124	18025	A	4148	376	202	HYNSKVFPGGPKRSFLFLKALSFFAP APIPFWLHSKIFFFF*DRVSLCHPGWK LR
4125	18026	A	4149	3	144	LFCDWTPTPGLKQSSHGLPQCWDYRH *VTVPGLPISFVFFFP
4126	18027	A	4150	3	188	QLQSQLLSSLRPEDHMLGVEGCGKLSL HHCTLA*MTE*DSIS*KKILKKCF*KK HSFLY
4127	18028	A	4151	83	358	GWARWLTPGIPALWEAKAISKLEDLNA* A*QTYAPS*EESLHPIMNTLIRDVVVT SFRVTVDTSTIARHWLFCWDLQASIGH ILILGPG
4128	18029	A	4152	162	1	TVWYWHKNKLSNQWNKI*FLELDPITYK HLVYDKTGISNHWVKDALVNTQCRA
4129	18030	A	4153	369	20	FQLLARQROENGVPNGRGAFG*PKSRPC PPAWGTK*DSVSKKKRKKSCFVHRIL KLEAYHSLGSNTAQLFVSCFHKILC LSISIPDPYLQFKMWVPPSPKPLYQIDW VGLL
4130	18031	A	4154	117	2	QIFFFFFFFKMESSHIAQAGVQWRHLGS L*PLPPRFKR
4131	18032	A	4155	369	217	FFSPPPFFKPPPPPKIFPP*KKKNPPP PKKKKIFFFFFFFFQTP
4132	18033	A	4156	214	283	ASPSEGQGLSSGP*GLIN*SDKPSVTHS

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						PKPHCETA*GGTSFLSSSGSSPQAPKSP HHGPDSPLSDSIPMVISPEPPPLRAKG CPQGPFGASWWGTT
4133	18034	A	4157	319	712	QDFVSKQHSYCLKNLKSSSLIQVAMNRA QVCLISSSKSGERHLYLIKVS RDKISDS NDQESANCDAGNNFICIMLYKIWLN*K RLMK*HWTAI*LKIYFSNKMKFSNLNLS SVINSFDVKERLNLNANTLN
4134	18035	A	4158	183	369	LKRKQSQRGGEVNF LKVTQPECGKAGILF IYYFFEMESHVSGQTGVQWCNLG*LQPL PPSSD
4135	18036	A	4159	190	336	DPISIKNFWPGTVYFLIETGFLHVG*AG LELPTSGDLSTLASQSAGITG
4136	18037	A	4160	10	390	QGILLPCFMSSEERGRISNTFSFFFF FWKGSPINPQGSQAKKER*REPS SGL TPQRPNGGPPPPPGQNFFFKKGG*PG GPGRA*TPGPRGTPPLGPPKAGNKRGGP RGRAKNFLKNQNGPT
4137	18038	A	4161	53	376	YLF AFFFFFSKREAWQGGQPGMEGAKKFF MAP*PSKGGGGEFSGLTTPPNQWNPRAQP PPRGELILILEKKRPAPNAQPGPENLGP REPSPLAPQKGGNKENPWPPPP
4138	18039	A	4162	1	356	GVFTILVSFNFAFFLSFFFLGKQILVLM PQPESQGNLAPQNPPPG*RGFPALTP PRTGNKGMAPQAPQFFGFLKKGGF SHGG QGGFKTPTLGNLPP LAPQGLGNNGLGPW PPFFFF
4139	18040	A	4163	345	26	APGFKPALGPPGGPFFSKKSKNLPLGR GSTLQAVGPTFLGG*GKRSLKPPGG*AS RGPWGPPSPPPGGPN*IPVSEKKEREGK KKKGREKKKETFSNNLIFLSF
4140	18041	A	4164	18	284	TLQGTSGIFEGNFFFLGTGISLYCPGW RAWGGDHGSLQL*PPGSSSPASTPLGRS WDYRHVPPGWASFFFKTLPNGVTQAGL ELWG
4141	18042	A	4165	377	30	FSGKKKFFQLGWGCGPPPLIPPLWGV*P GQPPRVGGFNPPLPWKNPVFFKKPKQP GVGCASPYSPFLGKFRPRIPTLGPESG G*PNFPPPPPPWAPKKNFSPKKKKFYN CLW
4142	18043	A	4166	305	1	ESRQVLT SRLTLLSIHEFNLYLLNNSTYK HITS LPI NIRQYGD LKTLKKETKDLNK *GNIPCLGIGRINIVKMSLLSKLIYKFK AMPVKIPGELFLRNQQA
4143	18044	A	4167	394	78	BGKKQGRKKGRREGS*EGRREREKTR*K AEKEGMKEGGREGKKEGRKEGRKGRKE GRKEEGQKGGRTDGGWWVLRSLDTSQLI SFASGPKWREASSLVWASLCL
4144	18045	A	4168	1	431	CNTCVR*CAYWCV*MCGERLCWCVCSCN RVCCV*VERVCVLVCMVWCVCVCCARQ CVSVCHSRIESSRPSSGVPAPSKCQTHL YLPKLSAPPAAGLWDL PSEATASLSGSL CQPSCPRTRS FATLVSSMYHRPVTGELQ SIT
4145	18046	A	4169	3	423	YNAREIEAAAGRDHATALQPGYVRPCL KKKVLKLGQA WLA*F* NFFETGSHSV PRLECSGVISACCSLNLPGIV
4146	18047	A	4170	118	402	QICTCTPKPKMKVKKITMLSNMRYLYI

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						HLTQDI*DLDDIDL*NTADMNLKDLNK*R EIHCLRI*RLNIIKTSLFLKLPYRVHAI PFKISARSFVE
4147	18048	A	4171	404	285	RGCCEPW*HCTPAWVTE*DLVSKNKM QNDNLSHLSLA
4148	18049	A	4172	274	431	ESLVGQRNWVAKYFYRITAPGRAQLMP AIPAPWEAEVGGSGGLEIETLL*NNSSR PGAEAHACNPSTLGGGRGGRITRSRD*DP PGQH
4149	18050	A	4173	24	366	FLCLFHTCVLAFFVQQLCSVGWGCKVEN ADREEKQPCDSQAREEPRLCRRGFNRAP NINTRHEKLFVCLF*TSHSVTQAGVQ GCGHSSPQQLPGPKRSSHLSLRSSWDT GM
4150	18051	A	4174	397	1	TEPVLANETWGPWDRGPLGLGGLGPENT DNSHAVGADQLLKEPPFLSTRSIMEPM SLNAWLDSPHREMQAGTPLSLCGDTYET QVM*SWGIRGILPQQPWKMGASLSLTAS LSLSFAHTLKKHHTHTHTLY
4151	18052	A	4175	90	387	KGRWLFFPQGGGERGHNG*TAPPQTGGKE NPPPPPPKDRGKANAPPPGGIWLKKN GFFPIGQGGPEPPPPRGPPPPAPPKGGE KRGGPPHRPGKKLLK
4152	18053	A	4176	398	280	RRLKWEDPLNPRV*GCSKP*SHRCTPAW VTE*DPVSNFF
4153	18054	A	4177	253	395	LENFFFLVKMGSRYVAQAGLKPLA*GNP PASASPRAGITGGSHTQF
4154	18055	A	4178	366	48	PWASPGISLSFSFLRTKPTVKVR*YRVG PQRQPCPSRWAPPACPFMSFPPAWVSPP GSAASRPDRHAGSQVGATASPPPAQGLG APAWTAGLGEKQKLAARMGT
4155	18056	A	4179	44	413	GDGVNSAFFFFFFFLEKKVWFIPPGGGPK PEFGFRAPPPPGVKKIFGFTPLRTGE*R PLPFPFGKGF*FKKNGGSPMWPGGV*PS DPKGAPPPGPPKGE*RGEPWVGWNF LLKERKPLFKE
4156	18057	A	4180	396	235	HEVSLCCPDWS*TPGLKYSSCLGLPNCW DHRCRNHGPCKTQLEQGHQVAGLSR
4157	18058	A	4181	85	408	YTCSLRITQDHFFFFFFFLGKKIFFFPP GWGAGGQILTSKTPPGVKGIPLNPPR GGGPGGPPPPPTLFLGF*KKRGFPGGGQ KPRPKGDPPLPPKGGGLKGGPTP
4158	18059	A	4182	1	149	NHLNL*GRGCSEPRLHCTPAWVTE*DS VLKKKSYIHLGQNPTVRKVL
4159	18060	A	4183	310	3	ATAPSQFIRIN*RNHCHYIEVQSEASA NLETAVNNPENLGKIMDEGG*MKKQIWK EMTSRIFIVEKSMFGKTSKAQALILGA NIAVNFRLLKPMIYHLEN
4160	18061	A	4184	1	359	PTRPLVLDLDRPPFFFLGSGKKKNPGV FLYFGGWTPPKKKNSLWGGGGLKKG GGGVFFKPLPFLGGGPFLKNSGGVDKKG RAPFFFTKTPL*KKPPPPFPKIFKARG FW*KMGEPPFFCPPPPSFLKKGPPPKKE GV*KKPPPPFLTPPPNQGNFFFWGG STPPQNIKKPLGFFSSQTPKKKKRAADR DLELADAW
4161	18062	A	4185	1	362	HFTKYLFISSC*K*LLCWMQDCCKGIP MNTNVIQEKATSLYGLKHKEGEPKAG

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						EFNASKGWLDFNFRKSFQFKNVKITGEAA SANQKAADKFPDAIKKIIIEKGYLPEQI FNAGESAL
4162	18063	A	4186	366	47	AALFLVDPPGRGGVKGPPPPPGPFVFF QRRGVPLPLSPGGFFFRPPNSPPPGPPKG GGSGGGPRGPA*THGVFLKKNPPNCGAG KKKGFFLKKKKKPKVFFVFSVK
4163	18064	A	4187	394	112	KNTENLKISAWWWHVMVSAPNEAETGG STEGTGCSKL*SCHCTAWVTVRETLSPR KFFKKRANYLTFRI*KVCSLYHRKTKNS FKKHTQGRKF
4164	18065	A	4188	230	372	KPMFLPFNPAILLLGIYLKEYKSF*HKD TCMRMFITALFTITKTWNQ
4165	18066	A	4189	149	2	NRSLRFMRFKEGSHLPPI*VQGKAASAD VEAAASYPEGLGKTINKGGST
4166	18067	A	4190	2	159	MHQPWLLRRPKQENCLNPGGGGCSEPRS HHCIPA*ATERDSLKSKKKKGGAF
4167	18068	A	4191	180	415	LGFLQLLLFVGRSMFIFALELSHGWLGS SLSF*PVCVKQSSHLSSSWDHKHMSP YPANFCIFCRDKTLPCCLGWAQ
4168	18069	A	4192	424	41	PPLLRAAPPKGLL*PKNSFPFGAPP*IPF PPKKIKIFKFTPGGGGAPLFLPRQVKA EGSLPPRVFGPPPPFFPPLPSPLGAKPN PFFFFKKKKKKEWLHKSLSFYSAHFVLC LKYSLSFFYQSVKTK
4169	18070	A	4193	105	424	ELKRLVLIKIRGIPEKGAQCKEIQKLA QEVKGEIFMEIGSLKKQ*KIQETLDTL LKMQNALESLSNRIEQVEERNSELEKDV FKLTQSNKDPSQIKKKILYNV
4170	18071	A	4194	3	240	LCLQSOLLGRLRQENPNLRI*GCNEP* LHHCTPAQVTERDPVSKENKGSFIPMKI GKLVSLTLNRMCKNCKNSEKENV
4171	18072	A	4195	385	1	KMIILTCKMEIKHKDEKELQKTEVDLKI ENNTTRARLTNNIKKKPPESEKTNKTNH TKKSL*DQDTKKETRPQKKKNPFKSR*V RHWRNILNLESNRNGKKNPSGVQKRDS VPTLITQTQETWWWCF
4172	18073	A	4196	3	272	LFYLIMALKHKSSDVGNSNIYAKEKLES ASFKERI*KSYVEVAKIYGKNEYCIYEI VKKEK*IMHSIYRVQYYLQFQTSLEVLE RIPHG
4173	18074	A	4197	236	379	GGRFKGSNFTSPGLQNSFFMGPPKLS RAGV*QRREGKNPGVPQFNR
4174	18075	A	4198	375	1	NFKIPAPPPQNGKPLRVGTPPFLIFSP GSPPKSFPAKWARDRPF*NPGETLQE G*VFFSGRFFFFFFFRDRVLLCHPGWSA VAQSRLTSSDSRVHTILLVGRGCSEPR SHHCNPWVTRVK
4175	18076	A	4199	1	270	PSRTGPQIPRRPTRSNCPNQFLGF*GCG EPRSRLCTPAWATEQDSISKKERHGLLV FLKGFHYIRLLINLFAARGKRVLFA GGREMW
4176	18077	A	4200	388	1	PPGIINLFDPL*PPPPWVMGPPPS*KL ISPQKKKNKVPFPVPPINIFSGPPPTL VFWVLFFVSLKRQLIL**KSGVSAASLV RHDGAPRLTSSAGKGHAETPQPRPTH RNACSFVLIHQSYKVF
4177	18078	A	4201	298	158	FKIVINFQFLTPIFAPSEGGRCG*GRGE

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						LRSCHCTPAWVTE*EPI*KRKIKGKKRT EQESRRQNL
4178	18079	A	4202	128	358	KLMIPSPGQPPRPGGRWGHPARPAAPSGR*GAPLPGRPY*EKRIPTARTPRLGGWPSMSLRTGHDDNGGVWE
4179	18080	A	4203	406	1	FFFFFLRQSFTLVAQAGVQ*RNLSQQP LLPGF
4180	18081	A	4204	322	2	KPRPRKTPGGPFPI*GGGAPPPRGAPKGGSPPPPPPPGGKGGKKNNPPGG*KPWGGFFFFPPF*TPPKRGFLKKKKTQNPKKKKGGRSRYRTSPRV
4181	18082	A	4205	3	127	GFHRVSQNGLYLLTL*STRLHLPKC*DY RSEPLCLACFLFL
4182	18083	A	4206	1	216	GFRRVGRDGLDLTS*SACLGLPKCWDGR*PPRPAHLGGNSNAKEPLPACPLLSGHMHRVWVRWATATL
4183	18084	A	4207	427	0	LFETTNNFFWARVFFLPFFF*NPPPGFF FLPHKKKNFPPPPGFFFFFYAPPPFF FFFFFFFFFFFFFFFFFFFFFFFF PVVLKTVVSC
4184	18085	A	4208	2	404	PRVRLGIWCKERLFLCYFFFFLERGFCLAQGGGPGGNFG*RAPPPGEEKIPGPP PRGGGEKGPREGPKRIFGLKKGGGPGF GPGGVGPPKKGPPPPKPKGWGYGKPP AQKRGGFFFGKKRAPFFNWVNG
4185	18086	A	4209	40	412	PLFCLSEKPRYFEYAILMLSLKFLESC IMSVNSSAVSASVYYY*W*KIEREPLTSW TLEKLDPEVFHQKFAFT*RAKAILRKKN KFEGTLTSGFKTHYKTTIITTVWY*HKD TQIDQWNRIESS
4186	18087	A	4210	219	392	HFFFLNYNFLGKGVSCFPAEGQGRNLG *LHPPPPGLKQFFCLTLRNWNHRLVPP PP
4187	18088	A	4211	409	2	LERKTVFFSPPPIFFAPVFFLSPFFYT PPPLYIFCPKKKKIFPPPPGKIFFFFK GPPPIFFFFFFFFFFFFWS*FFIMYQ IVENISYNLIKVDSHLYLFKDKKILLCT ISSDAW
4188	18089	A	4212	24	399	ADAFSTTNLHGLGPDFTPTTQLYINLG MAILL*AGAVNIGYRSKIKNALAHFLPQ GTPTPLIPILVIETINLLILATALVWH LTAIITAGHLLMHLIGSASLAGSTISLP STLTVFTILILLT
4189	18090	A	4213	411	197	SWLTAPSFKRFSCLSLSS*DYRLVPH PDNFCIGSRDGARMVIS*HHDPPASAS QSVGF*APKVLGLQT
4190	18091	A	4214	218	126	KEPEPLFRSSWSVGAILDNVMRRVLI KSCTPGVVAHTCNPTLGGRGGQITRSG DRDHGP*HKSALGSCASCFIYLWDLHLH IVFE
4191	18092	A	4215	1	332	MAPSLCLSNKKRGFIGPGFAGAPKHPGR GQGHPREKLAFKKGPKPKGLKSFLVLK TPPPKPPFFLSPKGGALKTEEP*TKKK GGAEEKPPGKRPPLGPFCKPKPNWG
4192	18093	A	4216	1	185	KLYLSILISLQISLIITFTATELIIFYI FFETTLIPTLAIITR*GNQPANFLYLLV SFHEN
4193	18094	A	4217	1	388	LRFCWETLFPPLYPNPFHFHFSFLFFSFS

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						FFFFLGGKFCFCPQPGGGPNLNLRDPP PRG*KEF*APPPPRGGENQGSPPPPNG GGF*KKGGLNHGGGGGFKPPQKKPPPL ASQGRNRKGGAPPLLK
4194	18095	A	4218	3	195	VIYSTIFAGTLITALSSH*FFT*VGLEI NMLAFIPVLTKKINPRSTEAAIKYFLTQ ATASHPA
4195	18096	A	4219	261	1	EPRRERKERKEKKKGATPSRICMKRER EERFS*ERRERGEERGEKEERERGER ERERSEERERERERPKN*MRLNGRTRR TRG
4196	18097	A	4220	5	375	DEMLHLKFTYILN*TLKDTIIPKVNENL YN*DFLNSKVQGTTPPPRPSRPPSSPSP DPPPGPPPAGARRARRPGRGSPPGGP PAPPPAPPRAGRAAGGRPPARPGR GPAARPAGGGG
4197	18098	A	4221	258	267	GGGALKKKIYCGGGGNNFFF*SPPPSFF FFFFFFFFFFFFFFFFFFFFFFFFFL IYFIFILIF
4198	18099	A	4222	127	330	KKKKKKKKKKKKKKGGGPKKKKFLPR GGGKNFFF*GGQKKLGGGVKKGGGKK PGAKKKKRGEK
4199	18100	A	4223	1	377	RRFHLRRENLEQKQTMGIFFFFGVAGP PGPGGKSFSPPSFFF*GKNTFFTTPPGG GGQNLVGENSNSNPPPRDPPSPGPSEK I*KKTPPFLVGPNTKKNKHFGGGGSPK KKTLLPPPLDPF
4200	18101	A	4224	223	431	IRKTGPLGFGGONNPLPKV*PPPGLTFF QKGPPPPPPPPFQKPRFLKFYKREGPP PPKVGLTPPPGLL
4201	18102	A	4225	173	2	RCKLHCLFPTLAIITR*GNQPERLNAGT YFLFYTLVGSPLLLIAIYTHNTLGPTR P
4202	18103	A	4226	11	377	FLTUVFICISLFGRLMGI*FFVNFFCEL FFHAFSLFLKTDIIFSIDLLEIIYAH VCHICCNLIFSLSLYFVFYNGSLKYIKC* NLFAIILDFADVSFLIFMFRGTGRQNDN QFSLKILIGF
4203	18104	A	4227	1	412	KNSKVKNATDLLKNASESPHSRIDEAEE RISELEDRLFENTKSEETK*KRIKK*SM PTDLENSLKRANLRVIGLKEKVGKEL*V GSFFKDI*QNVPNLEKDNIQAQEAYTT LSRFNPKTTSRHLAIKLSKVVDKER
4204	18105	A	4228	373	163	IGVFLGGAPFFFFFFFFFPQGPKRGGG KGGASGKTG*GGGGLKLGGGKQGWPPFF FLRTWPTFTTRAPGL
4205	18106	A	4229	392	3	PPC*NRAPGFNFGGPFKKIYSSPPPRGK FGSLKGPPPPFFSAPPGGPKFSKGGGPL FFGAPDF*GGFGKNYFWGQGF*PHSP PPFSGWPKRRAPFSKKKKKKRRRGWGE GEGQGSNHLKHYFQI
4206	18107	A	4230	211	400	YALIWLVCILNLYALHSVFFWCFCFLI FKFIYVFLNLLFLFAF*LVLCCLKVQNH SGSLSVSYFPLLEACRIFPLFLF*NL *MICFNMVVLVFKQLCSALSFLVFLFLF FNF*YLCIFKFIVFCFLRRNPTLAQA GVQWHDLGA
4207	18108	A	4231	69	386	KRIFFFLGPRGGGKGMWVNGNPPPKGK

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						GNFSA*PPQGGPKGPGPKNKVIFGFKK KRGFYGGGQPPNLGKELAGPPKGGEKRG KTHPGGKFYAFLGGGLFSKKRN
4208	18109	A	4232	394	287	FKEKKKKPPPPPLFSPPFF*KRGGGDPLF SPRGEKK
4209	18110	A	4233	442	112	LLGRLRWEDGLSPQGRSCSEP*SCHCTP AWATQ*DPVSNTNNKNPNQACSSSLNP SLPWTAAVVRTLGEHCNGREALPARAKN ATKAPVLTTHHCQTVRTISCALLPH
4210	18111	A	4234	415	58	SLQKGHFPPFQELDPQNPGRSGWSPVLP TTGLFFSLDFIRFT*FMAGVLVGYKHCW EWTAAALVLLFLRDRVSLCFPLIHTLG LKRSSCLSLSSWSYRHTIPHPAST*FF G
4211	18112	A	4235	406	168	HGETPSFLKIQKLAGRGGLL*SQLLGR WRQGNHLNWGGRSSVYIYTEKHTVHTQQ SVTTPFMSMSQTLAYSPLSLKSS
4212	18113	A	4236	247	397	TVCFSVYIYTELLPPQVK*FPCLTLPSS WDYRSPVPLPAYFCIFSRDGV
4213	18114	A	4237	36	405	RLYCFIKGLNVKNKTRIVFFFFLETNF PFGPQGGGEGANSFGPEPLALGVKKGPR PPPPGGGE*GAGPPGPGNFGLLKKKGVP RGGGGGPKPPTQRFPPGRPPQKKKNFFG PALGKKKVFFF
4214	18115	A	4238	407	3	KKKKKLTRPGGGGPFSPLPKRVRQKKGG NPGGGFSKKKSPPPPPRGGKKKKPFSK KKKRFLSGNNTGKNRLGKDPQS*PAGNA RKKPGWERALARGRAPGMTDRKPQESGL DGSQQSGTGQEPGNSGPVPKVH
4215	18116	A	4239	144	405	PTVKLVLLYLVLKVAVSKNLR**GGLT V*QQRQILWKRLISNTEFLYLRQSKMMH LVL*PTVNTLKSLSKSGQARWLTPVIPAL WEA
4216	18117	A	4240	369	40	PLLQGTASWPRWGRAGDRPRKEG*LHP RETRVPPALHHQPAPAGVSLTSPGPPFP LSLQRLRGHSSDSLPAVCQYSGSWREE KAAAEAPALTPAICTCTICSVLTVVL
4217	18118	A	4241	397	1	ISKSLFFPIPFWKKKKRGFSPLNFLGG VFFFFFFLKIIFEIFFLKRFFPIFLGAPG FKIFKKYFPFPRGFKTPPKKKIFLNPF KKKGGGGGALFFFFFFETGSRSVTQAGV KWHDHGSLQP*PPRLK*SSDP
4218	18119	A	4242	230	393	ADRPGLPLSAPETGSHSIAQTGVQ*HN YGSP*PLTPGLKLSSCLSLPNCWDYR
4219	18120	A	4243	434	104	KQPTFQSTTGSPSAGRPPPPRAKKKKP PFF*KKKKSGNIGGPLPPPPPGGEEKK NLFPRKGEGSHKTDSSPPH*RGKKKNL SPKKKKKKAWCWDYRRKPLCPATYF
4220	18121	A	4244	2	425	FVFKIILKNLSEIQENLQFSKIKKTIHD LNKKFNKETGNITKNQTEILELKNMSSE IKNTVKSFNNRLNQAERISELEDRSFE MTQADKKRKGESLQDVLYTMK*TNIL WSFQKEKRKEKGLQNILNEIVAENFPSL
4221	18122	A	4245	12	424	IYYKTLNCT*IF*FGGALACFHFSYFF IHYVGFVPSFVYLFSSHVIISVWTSGYLL YSLGCNPILSLFIFLLKLFHFGYLTIOV GIYVWILFVCLFLSNSFINI*FTYHAIP IPIYIPLKVNSMFYSIFTTK

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4222	18123	A	4246	215	425	LSIQISQIRNLTYLFINIMGKILRAKRRK *GTSDAVVNQITIFLRPRTVAHSCNPSTL GGRGGRITKSGDRE
4223	18124	A	4247	413	2	WEVESFSLGKAFMWGCATENPGPPHPKF LLFIMKAPPWRVGFQDCFPNPKDGRFT* PRTPPCPRARGAKKNSVSKKKIKIWK WPPTPLPPPGNGGTRKFPSSPPPPPPPT TPKITPPGGERQL*PQRAEGAGDTK
4224	18125	A	4248	61	281	ITWKDFDSFVSLRVSKAFHLALPAFTGN CIKCHIKMGIYPEEKFKNIHKYLYLEID VCGH*TWKKIFFLFFFLRQRTTLFAQAG GQWLDLSLLQPPPPGFKRFSGLSFLSK* DFDSFVSLRVSKAFHLALPAFIGNCIKC HIKMGIIYPEEKFKNIHKYLYLEIDVCGH IRLGKFFFCFFF
4225	18126	A	4249	23	13	RVRPFASPGGREVTVCGLGREGQERRL RWHKPFPLAATSCAVVPSVTPSVTS GSADGDGQSLAVGAGTLATVGGLELLNS NDPPASASQAGIAGVSHRAWP*T
4226	18127	A	4250	182	342	KGFFFLPPGGGGGGEF*FNEPPPPRVKG IFPPPPPGKGEKPPPPPPPGYIFVF
4227	18128	A	4251	2	219	PSLRKMQKLARHGGLTLLWSQLFGRLLRE DCLSSGGRGSQTHGSEL*SYHCIPAWAT DGDVSKNTKFFFFFFF
4228	18129	A	4252	223	324	LGAVAHICNPSTLGGRRRITR*GVRDQ PGQHGE
4229	18130	A	4253	165	336	ESDAQGHQVAARVSHVLEKDALLVFRSL CKLAMKPLGEGPPDPK*ADSSSWPPSVQ
4230	18131	A	4254	3	233	ETAFCHVGQAGLELLTSSDPASGLQHA GITGPATKSAP*WS*VSGPHLGAFDSL MLLAQDWRALLESAKFFPLL
4231	18132	A	4255	394	44	AKIFPPGVKKFFFASTPPGGGKKRGPPPP PVNFFPFKKGGGFPPWPGGV*NPAPINP RPWPPKRWGFKGEAPPPPKLNLFFPQG GGGKNFFGKKKGAPTGGPPFFFFFEME FHCPRD
4232	18133	A	4256	152	2	YWSPPFYCRSCCIRQGTVAHTCNPSTLVG QGARFTRSGVRN*HGQRGESPR
4233	18134	A	4257	404	190	AQLIRGWRQ*DHLSTLGGGGCNEPSSCHC TPAWITEPNQSLSQSTQKQKMLIPN*YG *TVSPPKSHPELQFS
4234	18135	A	4258	288	407	ENCRPRAVAHACNPS*ENCRPRAVAHAC NPSAFGGRGEQIPRSGEQEPVQHG
4235	18136	A	4259	406	163	GWGVQTHPGHHGETLFFLKKKK*VG GGGPTRYSPIFGGVGPQGNLPQGGGSKNP KLNPLLPWQKGVFFFSKKKKKKERD
4236	18137	A	4260	101	276	LTSIVPSLWEAEGAKRLGLRPACRESS LCHCTLPPWVTG*NLVSKKKKKRGGALG FF
4237	18138	A	4261	2	414	WVAATPNLVFVGRGNCQDWFTGPFLTRG GWGGVLFPPVKRVIKGLVAPFSGPIPIR KNHQKVGGLFEPNKTNFKE*NFVENKNT RRGIKKNVPEKKKPQKGIPLPPQIFNEN QTWGDFFDFFFAKKKKIINSFLGWA
4238	18139	A	4262	337	382	RDARFLHCSLV*LIT*LQKEFFVVGQAG VQWHYFGFLQPLPSGFNFQFFCLSLLSRW HYRGPPPSLGKFLVGLVGLVGFETKFW FCWPGWRAITGFVWPATYTRVQAIFL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4239	18140	A	4263	406	184	QLLGRRLRQENCHLGEGGCS*LRSPFCTIS AWATKLDPVSEKPKTKNQKPTGLGGLNQ GPASLLKKIRKLGGKRRPG
4240	18141	A	4264	233	440	LPVHHGWGSLRKLTLTGKEANPSFFT GQQGKAKQKQKQPGAGAHACNSSPLGG QGR*ITRSGVQDQ
4241	18142	A	4265	2	230	GARL*SHLLVRLRKENHLNLKGKNCREL KWPCHCTPAWGTTKDSAAKNKNQPLPPPK GVKSPPPQREHGLIVTCMFVQ
4242	18143	A	4266	1	349	HKTNIHFKLVMVSNVFTFFFFGKGFSFC APGGRAGPLFGLVETPPGREKAFFGENP PRRGE*RAMAPCPGKILVF*KKTGFPRG LNFWPGGPPFFGLQRRGNGGNPWPGPE FFWF
4243	18144	A	4267	2	375	RSEOPAGSASSGNEGLSTRASGCGGCTG SPNSASPPALCSISRRALAAFPGRARD LQPMPEPPTHSGVSCAAKPPR*APPPA PRRPVPSTTQGLRSAGAQRGTGRHLHLQ PQCRHWWKPGAG
4244	18145	A	4268	377	3	TPAWMTERDCIWRRTSAPGGSWPSGPV PSPCAQ*RPSPQGLGLWWAAAAAPRC*T APGPRPPPHGPGSPQGASPPTRPPRCRP HPRAGSAGPTGATPPGSTQGRRRHSQ LPGHPGHRVALG
4245	18146	A	4269	1	294	LEDWGGRGARAHYDGSLEPESDHYRLR LGQYHGDAGDSLWHNDKPFSTVDRDRD SYSGNWALYQGGCWTACQAQ*ILDVAVY ATGPKYQVHCEALH
4246	18147	A	4270	2	218	TGRIITLSQGLQTLPLIAF**LLASLA NLALPPTINLLGELSLVLTTF*SNITL LQKKKKKKKKKKKIF
4247	18148	A	4271	32	443	LHSDVDQLAGLVFPGCPWPLASPARRAP AGPWPRRAAAPPS*DAPAPRLAVSAGSP AWPPST*GLPAPAAVVASPASASPTSA RSRS*ASPTARRCRPGPGTAAPTASARQ CQWRP*PCQRSPPSGTCSSAAAPT
4248	18149	A	4272	434	57	HLSFPPASAAKPLPQAASLWSSPPSIV LAQVPPMNTDPCPQPSA*PAELSPEMP PARPQAPPENWSHP*GCGAQTVAPLVPG ATPAHRPASPSVTLPLVLTAGGHCIFYLY TYQIFLKFHYIKR
4249	18150	A	4273	288	424	GLSLVAQAVVQWCDLVSL*PPPPRVKQ FSCLSPPRIWDY*HPPP /
4250	18151	A	4274	1	429	NTRGAAGPPQMPHPPRASAFPENPCGRK N*GOVSGP*ASGSSPVKWAGPAGTWRKG GLGWGPTRVGRGPRRRPGASSGYARQQ GPGHFGFPSPRRRLSVPACALCPGQTS GTRAGLAVWPQIGLCLKAQGARSCPRDH SSD
4251	18152	A	4275	253	3	PHQFNAVIFYPPSPVSRGCPNNALYSPFV IVVLCFVKTVGSVTQAGV*WHDHSSLQ P*TAGLKRFSSTLILSSWDYKSTPPCI
4252	18153	A	4276	406	3	PMVSGQGVCAK*QARAIPEGIFRRSAD TQVVREVQQKYNMGLPVDFDQYNELHLP AVILKTFLRELREPLLTDFDLYPHVVGFL NIDESQRPATLQVLQTLPEESYQVLR QTAFLVQISAHSDQNKMTNTCI
4253	18154	A	4277	373	3	DGVSLCPPGWSAVAQSWLTAVL*ALGFI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FLFPVGGTLTGIVLANSSLDIVLHDTYYV VAPFPYVLSIGAVFAIIGGFH*FPLFS GYTLGQTYAKIHFPPIIFIGVNLSSFPQH NLGLSGMRRCI
4254	18155	A	4278	71	176	AGGRGCNESRSRHCTPAWATE*DSVKEK KKGLFFW
4255	18156	A	4279	2	379	SPFVPLQSSLGNKSETPSHGRKKRRKR KRTDENQP*KHPLRARPGFAPRAQGGGA QSGSGGRRAGPCRKLVRHGHTGNPKREP GLIPQGEGRSLGIHPSNGCHKPCPSRGR PPRPKQGRGRMQN
4256	18157	A	4280	2	338	CDMPRRKLDPLSGRNTLGFVCCVWAQTS GLK*SSCLCLPKCWDYRHEPLRPVWVYF KLWHPSPWKPGFYFVSFFPYLPLCTTA SLFCSCLPCCSRVTLVGSSESSCLWPAG
4257	18158	A	4281	407	1	EERGVATGHTAERGRADNNEERGEVANK RGGREVOPEARRMTTATGTTAATRGAR T*TAATTATAPVTRTAAPATTASSTRTL RTPRRARTASVLWARCSRWSATWRASR TDCRTASHSRPTATRSRTARMA
4258	18159	A	4282	367	225	PCDSACLGLPKCWDYRREPPRPAGVLF *ASF*QSKEVYVCKLTHA
4259	18160	A	4283	452	1	NTCGLQSVCRGTQRGGPKRCPCHPRERW DLGDEQESSKEGRPGREGVQGGGLLGAT PGAQGS*GL*AEAAMSSGHALPGQVVP LTPLSPSPNPHRRPRAGRASRQSRST EAQRAVPSQGAAPGWETDWGSSHQWQPC QAQGEGRTR
4260	18161	A	4284	436	22	CHVTGTQPIKVSWAKDSREIRSGGKYQI SYLENSAHLTVLKVKGDSGQYTCYAVN EVGKDSCTAQLNIKERLIPPSFTKRLSE TVEETQGNSEKLEGRVPGSQPITVWYK NNIEIQPTYN*EITFKNNCIAAARRI
4261	18162	A	4285	301	403	LSIS*PCDLPALVSQSAGITGMSHARP RVKSLI
4262	18163	A	4286	380	2	AQVLYSSREQERRQDLPEQVIAEGE*V KASACQLTFEEDAEAMESGPAALDKDFQC TRKHHFAEVQGSPPRCMSSRYLVDGCPKT FAEAQNVCS*CCEANLVSIHAFTFILRI QWCTSTVNQAQVCI
4263	18164	A	4287	453	3	YIYEGSTMEEPKPKVPGPLGLHCPGKF QG*RNSYNHHA VRVGTCAPEGVKDLTS SLQSVITKPEQNIQELMKHFKEKSEAE NHIRTLKAESLEENMAKIHGQLEKLLK SQCDRLTEELTONENENKKLKLKYQCLK DQLEEREDV
4264	18165	A	4288	52	400	LDLYFFVYRQCLALSRLQRSSAILAHCN LKLGLSGDPTTPASQSKBITSMRYHI*P NL*NSMC*NCVFDTHRIGENIWESYI* *EINIQNACRIPKTKQKTHFQNKQGLH SNLN
4265	18166	A	4289	2	263	IHGHLWSQLPGRLLKWDERRSPSGRCS EL*SHHCTPVWVTEGDPVSKKRINICKQ NLNEKTNLTVDTPRHSFTHKIKSLNHFQ MFL
4266	18167	A	4290	3	142	YLGVHRLSIDGLDLLT**SARLGLPKCW DYWRDPPRPANFYFLFK
4267	18168	A	4291	324	19	EMSKRHEQKPHRRBIQMANKHVKRTSLA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						IREMKIETTMKYYHTPIQMA*VRNNDTS QVQWHTLQVASPLVAEVGGWNEARNLRL QIVKMVPMNSHCTPAWVT
4268	18169	A	4292	2	204	THFCRDRDSLCCPGWPRTAELKQSALLG LPKCWDYRH*ATKPGQLQSVFLGLKIFL LLVVRGVDRYL
4269	18170	A	4293	427	3	RKKTVTVPRTGERGIISNEDNGLCKAVG NIPGSPLCNVSKLNIMKHAPGGHAARFC IWTESAFRKLDELGYGTWRAASLKSSYN LPMHKMINPDLRSRILKSPETIQALRAPR KKIHNRLVKKNPVLRPL*RIKLTSRHKR R
4270	18171	A	4294	24	372	FICPLQDYVICSDVTSCVVKILATTGR RLRDDSVQSFSSFFGKGSLLAPRVKEQ GGDLG*WNPFPRLREFPGLALPRCWN GLAPPPPLILVFLEKRGFPLAGKMGLNL LHSR
4271	18172	A	4295	1	332	IHSSYFFPQS*FFGTINTSDKPLRLIK EKKREGTN*HIMHEPWKFGIDPEDIKV KKKYYKQLCTHKFDNLEEMVHFLKKKTI HLI*NR*FE*LYKYYRN
4272	18173	A	4296	407	30	WSVIYGEN*ESLGWAHPSHVANIRVTG LRYLFSYGRHALDMLESSQDNMRSWVS QMSSEIDVDNLGHISLCNAVQ*IRNLNP GLKTSKIELKFKELHKSCKDAGSEVTKK EFIEVYHELYAVG
4273	18174	A	4297	350	1	YKTVVMNKEKW*YVGYNIEQEQLALKT TVLDEWYTLDPGRIIKVGGERFEAPEAL FQPRLINVEGVGVDELLYSTIQAADVGT RSEFYKHIVLSGGSTMYPLPSRMEREL KQHV
4274	18175	A	4298	623	1	SRRGCAATCDGSI TAWPQRQAQKPSV HSKLEAEAKPTPGDHAASESTGFSCG GGVHKTAHAHARNMPGDSNTGSGQSPAG RRWEARGAPRHHPTQPDWTHPDALRQA MARNPASSF*SF*RCCTAASPVPVTPPS PVLMRGPVPGGGGQKIRPLQEEAPPP SSPVVLSR*PQAGTPSSPAVSSLYHGGL SPTGRQDRWGR
4275	18176	A	4299	469	3	PVRNCLGARFRVSGRAAHHAL*QSASTL QGDPRTRKQALISA*SSAFDVQDVSHVTL PFYPKRAQSKDLIKEAILDNDFMKNLEL SQIQEIVDCMPVEYKGDSRIVKEVDVG SCVYVMEGKVGVTQGVKLCVPGPGKV YEELAILYICRRPCI
4276	18177	A	4300	506	321	KPLSLLKIQLAGHGGSC*QLLRVR QENCLNLGGEGCSGLPKFWDYRCEPPCP DCWPS
4277	18178	A	4301	454	1	NGEKPTYSGKKYVFLF*NTRRPTLFTWG KTN*GERPRSSVYSCSSWRLSSSSLGRS *NSVGSNLILATLTAQELSNS*ANNLI *LAYTIAFIVKIPLYGLHL*LHKAHVEV PIAGSIVLAPVLLKLGYGIIIRLTILN PLTKHIAYPLY
4278	18179	A	4302	3	463	AVSLPLPLPRFGRLLPRLVGVVCPLRCH ILRTQRLGAPSR*QTGAKQAGVVEELR SRLSLGPELGRIRPYSGDPGQVTDSSGA LASSLERGCYPAALLVGEGEEMYLGYPY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						HPT*DGLKRLSLAKPPGGETRLTRSGHTFWGEGIPPSAVCL
4279	18180	A	4303	469	2	FFFFFSETESC SVTQAGV*WHDLGSLY
4280	18181	A	4304	194	3	FFFFFSETESC SVTQAGV*WHDLGSLY
4281	18182	A	4306	517	254	VVEETAFLRLIGKTGIGLVTSGDLAASASQRGGMGTGVSHCNKREKFLMNIIVMSSGLTFLPFSPDEV*GS*GLSLFPLPALNTGLRN
4282	18183	A	4307	276	3	KIKMEGIPLHIPNPLVNLNLGLLFIATSSLAVYSIL*SG*ASNYSYALIGALRAVAQTISYEVTALAILLSTLIISGSFNLSTLITTLV
4283	18184	A	4308	234	398	KKFFFFFPLEGGGPITTIWSPPLPG*RESPAPPPPRGGIKGLAPPNLFLLDKR
4284	18185	A	4309	403	100	SGGQKAVGPPWAADPGYKQNTNKLGLPLPQPSTEGGAFWPTQGP KPTGLPPLPG*LNPRNPTPP*WPPPPPPFNTRSKGPHTPSP TPLCGPPPKNRLFFFF
4285	18186	A	4310	399	85	WKPIPLAPEWRGVIRFRALPPCRPLHCP TLKLTAPSVIHQRT*VHWGFLVGVLSVFLERESCSTQVECSGTLALRSLELLGVSDPSISAFQRAIGVSHHA
4286	18187	A	4311	230	2	WTEEDTRRCLVLFSSFFLSFFLFCFVLROREACCPGWSAVTQSQLTVASTSLAQAKRSSHLSPQRS*DYRHTPQCI
4287	18188	A	4312	1	420	NTSWGVGELSLIVIVINMLLPYVWLPKGKFFFFPQNSRFPSPAPPHSSPPGLRSDFSHSGGLFFHLEVLWGLPLPPPPPPASTHVRPLGTQGCP*LAWYIHLISASYQKANAA PQLSCILQDCIRSKGDLIFTFFTLCLS
4288	18189	A	4313	403	207	ESSEG*LNPLAHLAMRYKGC PFKDVREKSEFILKSIQVRKSI LNTRMSLLQLDFTCRYSRCVCFY
4289	18190	A	4314	469	328	TSEGGGFNELLRLCHCTP VWLTK*DSVSI SQRIRKKNLKTQSLVVRCP
4290	18191	A	4315	1	212	NTLPGVEVLKRLRWEDSLNP*GQGC REP*SCHCTTAWATEKDPVSKKKKKKNPGGFRPHSLSQPFPPK
4291	18192	A	4316	63	559	SNLTFWQCAVPAVETTPSSLCGPVPSPTSSATPKPIPS*AACPPPDCA LAEVRALPAAGRPRFSEACLT PQPNPCVLWPCLWDHSPTSCPTGSS*APHSCAFLVPVRLGGG MTTVHPTVHLPIHSSLTFAWE*PSP PACLTAPRPTGHCLLSVPPSAYSSSSPS
4292	18193	A	4317	135	405	PAPPSPHPKPDSVSCVIPS*PAPPSPH PKPDSVSCVIPS SHVAGPSGLPEMTLLEPRGPCPPEVPPTSPFVG*AWWPHPPARRASGRMDGRTDGRGRHLDLRSTHSLTP
4293	18194	A	4318	413	1	LYLVGRA*SFHRSFPGQERIHPPGGKPYDCKECGETFISLVSIGRMLTHRGVVPYKCKVCGKAFDYRSLFRIHERSHPGKPYE CKQCGKAFSCSSYIRIHERTHTGDEPYE CKQCGKAFSCCKYIRINERTHTGGV
4294	18195	A	4319	479	342	GVGVNDNGILVLGATNIPVWLDSAIRRR*DNTVNILFLTADVTSR
4295	18196	A	4320	400	26	HSEAVTTVRSHHSPVGHISLNA PPTVALTP*YNKPLNIFV*ARAQKIQQGFLTHTIPHILLVITRDTSRACVVCVVCVVCV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						CVYAYIIVCMCVYIYVCVYIYICNYTFI PTLVHLPINKMY
4296	18197	A	4321	370	1	SDRGQKGKAGQATRLGSRQTGQDEDKGTE KSIPSWDKGPNNEFGKSVNVSSNLVTQ EPSPEETSTKRSIKQNSNPVKKEKSCCK NECGKAFSYCSALIRHQRTHTGKPY*C NECEKAFSRNV
4297	18198	A	4322	342	82	GLGLTTNWLLTGKSAGRGCAPSSGGLWL AVGDSVYHRETEGGKPSGPRPCC*PS* AGLAPSPPPPGCPEAPGSCCLHYRCLL TAH
4298	18199	A	4323	284	3	ITKKFPRVIGGGCFSPFFMGLSKKNGLF PEGALSISLIFGPAIPGGAQVISSAKE KKKVLSPRGVVAHACNPSTLGG*GGRIK RSRVPDQPV
4299	18200	A	4324	365	3	QVEVYVVENHPPFRLEESIYQ*CRLEGAT SVAGEQISEYNISMRAADGGSPPLSTET HITLHVVIDINDNPPTFPHLSYSAYIPEN NPRGASIFSVTAQDPDSNNNARITYALT EDTLQGVY
4300	18201	A	4325	253	3	PSFLSRD*SHIHKRLECSGMISADYNLH LPGSSYPPTSPSQVAGTAGPSMSLQGR ASHDITSSSRSIGAKELLRPADHPQCI
4301	18202	A	4326	307	95	FLFLKDKILLSPRLECSGTTIAHCSLK LLDSSYPPAVAS*VAGTSGMCHYTWLRL KNHLSPGIQGCSEI
4302	18203	A	4327	371	2	WAPNHISPTPRSGSTTRIWAPTPPSNP RPCQDPGHRTPDPWYPPEEFLLTNPDPR APASWSFPFQEKRLHFPALPCP*HLDSS LGPTTLFSFSFPPTSIRPSQTNHSGKTP PPLSYAQHDCI
4303	18204	A	4328	409	1	RLLEARQPELEMAALIFFTLKYKHVERE QKYHQLODEYFTSAVVLTLILAALFGLV YLLIFPQSVVVLVLLVLCICFLVACVLY LHITRVQCFPGCLTIQIRTVLCIFIVVL IYSVAQGCVVG*LPWAWSSKPNLY
4304	18205	A	4329	262	2	LHGAYLVLDITGAQNRKPRYSFKWRVGO FFFLVFSPRDSLTLPLRLECSGTVMABC HLDLLGSGDPPTSAS*I*GTTGAYHHTQ HV
4305	18206	A	4330	1	399	NTF*FLKGMGLVNHVFTEDNLKKLYVSN LGIGHTRYATTGNV
4306	18207	A	4331	408	3	SSVGIHVTRHTGKPYECKHCGKAFSCH SSLREHVTRHSGEKPYECNQCGKAFSHA QYFQKHVRSHSGVKPYECTECGKAYSCH SSLRVHVTRHTGERPYECKQCGKTFRYL ASLQAHVRTHAGA*IKYSGHV
4307	18208	A	4332	110	426	GLSPGTWSDMTGGPAVTAFFCTLTGTHA GHIIDGIDIAKLPLHLRLSRLSILQD PVLFSGTIR*APPPLRPTQPQAGSVPSD LEHKEEGVGGDQDPRGVSCSC
4308	18209	A	4333	133	1	EPCCPSALAAPEVLGPEKYDKSCDMWSL GVFMYIL*VPSPPPPLY
4309	18210	A	4334	165	1	IILTFFKNERKVVKAQYQW*KNR*VDQ WNRIASPEIDPHE*SQLISDKAKECI
4310	18211	A	4335	42	440	SARRAGDPARGAPSRNNASLPDPRELGT RPAGGLQ*GNCPAPPTPQLPSPSVSRPV SGRGPPPPPSFGDPRANRPQNPKGAKVV

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						LTVMGEPGEIRRAACPQLSWAMTFPGS LPEPKRTGPGIQKSPPSRRGG
4311	18212	A	4336	1	160	NTCGGGAQL*SQLLRRLMWEDLNSGSQG CSELRSHHCTAA*ETKGDPLSINEY
4312	18213	A	4337	236	1	QRSLLCYIMEIRTAVRIVAIGVESEV YLAMSEEGTVYAKKECNEYGIF*ELVLE SHYYTYAAAVLRPVCCIESKVS
4313	18214	A	4338	408	3	CQSSVSKKERTNGAQNPAAKQGNNELR DSTEQFQEYRQRLRYHQHLEQKEQQRH I*QOMLLEGGVNDQEDGRDQQNRNEQFL NRSIQKLGEELNIGMDGLGNEVSALIQQC NGSKGNGSNGL*VNSFDTPPHV
4314	18215	A	4339	363	1	RSQSSLPKSFKRKISVVSATKGVPAGTS DT*GVQPGWQ*RWGASTATTQKKPSISI ATESLKSLLPDIKPLAQQAVIDLHADD SRISEDETERNGDDKTHDKGLKICRTVV RARYSINEV
4315	18216	A	4340	1	353	DVFLDTLAREPLRHSCNFFLCYLL*DFFK FIPQFFYWMFYFDYIFISRRNFYLLLT HFFTLPLFLVIRIQCLHLFLFFSFFFFF FGKGNPFLPPGWRARAQFWVNGSPPLRV NALLP
4316	18217	A	4341	376	3	LELREGGFLPHIADEVREERSPALDDR AGRCQGQPRIQVCLTPKSMFLAFHM*T CEHCLEQCFSTSL*PIEIRTLH*D*GCV CMCAYVCICVCHMCMCAIICICVARMA KRPLESIHSTCT
4317	18218	A	4342	158	2	LAFFFFCETQSCCQWHDLSLQPLPQRF R*FSCSLSPSSWDKKHTSPHPTCI
4318	18219	A	4343	145	2	IFGEQVVFYDMNKFSGDF*DFGASLTQ AVHTVPNV*SVIPCHPPRV
4319	18220	A	4344	1	434	RSLIFRATAYEYRYIDQADLKLPAKRS SCLGLPKGWDYRHEPPCLARFIWQIFI AYKLR*KHYKSRQSLPSRGSC*CACDT FVSDPSHWGTMAQILGWITLGQVQRSC LADQPLLPLLPPTLAPCLP*NDVLLFFF TQSQ
4320	18221	A	4345	4	475	KHSCRSLEHLDRPLPALQETCPVRAEP LLLVRINASGGILIRMGAINRCLKHPLA RDTPVCLLAVLGEQHSKGSFLLNHLQ LPGLVRAGRGRREAGSKDGGSCLEAGS GIPVCGDKEPTN*CSPPSPQLQESGEGGR PRGGEASLQGCRRWRANG
4321	18222	A	4346	313	442	DSTLNFFFFFF*TESYFVAQAGVQGHNLS SLKPPPPGFKRFSCSL
4322	18223	A	4347	437	338	AEVQEFYGDYIAVNPHLSLNLGCGG RNWDPAQLSRTTQGLTALLSLKKCPMI RYQLSSEAAKRLAECVKQVITKEYELFE FRTEVPPLLLILDRCDDAITPLLNQWT YQAMVHELLGINNNRIDLSRVPGCMRPL *RIHPGTLERSIRLLFMPSSSWTMA
4323	18224	A	4348	409	118	GLHDASFVAAPSTQVYVFFFEETASEF DFFERLHTRSARVARCKNDVGGEKLLQKK WTFLLKQALLCTQPGQLPFNVIRHAVLL PADSPTAPHIYAVFTSQW*AAGPSGRWS TSSAAAFRRPRHSCL
4324	18225	A	4349	2	418	YTLPDFPHPHRLSHCRLLQSRTAETYQ SPGACTPISQGHGQRSSPCSSSNPAC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						*SSSSCGSTGFRCPGSAHPGCCSYVL*MGR*RSSQAPRASPIAQGPRSAAPAGRAGHPALPSPPLP*GAPPPPSAASSPGL*SPA
4325	18226	A	4350	401	276	DFLNVGGGGYS*PRLCHCSPTWVTEGDLVSKTNTHTNKKHL
4326	18227	A	4351	446	277	AQDFVLIKDGEVIGGICFRMFPSQGFTEIVFCAVT*NEQVKVSAAPRPQPQSTAH
4327	18228	A	4352	408	3	PKSSLFTSRPNGKSWSTKRPAISLAYSNENAQGSWNGDQDAGPLLVENPRDYSTELSVTIAGASLLFLNLVLAFAALYSRKDTRQ*PLCQLSPHRGIGASELGHAPQ*ELPALLLGPRIHCEAGPPHDTLPV
4328	18229	A	4353	62	280	VRIGCLTSVPEASSCGLPTTPGCC*PLGLPFCRSRSTRSRFRSRSTRQSRSPKTYSPGRRRRSRSRSPTPP
4329	18230	A	4354	364	3	PVGEKGSLVPKSPVEEKGKSPVQSQSPVEEKAQYRVKSPVEEAKSAEVGKGQDKEE*EKEVKQAPKEDKVEKKEKPKHVPEKKKAESPVKEEAVAEEVVTIAKSVKVQLEKETNEECI
4330	18231	A	4355	3	558	LGPTLLWRRGKVPKANSPIPTSLRRTLPRASPGPSRGPFLMRQAGSTPMTLPRSTPSMSPML*MVWPPTAVPVP*KPLMWAPPAPLVLLVTILTETIQEPATPAPLTQF*KPTSLMVS RPVCPVVQGPRTTRSTLCATTIAPSHATLRPGLSTTTSPWQTL SLLLEGQASLPKG*NTSITLPSVS
4331	18232	A	4357	258	1	LGFHDPGPAGWSQPHGGRSAQAQ*PPQPPTVPRTSLADVSDAPLPCCGHSRPQHHPFRLPHTSFSTPGLSAVCLIVHPAARVSRCI
4332	18233	A	4358	97	343	DRDLGDEYGWKQVHGDVFRPSSHPLIFS SLIGSGCQIFAVSLIVIVAMIEHLYTE*VPTLNCIMSLFLNLFNHNWLLSQS
4333	18234	A	4359	182	2	KDYFGSSVENGGEEELKQEDQLGGYSVI*ARDEDEDDDDDDDEDEEDEDDEDDDDCI
4334	18235	A	4360	88	2	RGSRTDTG*RGSDRG TG*RGSH TGTR*RGSRTDTG*RGSRDTGTGGRSRTGTGGRGSRTGTGGV
4335	18236	A	4361	2	250	ELRDEGKASSAKQRLKCAGLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLT KVHTECCHGDLFGCDEESAGLAKYIM
4336	18237	A	4362	169	456	EQLLCAGQGQLSCEPLHLPCPVGPQTPAHRPGRMAPGPPSFLSPGSPCGLGLAIPCSCQPPWAGVPDHHLPSPMGRAGLSPEERSAGEGVIPWP
4337	18238	A	4363	1	419	PEFKLQKLKRSQNSAFLDIGDENEIQLSKSDVVLSTLEIVIMEVQGLKSVAPNRI VYCTMEVEGEKLQTDQAEASRPQWGTOGDFTTTHPRPVVKVLFTESTGVLALEDKELGRVILYPTSNSSKSAELHRMVVPKN
4338	18239	A	4364	375	448	PGAVAHACNPSTLGGRSGRIMRAG
4339	18240	A	4365	1	444	DFLTNYHLHFLRIAGSQLTGLGTAVQQLY SAYEENNRFTLLAAVKRNHNQYVNP SGVATFFESI KEILLRQSGVKVSVSDHDS CVHGPCQNGRSLRKLAVSSVLKSRESLPV IIVANEPLQPFCLKCLPGYSDSWCEIDI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						DEWLPFPW
4340	18241	A	4366	52	402	CPQEVWFHFSFCHCTSAFMKDLYFLCLVR FGDLKEDKVTRHDGASSDGHIAHIFRHA AKELFNEDVEEVITYRALRCGAVSTACLC LWLARVHGVVPVWICACGGSMDGVYTSQN QKDF
4341	18242	A	4367	119	247	WVLLSFQLHGVAVLGLIALIAMEEIGAE MALRTFGHLLRYGEP
4342	18243	A	4368	2	430	GGTVVDGQPGFHDGSLSKAPGMNSLEQG MVLNIGDVSSSAVKTVGSVVSSVALTG VLSGNGGTNVNMPVSKPTSWAAIASKPA KQPIMKTKSGLPPSPIKHNDIGTWDN KGFVPKAPVQQAAPSTQACPQSQQVQQT LP
4343	18244	A	4369	1	406	ETSTPEGEAGPIQRLDIPVENPVESKNI FLGAPLIICHVIDKRSPLYDISATDLAN QDLEVIVILEGLGETTGISTRARTFYIA EEIQWGHFRFVSIETEEQRPDSVDYSKFG KTDLVTTSRCNARELDEKPSILI
4344	18245	A	4370	2	284	GTGTLCDLTALLSARYDGVRTCILPCWK TISTIPVALLIHYHQNQASCGRKRAILE TRQHRLFCADPKEQWVKDAKPHLDRQAA ALTRNGGTFE
4345	18246	A	4371	3	184	EDYNILLSIMKGTTRPINKEIEALNDTV DQLELTDLCRTLTPITIAEYSFFSAPKV LIQP
4346	18247	A	4372	44	304	GLFRSIGCQGLPRLPEWPTWVGCHRG LIMPSVPTQVSRPLMFLDTPGVLA PRI RSVETGLKLALCGEPGLGLGLPGPLPP HL
4347	18248	A	4373	1	422	LHLFNPAASAPSRSLFSGPILDPLSRAL GVGPGICGLASSPGISEGWDQIRSWTHP PDPDHLSGFCRSQVYMHPSLSPSTMIL SGGTALKPPYSAFPGMQPLEMVKPSGS PYQPMMSGNQLVYEGQLSQAAGLSASQM
4348	18249	A	4374	2	423	NSGTHTPGLELDSLKNRLEIPLVNG CSDLEDSFTILQSKDLKQEPDLDPTCID TSETSLSNQKLFSDINLNDQEWQELID ELANTVPEDDIQDLFNEDFEEKKEPEFS QPATETPLSQESASVKSDFSHSPFAHVS
4349	18250	A	4375	292	429	LKISVFPSSSTEISLQQRLEYIARAILTA KSSTGIASISADGESLRE
4350	18251	A	4376	544	32	ALHACACGLGSPEACFLHLLQLTGTSPG PVDGQGLDNQGFRLKAILGVSPAPEPV HGASEHNADTGVSVARACVLPTSPTLAR TAAAKDESPPLAGLTMGPSREPGGSCLP LPSGLLSSPTRLALPRPPSVSVWQDAG SSGSMPTEPLVQCCHRFYGTLSWAVMV LK
4351	18252	A	4377	378	232	PAKRAEEELLLHDTRCWLNGGAMPEARH PRTGASALHVAAAKGYIEVMR
4352	18253	A	4378	291	1	QMLSVDVASRYRAPSTYVLNSLKEGMDG LHGESSCSFLGSPVAMNMQTAGLEMGI CDGHFRQNVGCGYVLKPDFLRDIQSSLH PEKPISPFKGQSL
4353	18254	A	4379	171	458	RGPLFLTLHIVNSLQGNFRREYIVTQG PLPGTKDDFWKMWQENVHNIVMTQCV EKGRVSKQLSWHQSFACHLDRILPHHQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SETPQNNVIGIM
4354	18255	A	4380	214	410	LDHLPTHPSPTGETIEVKWFRAVQTGLPM CILGAFFGPIRLGAQSLQVLDSELIPWA VQNGRIAPC
4355	18256	A	4381	2	74	IGDSGVGKSNLLSRLTRNEFNGL
4356	18257	A	4382	290	119	IATVSLNIVKMPRLPKATYRFNAIPKI PMTFFTEIDKTIKCMWNHKIIPGNSPA H
4357	18258	A	4383	2	423	LERVCWIKDIVVAVTGENMEVMKSIQK YQHKRISLVEAGVTRHRSIFNGLKALAE DQINSKLSKPEVVIHDAVRPFVEEGL LKVVTAAKEHGAAGAIRPLVSTVVS PSADGCLDYSLEERARHRASEMPQAF LFDVIY
4358	18259	A	4384	356	1	WYPCCLLASLVCVFRGLFYLSLCLVLR VPPLCLQFPGSLLGSLLFSLLRQGLAL WPRLECSAIRAHCSLELGSNDSPASAS QSAGITGMSQCAWPLSLLSVSPRPGLS SVPLIF
4359	18260	A	4385	1	125	SGSKTLRSSLSEPTILDIKHFHRESFF YTHLINFSGKRYC
4360	18261	A	4386	53	215	WQLYWTTCQKISRNOGLAHVPRMECSS MIIAHCNLKLGLSSDPPASASQIDPS
4361	18262	A	4387	2	390	PSLAARVLARGYGNFVSFVLWLKNDRM HGECAPNVSVAVSTSHTTIIGGGIRGGG GGGYGSGGSSYSGGGSYSGGGDGGGR GSYSGGGNYSGCAGSGHGSYCSGSSS GGYRRGSGGFGSCNSGG
4362	18263	A	4388	2	441	IKTRISVIHKEEFGLTPIEGATEDMKNK TLQLAFAINQEPDAKMLQMV LKGSEGA TVNQGPLEVAQVFLAEIPADPKLYRHHN KLRLCFNEFIMRCGEAVEKNKRLITVDQ MEYQQLKKNYNKLKENLRPMIERKIPE LVKPIF
4363	18264	A	4390	242	24	KLGNFLGGCVKESPFVPGGGMQWPDFGS LQHPPSRFKQFSCPTLPGNWNFRNAPLR SGKFFFSPVFLVETGY
4364	18265	A	4391	1	244	VDQMRQNLFTTGAHHLQQANIQFRTDI ARTEYLSNADERLRWQASSLPADDLCTE DAIMLKRFTRYELGCGQGEAWECEGW
4365	18266	A	4392	2	146	LDLLSQPCRAVYIFAKNDIPFELRIVD LIKGRSSLGFGEPKSEQEGR
4366	18267	A	4393	204	489	GAASEHPKPGESHGTSKASSLCADAGP AGHFASVYNPLAWTVTTIVTLTVGFP GV RVTDEAGHPVPSQVSGIQRCLQGMKAPP VTVTVSGEKGS
4367	18268	A	4394	2	171	LSDFGQPSRSIIFASWSAGDFGSGV GATE WLEVFFIIPSHIGHELVLGCCPEVMFL
4368	18269	A	4395	2	197	WLELLKFYTLDCALEEYVICVRIQDILT RENNNWPKRRIAIEGEMICCSIFVEYFI CATHYLIQC
4369	18270	A	4396	2	285	TVDFPFQPYKQEQEYMTKVLCECLOQKVN GILESPTGTGKTLCLCTTLAWREHLRD GISARKIAERAQGELFPDRALSSWGNA AAAGDPIGPS
4370	18271	A	4397	366	461	TSNFSCSLVLEEEASDYLELDTIKNLVK KYSQ
4371	18272	A	4399	157	3	DVLRNNFARSAVLYLFIDRVTLWNAPRL ECSGAIIAHCSLLKLGSDNPPTS

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4372	18273	A	4400	2	343	DIDFKYHFDFFSVNFNEELVALYGGSLQ KQTKFVHECIKTILKLYKQEFAPKSVA IIGHSMGGLVARALLTLKNFKHDLINLL ITQATPHVAPVMPLDRFITGSTGWLKDH G
4373	18274	A	4401	214	430	ELGNILNVVVRWEAEELSNRWFNGQAV HGELSPVTDFFRESCCRQYEMGECTRGGF CNFMHLRPI SQNLQRQ
4374	18275	A	4402	3	227	LTQVSPQMTGHAGLNTAQAGGMAKVSEL KHFQYFLPNRGLSLRVMKMGPRGPLLF FLLGSPRATHAWKRQISF
4375	18276	A	4403	158	313	NRDEFCHVAQAGLELLGSSSPPAATSQS ACITGVSYHVRPTLSNKGCCSSL
4376	18277	A	4404	3	628	HCIREGGQDVPSNKDVTSLDWNSEGTL ATGSYDGFARIWTKDGNLSTLQGHKGP IFALKWNKKGNFILLSAGVDKTTIIWDAH TGEAKQQFPFHSAPALDWDQSNNTFAS CSTDMCIHVCKLGQDRPIKTFQGHNTNEV NAIKWDPTGNLLASCSDMTLKIWSMKQ DNCVHDLQAHNKEIYTIKWSPTGPGTNN PNANMLLASASL
4377	18278	A	4405	35	180	MCVDYHYFFCLLGPNNNNPQTSAVRPT QTNGSNVPFKPRGREFSFGK
4378	18279	A	4406	1	438	DFQRPRDDHGDVDWEKLVLLTDCSNLQ DQTYILYILYVIKGPSWDTNLSGQNGVT VQNLLGELYGKTGLNQEWGLIPYISSLF RKKVDVLAEEACTDLLSDQKQLTVGLSDE PREKIIYAPLPPKELTKLIYEASGQDII IGVLTQ
4379	18280	A	4407	1	428	TESVNAYFKGADPTKCIKVITGDMTMSF PSGIIKVFTSNPTPAVLCFRVKNISRL QILPNAQLVFSQCDSDNTKDFWMNQ AVTVYLKKLSEQNPAASYNVVDVLYQV SLNGIQSTPLNLATYWKCSASTDLRVD YK
4380	18281	A	4408	174	383	KNSWPGAVAHACNPSTLGKGQRQITRSL YRDHPVQHGEIPLYLKLTAVALTFLGLL TGLHDLTLTNLT
4381	18282	A	4409	1	288	LMAEKDSLDPSTFTHAMQLLTAGKGASRV PLGRPAIPGMSGPGFVPLASRPLGTEAV GSSGLILIFGSLDSTFPFPQPGVRGRISR LQWRPEGDFAIP
4382	18283	A	4410	292	422	LVHSSCFQVSSKILELARKQRMNTDIRR NIFCTIMTSEDFLDA
4383	18284	A	4411	412	238	FFSRHRVSQWDQAGLELLTSLDLSALAS HSAEITGLNHHAQPLTNFNKYCWISLQ VH
4384	18285	A	4412	1	405	VTSSDKSLKVLDAEDKVFNEIRNEHFS NVFGFLSQKARNLQAQYDRRRGMDIKQM KNFVSQELKGLKQEHRLLSLHIGACESI MKKKTKQDFQELIKTEHALLEGFNIRE TSYIEEHIDRQVSPIESIRLMCL
4385	18286	A	4414	2	149	GFHHVGQAGLEVLTSDNLPVSASQSAGI TGVSHCAQLRSDGFKKRSSPA
4386	18287	A	4415	1	366	DICHRKLGVECPSHASINRLVVQVSSI TASLRFEGPLNVDLIEFQTNLVPRIH FPMTAFAPIVSADKAYHEQFSVDITTA CFESSNQLVKCDPRLGKYMCCLLYRGD

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						VVPKEVNAAI
4387	18288	A	4416	1	164	RRRCCEMSTMFADTLLIVFISVCTALLAE GITWVLVYRTDPFGTLAGSEGGPGGRY
4388	18289	A	4417	2	141	DIAIPCNNKGAHSVGLMWMLAREVLRM RGTISREHPWDLTSSVMG
4389	18290	A	4418	136	1	EQTAKFGQLHKVLGMDPLPSKMPKPKPN ENPVDYTVQIPPRDPMQ
4390	18291	A	4419	1	280	GNCKYYGYRGPSCEDGRRLVLKPEWFR GRDVLVLGCNVGHLTSLACKRGPSRMV GLDIDSRLIHSARQNIHYLSEELRLLP QTLLEGDPGA
4391	18292	A	4420	3	446	TVSTSQVRQNYHRDSQAAINRQISLELY ASYVYLSMPYFDRDDVALKNFAKYFLH QSHEDRDHADKLMKLQNRGGRSLLQDM RKPDCCDDWESALNAMEWALHLDKNVQA LLELHKLTTDKNDPDLSDYIETHYLNQ VTAINELG
4392	18293	A	4421	6	182	DPSFCSEPRSCHCTPTWRTEQDSISEKK KKRNILKNWAKNYITLSEKERKSKQRS RR
4393	18294	A	4422	1	456	GPISYVVVMPKKRQALVEFEDVLGACNA VNYAADNQIYIAGHPAFVNYSTSQKISR LGSDSDSRVNSVLLFTILNPIYSITTD VLYTICNPGCPVQRIVIFRKNGVQAMVE FDSVQSAQRAKASLNGADIYSGCCTLKI EYAKPTRLNGSK
4394	18295	A	4423	2	257	FHHVQGAGLKLISVDPPALDSQSAREIT GVSHCAQPVLCILNQLCAKAVLSPDSHP YPPKSGRHEGQVREQMSPCSYIYFKRT V
4395	18296	A	4424	106	259	CCCFKYFFSNVKICFYRDLKPENILLNE DMHIQITDFGTAKVLSPEKQGV
4396	18297	A	4425	3	364	MDEIEKYQEVEEDQDPSCPRLSRELLDE KEPEVLQDSLDRCYSTPSGYLELPDLGQ PYSSAVYSLEEQYLGALDVDSEYLTVK VISLHLVFQIGVIFLFQVPLTDPDPRDIA AGRITYGRI
4397	18298	A	4426	2	241	HHVWLICFVFFVCVETGFCHVAQVGLER LGSSDLPTSVSLSAGITDVNHWAQSKPS PSKGTGMNRPIGLRVKGQVWSRL
4398	18299	A	4427	2	438	TRLIGPNCPGVMNPGKCKMGIMPGHCHK KGRIGIVSRSGTLTYEAVHQTTOVGLGQ SLCVGIGGDPFNGTDFIDCLEIFLNDISA TEGIILIAEIGGNAQENAAEFLKQHNSS PNSKPVESFIAALTSTGRKMGHAGQLL AEEKV
4399	18300	A	4428	34	427	AGMLPAVGSADEEEDPAEEDCPPELVME TTHSEEEKSGLGAKIPVTIITGYLSAG KTTLLNYILTEQHSKRVAVILNEFGEGS ALEKSLAVSPGGELYERLELINACLCC SVKGNGLIAIENLMRQKGE
4400	18301	A	4429	330	8	YSDRISHWIDMCPKSYIFRGVPVHPHIS TFLHTAHNLVARGNYENMSPHDEEKGAY QRKEKCCDDPMAGARIHFLCFEFGFR SVSQAGVPWPHITSMQPQPPRIK
4401	18302	A	4430	446	222	LTSSDPPASAPQSAGITGVSHRPQPIWG VSIQLYFSGCPDTPGQGRLTREHCDGQD GEQGGPCSESAQFCHDWS

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4402	18303	A	4431	3	243	AREDSADVFVSFFPDFVWTLRDFSLDLEA DGQPLTPGTSQKDNFNFLRLCIRKFTS LIRTSRSYQSPDTSVASSRGAR
4403	18304	A	4432	433	0	PPPSPPPPPPPPPPPPPPPPPPPPPPPP PPPPPPPPPPPPPPPPPPPPPPPPPPPP PPPPPPPPPPPPPPPPSPSSSS
4404	18305	A	4433	25	185	ARWVACSELRLRCCTPAWATEPEPVFKK KKKVQQQGGWPGGLTPVSYRFGRLT
4405	18306	A	4434	2	329	VRDIKEKLCYVAVDFEQEMATVEFSSSL EKSYELPDGQVITIGNERFRCPEALIQP SFLGMESCGMHETTLSIMKCDVDIRKD LYANTVLTGGTTMYPGIADRMHNEI
4406	18307	A	4435	2	374	WVTFISLLFLFSSADSRGGFRDHAHTSE VAHRLKDLPEENFKALLIAFAHYLHQ PFEDHVELLNEVTEFAKTCVADESAENC DQSLHTLFGDTLCTVATLRETYGDMADC CAQQEPERNECF
4407	18308	A	4436	2	352	KVRRIDSRLAELDREIRNPQISCQLIYS PSLFLGAFLLFFFGFFPPPYLLAPKN QFNPPPLCTGGPVPRPKPPIPPWEPPRP APPLFSPQWDLGFQIAPFLWVINGGGPS GGSRA
4408	18309	A	4437	2	369	QSCETLFHSHWKDVEVCSSALSCLSQVSV HLQGLLESFLIPGMVEVQRDSQMALVES LEYVRGEISKAMADFTTWKTHLLTSDSQ GGNQMLDEGFRDFSEQMEIAIRAILCA IQNLEERKNE
4409	18310	A	4438	2	231	SDTSRPLQLPCPAARERFPDGPLSLRPLP FFLSQVYNEQIHDLLLEPKGPLAIREDPD KGVVVQGLSFHQVVDWARVG
4410	18311	A	4439	1	365	MAHAMEEVKKCLGPDMMDDICHEQFLEL SYLNGVPEPSRGRGVPRGRRAPPPPP VPRGRGVGPPRWALVRGTPVRGATRGA TVTRGVPPPTVRGAPAPRALTAVMQRI PLSPPPATK
4411	18312	A	4440	92	510	LAALPDGGQELHIPRSRAGPAGELSWAV VGTGALSLSILFQMARCRPWPLRPNS PLQGWIFNVVPWLVAIPASLFSGFLSDH LINQGYRAITVRKLMQGMGLGLSSVFAL CLGHTSSFCESVVFASASIGLQTFNHR
4412	18313	A	4441	2	266	FPPHLPELGKWECPWHQCDECSAAVSF CEFSPHSFCKDHEKGALVPSALEGRGCC SEHDPMAVPSPEYWSKICKKWSQDHGE EVKE
4413	18314	A	4442	2	279	KGAELVFLPSNTRSLMYPLDQGVVTRFK AHYAGYSMERIVSAMEENPGREKIMKKL LKLSSPKEIPAGEKLCPNDAHDFTELDD RVIHENHE
4414	18315	A	4443	2	371	KWVTFISLLFLFSATDSRGVSRLDAHTS EVAHRFKDLGEENFKALEAIAFAQYLQ WPFEEHVELGNDVTESAKTCGADESADN CDKSLHTLFGDTLCTVATLRETYGEMAD CCSQPEPCEKG
4415	18316	A	4444	2	372	WVTFISLLYLFSSGYSRGVFRRDAHKSE VAHRFKDLGQENFKALVLIATAFYLLQ SFEDHVKLMNEVTEFAETCVADESSDDC DKSLHTLFGDTLCTVATLRETYGEMADC CAQQEPERNECF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4416	18317	A	4445	1	283	FRKNAEDILTMEGLRATMKHELEAAQKK HSLWELLRIPNICKRIWILSFVRSAGVC WRSTPDPVCLGITSGGCRTAQIPACSFL WKLHSLGAPA
4417	18318	A	4446	173	2	KKKKCVLYPEGHGVFHALVCVCVCVCVC VCVCIQVNFNFCFISWINLSVQVSLLD Y
4418	18319	A	4447	104	221	SCHLHYSLGDKSETLSKNHHYHHHHHHNH HHHPAGYFKMK
4419	18320	A	4448	241	1	WVSWDKAPSWVRGLGSGSRGGVWGGGSP PHRVTDVSCSFLPDGRHVWEMEAKTDRD LCKPVSFAAGAATVGPQGLGGRC
4420	18321	A	4449	229	349	WKRSHSFGLDVVAHACNPSTFGGQGGRI MRSGVQDQPGQY
4421	18322	A	4450	76	189	TESKPAATTRSSGGGGGGGKRGKKDD SHWWSRFQKV
4422	18323	A	4451	40	359	SGEPLFPFFFLARLIPGVCFVEMHTRV RLIGLKIWEKKVPQVSTPTLVEVSRNL RKVGSCKCKHPEAKRMPCAHYLSVVLN QLCVLHEKTPVSDRVTKCCTES
4423	18324	A	4452	2	371	KFQNALIVRYTKKVPQGSTPTIVKVSRL LGKVGIKCKKHSEAKGMPCAEDYLSVVL NQVCVLHEKTPASDRVTKCCTESLVNRR PCFSALEDYETVVPKECNAETFTFHADI CTLYENERLFQ
4424	18325	A	4453	118	369	GRYILLKTKKQTANNNIKTPOYLSNMS KKFRHSEFFFFYLLKWSLALQRCNLGSLQ PTPPRFNQLSCLSLPNSWDYRCVPPNLV
4425	18326	A	4454	364	3	GHLSLQRLLLPFVWLCPAPRGGAAYRGRQ ASLSCGGLHPVRASRLCLPNQACTMAG APPPASLLPCLSLISDCASNQRDSVGVG PSEPCAGYNLLVCRFLSPSEKRSPSAGV MRFSRCRL
4426	18327	A	4455	1	379	AAFTECCQAADRAACLLPKLDELDRDEGK ASSARQLKCASLQKGERAFKANAVAR LSQRFPAEFAEVAKLVDLTAKVHTECC HGDLLCACDDRSDLAKYICENQDSISSK LKECCEKPLEKSH
4427	18328	A	4456	1	362	LRPARSLVFPWFAPGGSGRLGLKLEAK COGDGVSYEETTIPRSAYHNLFGPLI SRRDAEVLTSLRELDLALNQSTGLPTL TLPRGTTCLPPALLPYLEQFRRIVFWLG DDLRSWEA
4428	18329	A	4457	250	330	EWTHLWLNNEGFAWIEYVCVDHCFPE
4429	18330	A	4459	96	319	YLTIPFSQAMENCKDARLTTSIGAYNFN HRLLEMILNKPGLTYKPCVNQVSALL SFLFFMPLFLSYCQVSIH
4430	18331	A	4460	50	339	NSQTLKLSNVQCLKTRALFFFPKGIYPQ IKTLPPCPTSGPDPYVRVNLPLKKGKPC LKKISGNRKTLKPLFDKTLKFLVPMKEV PKSPLNVPVKNI
4431	18332	A	4461	2	357	GYDGVKRWTRDGDIFNKELLIPIHLEV HWSLISVDVRRRTITYFDSQRTLNRRCP KHIAKYLAQAEAVKKDRLDFHQGWKGYFK MYCKHLALSQPFSTQQDMPKLRRQIYK ELCHCKF
4432	18333	A	4462	182	325	IRLSSWLCDASCQVYEFVRKESSIIAP APAEDVDTPPRKKRKHRL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4433	18334	A	4463	1	338	SRHSPGPTPQPDCSLRTGQRSVQVSDTS SCSQLSSSSSGSSSSSVAPAGTWVLQAS QCSLTKACRQPPIVFLPKLVYDMVESTD SSGLPKAASLLPSPSVMWASSFRPLLSK
4434	18335	A	4464	2	343	IIDFFLGAYLKDEVLIKIMPVQKQTRAGQ RTRFKAFVAIGDYNGHVGLGVKCSKEVA TAIRGAILAKLSIVPVRRGYWGKNKIGK PHTVPCKVTGRGCSVLVRLIPAPRGTTGI VS
4435	18336	A	4465	1	371	INSTLKMSFVGENSGVKMGSEDEWEKDEP QCCLEEIFFALASSLSSASAEKGSPIILL GVSKGEFCLYCDKDKGQSHPSLQLKKEK LMKLAAQKESARRPFIYFRAQVGSWNML ESAAHPGWFI
4436	18337	A	4466	246	12	LCFTPLPSYILFFETKSHSAPKLECS GVITATSEVILLGGGCGSELRSYCCTPT WVTKLDSITKKRRKRKRKDL
4437	18338	A	4467	2	355	WVTFISLLFLFSSAYSRGVFRDAHTSE VAHRFKDLGEENFKALALIAFAQYLQQC PFEDHVKLANEVTEFAKTCVADESAENC DKSLHTLFGDKLCTVATLRETYGEMADC CAKQEP
4438	18339	A	4468	2	361	EDHVKLNVNEVTEFGKTCVADESAENC DK SLHTLFGDKLCSVATIRETYGEMADCCA KHEPERNECFLOHKDDNPNLRLVRPEV DEMCTAFHDTDETFLKKLYEIARRHPY FYAPELLL
4439	18340	A	4469	1	373	SSQPSSPSESVSGTVSVSPSSLSPSPCL SLSVCLLVCSLSMFFSLPVCLSVPLCV SPRPHPSVSHAHPRASALVNCPPWGPAP TSAPVSFYKQPSPALKTGQASPHPHPHP FPTSPMQSQK
4440	18341	A	4470	236	371	KVLGAVLKDKGGLFCFVFGDRVSLCHPG WSAVVQSQLTAAVTSQA
4441	18342	A	4471	345	201	AWMTAHLFMAWFTFYFKSTAQKKKFVFK TLLLDIDNFDPLWDSKEGKL
4442	18343	A	4472	1	144	AGFHHVGEAGLGLLTSRDPASPCKRAG ITGLNHHTWPFVILTYTY
4443	18344	A	4473	3	333	KNHLEASIGHPFFPDHSPSCPHLLSSS NYHSLSCFLGGFFSETGSAPSPRLCSCG VIAAHCSLKLGGSTSPLTASWVAGITG MCWLYSPAVSPRSPDLTCTSQLNI
4444	18345	A	4474	288	1	TSAVNRISIKSQADQEATEQKLRDYSHQ GIQILAWQKFEYKPGKVTMDPEDCILQL AKKKEEEEEEEEEEEEEEEEEEEEEED QEEEEEEGEEEE
4445	18346	A	4475	3	124	PRLECSGMIMAHCSLDDLLSSDPPTLAS QVAGTTKKISLH
4446	18347	A	4476	196	2	SCYEHPRIVYGFLFLRQDLAVTQAGVP WHDHGSLLQLPELKRFGTSHLLSSQG YRRAQPRR
4447	18348	A	4477	3	162	LLERNKELEGSLLQOMYSTNEEQVQIEV RALHVLHAHTPRGPLGLCVPLCNLE
4448	18349	A	4478	167	2	ACGISPFSLSSSCFGHVRHASLPLAFHH DCGFPEASPAMLPVQPSQLNLFIKYPV
4449	18350	A	4479	195	26	WVSMLDIHDNGPHEVAVICFVCFLSQSL ALLPRLECSGVISAHCNLPGRQSQTPS
4450	18351	A	4480	175	1	NRSATKCDWGEKRTSQELNLFVFFVCL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FEMESHVAQAGVQWRNPGSLKPLPPRFKR
4451	18352	A	4481	122	357	YHAFLYQWYNLKRHKRFRCSLLTIIFLG GERKLQSIQLWNISHYIQRVLEIPS GLGAVAHACNPSTLGQGGEWIT
4452	18353	A	4482	137	2	FYSYLKILEEMGPHYVPQAGLELLGSRD PFDSAYQSTEIIGMSHH
4453	18354	A	4483	347	208	GQAGLELLTSSLPASASQSAGITGAGHH TRPRIYFLKKYLAFLVLS
4454	18355	A	4484	411	268	RLNRRGGGCSEPRSCRCTPAWATEQNSI SKKNQKTKTKPLCCRLILL
4455	18356	A	4485	2	102	PCLLKMQQLAGHGGMHLSQLLRRRLRCF LHSYP
4456	18357	A	4486	1	113	HSAHSTHAGHAGHTSLPKCWDYRSEPPR LAKFLNTRY
4457	18358	A	4487	163	353	QVAATLNNLAVLYGKRGKYKEAEPLCKR ALEIREKVQKKGAVVFEIFVLCVCGFF FFFKRDP
4458	18359	A	4488	408	307	RGCSEPRSHDCSAAWLTERDSVSKKNKN KSPKKQ
4459	18360	A	4489	337	179	YSINFALILIFLFLVGLVWAAIINYHR LHGLNNKHLIMIMVGSPLRSCG
4460	18361	A	4490	229	345	LENETLGRARWLTPVIPALWEAEASRSR GQEIETILANM
4461	18362	A	4491	180	365	ENNLKTLVALDMSFYFILEFLFYFILFYF ILFYFLRWSFALVAQAGVQWRYLGSQP LPPRFK
4462	18363	A	4492	269	385	GNLQNLKVFYKIQHPMIKTLNKLVID RTYLNIIKAIY
4463	18364	A	4493	103	336	QLLVSLINLFLQAFKLQIDCGHTCMHFW RONLCLLPPTLPTRRNLTLSPLSCSG TIWAHRKRLRLPGSHHSPASATR
4464	18365	A	4494	305	379	YIKIENFCLGVVAHTCNPSTLGGRG
4465	18366	A	4495	47	224	ETATKTQRRWETALVPQHPHRLAPVTW VKTGNSTIANFLILVYLSFLFLVYSC IQQ
4466	18367	A	4496	3	129	ITLNPGGRGCSSELRSCHCTPAWATERDS VSKKKKKFPPPPF
4467	18368	A	4497	396	112	LPELEFEAAVSHDCASELQLGHQSKTLF QKKINRIINNNSHIAISLLGIYPKEF KAGTQDICTPMITASLFTIVKROKQPK CLATNELVYRM
4468	18369	A	4498	1	152	LSLPGSQTWWRALIVPATWEAEVGGSP PRSRQLQVAMITPLHSSCGRRG
4469	18370	A	4499	92	2	KRPGVVTHACNPSTLGGRGGPITKSVVR DQ
4470	18371	A	4500	116	1	AGIAGMCLHAQLIFLYFLVETRFLCHLQ AGLELLTLWS
4471	18372	A	4501	99	1	QGTPVHRWWKCLVQPLWRTVWSFLRKV KIDNS
4472	18373	A	4502	140	288	RQFHYVAQAGLELLGFSNLPALTSQSAG ITGASHHNQPTSRFLKEKKIG
4473	18374	A	4503	330	181	FFFFLFFFFFFFFFFFFXFFFFFFFFF FFFFFFFFFFFFFFFFFFFFF
4474	18375	A	4504	171	2	VETVSKESLRICLDIRYFFFTKPHS IAQAQVQWHYQGSLOPQLRLKQSSRLS
4475	18376	A	4505	345	74	SVERTCHSPKPLMLFLPLVFQARDDILN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GSHPVSFKEACEFGGFQAQIQFGPHVEH KHKPGFLEACHPYQTAEFASALTLDFA SRTVQK
4476	18377	A	4506	268	102	KNIRELWPGAVAHACNPSTPGGRGRWIT RSGDWLNLRTCEHVILQQKGKFRFLIS
4477	18378	A	4507	1	67	GLPKCWDYRREPPHAPRNCKYF
4478	18379	A	4508	339	180	ANFFVFFFEEMGFHRVAQTGLEVLGSSDL PILASKSAGITGISYSVRPQTNT
4479	18380	A	4509	174	3	NEPKVVIYIIPGDPFLFLLLLFFETESH YVTOAGVQWHDLGSLQPLPRLQRFSCV
4480	18381	A	4510	84	3	AHHIFTVGLDVTDRAYFTSATIIAI
4481	18382	A	4511	127	2	LLIKIHCWPGVVAHACNPSTLGVRGRWI TRSGVQDQPEQYG
4482	18383	A	4512	109	345	EIFLIQGHEGSCLCFLGFSFMCVATGF PHVTWLILTLNLPTSSYSRAGITGVSH HARANNLFCFGSMPSHGITGLNF
4483	18384	A	4513	290	13	RDLRPTPOKGPKNHTAPNPLQRAQTHVK KGRGPTPTPTPSKDPGPHPLRKPMPW GRVWGEKKKKKNGKPKDKGKKKKKKKE RKIQHSRF
4484	18385	A	4514	234	362	DGDVLSKFVNFFSFKVVEGTPLIDGRRL KYRLNGDFLFLRLKL
4485	18386	A	4515	190	330	CLALQSECFRRWSFALIAQAGVQRDL SPQPLPPVFKRFSSSLHPE
4486	18387	A	4516	2	199	LCVCVCVCVCVCVCIFFFFLSKKWGPPPL CPPGGPKTLGPKESPPLAPKNRNGSLT PPPPPTFFF
4487	18388	A	4517	94	339	SAYLGLKFFLFFFFFFFFFVGVPFPFF FNNKKLKPQIFFPPQKRPIFFFPFP PGGKNFFFGKFFFPNPREKGPKNLG
4488	18389	A	4518	95	3	LYLGPGAVAHACNPSTLGGRGGQITRSG VQ
4489	18390	A	4519	14	121	LIFFGNRNRLCCPVWSQTPGLKPSSWL SLPKCSD
4490	18391	A	4520	207	2	ISREKLCTVRIPDMHVIDSILFYLYFY SLALPPRLCNGTMAHCSLHLPSSNP PASASQVAGTTS
4491	18392	A	4521	169	1	ANLTQVGSYYSLSLHTLIQVTFKNIRA VRPGTVAHACNPRTLGGPDGWI TRSGDR
4492	18393	A	4522	2	82	GFILCVCVCVCVCVCVCVLYFIFF
4493	18394	A	4523	300	3	LFLPPSLPSQIPGGQKPLPIFPFRVP KKFIPPWFAPPLISPRFWVRFLGPPT QGNYPLGPGPPPPPPSLGFKKSPNPF FIKKKFSPPPKQK
4494	18395	A	4524	348	94	KPGEGGKGQNPFGGLKPGNPLNPGGG GSPEPNFPWPFGAKKTRPQKKKKK KGRKESRLNYGMEKRMKEKEKVFLSAL N
4495	18396	A	4525	313	161	RGHKPNLKSKEVNIRREAPGHPRNKKK TPNLKKKKKKKKENKKQKQK
4496	18397	A	4526	118	3	FFFFLRGSFALVAQAVVQWRYLSSLQAL PPGFKRFSCP
4497	18398	A	4527	153	2	KDAINKMKKWPGVVAHACNPSTLGQGG WITRSGAQDQPSHYGETPSLPK
4498	18399	A	4528	258	2	GGQKRGLPGFIKKPPFRKIFLKNLGE GKNSLSKFFFFFETESHCLTQAEVQW LNLSSQONKPPRFKQFLCLNHPSSWDYR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						R
4499	18400	A	4529	296	39	SIRIINIQILLGFFETGCHSVAQAHLKL LGSNDPPASASESTEITEMQHCTRLSIQ IFVAFPPYSNIKLSLKKEPILIKLLLYNC K
4500	18401	A	4530	292	37	SIRIINIQILLGFCBTGCHSVAQAHLKL LGSNDPPASASESTEITEMQQCTRLSIL IFVAFPPYSNNKLSTKKESILIKLLLYNR K
4501	18402	A	4531	3	138	GLWNGSCLCVCVICFMGMGACLVCICTC LYCCVPVNTCLCMDGR
4502	18403	A	4532	380	2	GGPPKKRESAKAPGGRNPQGGGREKTTP PKKKRPPQKGKKPTPPGGGGGPPRRGGG KKKPPPKREKECHRGGRGGGGPPVVTPE EGPPFFFFFFFFFFFFSLPFFFFFFCFPI FILFPNIVINGFY
4503	18404	A	4533	3	191	LSKITHASIPVPSVKKKKKKKKEKKKKK KKKKKKKKKKKKKKGGGPKKTLGGHN FSRGLE
4504	18405	A	4534	370	48	GPAPEVSSNNGKGKGGCPKGLGKPLGSQF NGVKGYSPKSSPLFQAPLGQGQFPKPR GNGGTTPPFPPKKKKKKCALGDGTPTS GC RRSWNHPETQDCGGWGSRVPR
4505	18406	A	4535	147	1	KGPPLFFFFFFFFFFFFFFFFFFFFFFFFF FFFFSFYFIYLFLSLRL
4506	18407	A	4536	198	1	NPPYFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFLSFIFIPLYFNFI SSNIVFIGFY
4507	18408	A	4537	2	356	QNRTGNSKTSQASPPPKECSASPATEQ SWMENDFDELREEGFTRS NYSELREDIQ TKGKEVENFEKHLHECITTITNEKCLQ ELTELKTTARELRDECRSLTSRRDQLAE RVSALE
4508	18409	A	4538	347	220	KCSGTIIAQCNIKLLGSSNPPVSASQSA GITGMSHHVQPKYC
4509	18410	A	4539	308	2	FSISCPHDTAAASQSAGITGVSHCARP IFSFCFFIFICIMCIKYLLRTGDSVMYF HGLCGFGLCCYLESYIRKLSHMKKLSIL ITSREKCKCILQINIGDR
4510	18411	A	4540	2	194	IKQVVSTALSRLSCSGTITAHCSLKL GSASASVVAR TTGTCHHAQLIFYSETGS HYVDVDA A
4511	18412	A	4541	101	2	MEENLGNTIQDIGRGKDFTSKTPKAMAT KAKID
4512	18413	A	4542	1	84	AEAEAEEAEAEAAAAAAAAAAAAEIKY
4513	18414	A	4543	3	183	KIQILFFVSSKTRLRPSAWHPRFVFCFL RWSLALAAQAGVQWHHLSSLQPPLLPGFK VDAA
4514	18415	A	4544	1	335	RKKKKKEKKKEKKKKKQGRKKRKREKE EEAKKKTKNKDK
4515	18416	A	4545	104	2	QKKKKKKKKKKKKKKKKKIYDFFLQIN CMCSHK
4516	18417	A	4546	5	108	FKRLSCRSPSSWDYRREP RPANFCIL SRDGIS
4517	18418	A	4547	131	1	RPRRPQVGLQDATSPIIEELITFDHAL IIIFLICFLVLVALF
4518	18419	A	4548	156	3	KGGQGMCSLSRSPSALLKFECRVISSYW ANWRAPVVPATRGAEAGESLEP

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4519	18420	A	4549	2	340	LNPGSAGCRELRSHHCTPAWTTTERGSVS KKKKKKKKKKKKKKKKKKKTFGGGGLW EREFLLGNFWEKKGGGANFFPLENPNGP QLKTWGGKKAFFPRKGGGPLNPPQGFYQG A
4520	18421	A	4550	165	335	PHYLPRRSIIHRPFKSHSPEPGAVAHAC NPSTLGGRGGWITSGQBFETSLINMEKS L
4521	18422	A	4551	123	3	GRVDRLSCLSLLSNDWDYGHLPHLANFC IFSRDGVLSW
4522	18423	A	4552	3	131	HPEVDIPILPGLGIISDIGAYYSGISEP FGYVGMVSYDPVRL
4523	18424	A	4553	87	364	ILASQSVVFRYAASAASGGLLETESQPS AAGTASAAVPSLEAQTPAAFRPTPPGLA PSSPPAPGPPAPTGKVCGRHFLRSESSA SGPLRALL
4524	18425	A	4554	114	0	LTWAPHSLIETIRNQIIQALLITILLGL YFTLLQRSE
4525	18426	A	4555	91	3	TTTTYIAIATACVVCVCACVPCVCVC M
4526	18427	A	4556	239	364	CIKITFSRPGAVVHACNPSTLGGQGGRI AMSRDRDHPGQQGK
4527	18428	A	4557	250	1	STEHVKQLRNEFMKISVILIFLEILLYI KVHLKLCTLTDDHLLLGKLSKILFRPG AVAHACNPSTLGGRGGRIPRSGDRDHS
4528	18429	A	4558	2	90	QDGLDLLTWGSACLSLPKCWDYRSEPSL F
4529	18430	A	4559	65	394	DPVSKKKKKKKIKNEKEKKFFGKKKPL KKKLADLILKPKKNFLKKREWKKREK GGDPFWKNKPQVGKTGNLNLGQNGLGK GPSDLKKNTPETKLNLVQKKQIF
4530	18431	A	4560	93	2	GIISAHCNLCPLGSEDSPASASQVAGIT GQ
4531	18432	A	4561	125	4	GAYTILYNKKSIRSIRPGMVAHACNLSTL GGRGGRITRSGD
4532	18433	A	4562	3	84	RSCHCTPAWATERETLSPKKKKKKNF
4533	18434	A	4563	145	3	GFYHVPPGGVEQSPCLSLPKYWNHYCEP PPLASIGFFFFFFETQSRS
4534	18435	A	4564	125	388	IRKPQILYSPQSENMQHLHISVLMGVT GKRGFMDILDVTERCRFSLKCTGIQE DLNKWEGIPCLWIIRLNTVKMAVFSKLI CRFS
4535	18436	A	4565	59	325	VARKGNLVSFLVIFYPLFDIEEVIEPLW VLISSEGEKVELEFFFFFVKKKSPF VTQAEFQWPNLSSLKPQPRLKQFFCLG LLIT
4536	18437	A	4566	326	3	PEKEFRRLVIKLIREAPEKGEAQCKEIQ KSIQEVKGEIFKEIDRIKKQLKHQETL DILLVMQNALESLSNRIEQVEERNSELE DKVFDLTQSNKDKAKRIRKYEQS
4537	18438	A	4567	333	209	EQAFDPYGTLSSQIFSPKPFEPFHKLMA RPAVALPFOVNLK
4538	18439	A	4568	125	2	HNQNSRSIDCSDPILGHCNLCPLGSSD SPASASQVAGTTG
4539	18440	A	4569	212	2	PICLSGKKCYGQNVVRVIKCHMWKHNHRL GVVVHACPNPNSLVGGGRFMRSGVLEQH EQHAETPSLLKTLK
4540	18441	A	4570	142	14	GRVDRSNPGRFLSTSNSSLYERPREIRE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						TSQAPSPVNHITST
4541	18442	A	4571	2	419	ARDSFLHDSQTSFCFSDSIPTPSNMEET QQKSNLELLRLISLLLIERSLEPVRYLRS MFANNLVHDTSDSDDYHLLKDLEEGIQ LMGRLEDGSRRTGQILKQYTSKCDTNH NHDALLTNYGLLYCFRKMDKVFETFLR
4542	18443	A	4572	3	194	HEGRQLSQQLRLRLRQKNCLNTGGGGCSE PRSHHSFPAWVTEHGFISQISLKLPLFIS HPEPFL
4543	18444	A	4573	2	286	CRDGLTYNDFLILPGYIDFTADHVDLTS ALTKRITLKTPLVYSPMDTVTEAVMAIA MALTGGIGFIHNNCTPEFHANEVRKVNK YEQGFITDPVV
4544	18445	A	4574	44	325	ROWLQEEAYITKEQKYSFLHDSQTSICF SDSIPTSSNMEETQQKSNLELLHISLLL IESRLEPVRFRLSTFTNNLVYDTSDD YHLLQDLEEG
4545	18446	A	4575	374	33	LRLARRSGASLCGSRSGGPPTCANICPR YAPLIIPPCRTSLLEAQGLVMVVGPDFRV RLVTSSERRFRYQPPPPGFNRFPCLSLP SNWDYRHAPRLANFNSLFFFFFLVETG Y
4546	18447	A	4576	400	225	PIFFVVFFLFLVFLVETRLCHVVQAGLE LLGSSNLPISASQSAKITGMSHPAWPRA EF
4547	18448	A	4577	2	372	ARETIFCFNSIPAPWNMDETRQKSNLQ LLRISLLILLYRTRLTLPCTQLHLIQT YKVNARCSHFHSSSTCGFLYSCTLVSL TGLDMKLCHSTLLKQNSALMSLLKIQVN LNQVSPVFNAH
4548	18449	A	4578	349	174	GCGEPRSHHCTPAWATRAKRCCLKKLKL QLKNVVKESKHQPLQNFSLTSTINTQ EN
4549	18450	A	4579	3	124	HELLNPEGEGCSEPRSCHCTLAWVTRAR LRLKKKKKKKK
4550	18451	A	4580	181	1	MSSYYFSPCSRLLMATVYNLHLPSSSNS PASASQVAGNAGARHYAWLIFVLLVETG LCSC
4551	18452	A	4581	227	3	HRKRNRCVSR TALLFLSGDGVSPCLKII IIIKVLFWLGEVAHACSPSPGSRGRI TRSGVRDQPGQHGETPSC
4552	18453	A	4582	257	2	RVRQLGAFSLSPGSGSFSKILGALKIMG PPRAGPVGSPRYSRPLGGPGRQIPRSGD PGPPGLPRGNPVPLKKNPKRSLILPAR A
4553	18454	A	4583	3	94	HEIAMAFLILTERKILGYIQLRKGNVVG GP
4554	18455	A	4584	345	50	IYIYICIFLNRNRVSLHCPGWSKTPGLK QSSHLGLPKCDYSHEPLCPAKTSHFKA QDRIPKNDPCTPSPAQMSTNLIGWASS YLOSYSPAPYNNKN
4555	18456	A	4585	338	19	FQLSRRFRPKNGGNPGSGACSEPRLGPC PSAWVTKRDSVSKKKKEYHTLSGLSTTG IYFSQFWMLGVQGASRFVWVGAVSWSI DGAVLLRPHMAEGARQLSGLGF
4556	18457	A	4586	2	224	ARGVGRAGLELQTSGDPPASASRGAGIT GVSHRVQLLGDRAKFLKKKKRGIILPG EFYSPKKRFTLNTPDNP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4557	18458	A	4587	344	168	PPGTVVHTYNPSTLGGQAGRIGSLGVQD KPGQHRQGLSLGVEDKPGQHSPTSVQS NP
4558	18459	A	4588	212	328	GLAVAQAGLELLSSSNPPASASQSAGIT GVSHHTQPYF
4559	18460	A	4589	110	323	LSNQKNQLYNPNNLLIYCVVRKLKSSYDK QAEVQGSKLGLQALPHGFTPLSGLNLP SSWEYTRPPRPPTNF
4560	18461	A	4590	2	127	ARGCSEPRSRHCTPAWATEQVSKKKKKG REKTFGQFFFWVI
4561	18462	A	4591	211	2	ARGSLEAGSSTPAWATINQSTNKKTDKT ALYWKKMPSTRYKARQKSMGFKSSKDR LTLFLGAKVSCLV
4562	18463	A	4592	3	120	HEKTKTNPIKKWAKDMNRQLSKEDNDN KINGWPGAVF
4563	18464	A	4593	388	227	GHVGQDGLELLTSDAPPSLASQSAGITG VSHRAQPKWLLFQHRSPCLPEAAGK
4564	18465	A	4594	1	348	PPPPPPPPPPPPPPPPPPPPPPPPPPPP PPPPPPPPPPPPPPPPPPPPPPPPPPPP PLPPPPPPPPSSPSSSPNPPATTSSVA C
4565	18466	A	4595	2	138	ARAARGFRHVGQAGLELLTSGDPPASAS RSAGITGVSHHTQPTNF
4566	18467	A	4596	315	2	ALKPNYSSTSMNIKARLPQYNINNLNLA PLYSSTSNQINIIVILINKENNHTLFP CLVSNRLKQSSHLGLPKCWDYRRELLC LACDKFFISYSAPAIQLLSC
4567	18468	A	4597	1	146	GTSVDQGSLELLTSGDPPASASQSAEIT GVSHRTQPLTIIQLYLYC
4568	18469	A	4598	293	3	GGTPWPRKKLGQRKFPHRPPGGSGNPDF SLLFFFFLQSFALVAQAGVQWCDLGLS QPPPPVNPFLRKQFGFSTSCFPILEAS GSFFGREASASC
4569	18470	A	4599	174	2	RSVAPFLKSARPTYRKEPTPDGTGSPQP PPPRFKRFSCLTRLSSWDYRHAPHPAS C
4570	18471	A	4600	59	252	LAPFGHELGTSES AHQTDNRHRLEGYOK RLDASGLERASYPLAEFKVGGRCSSQ PLTLCGY
4571	18472	A	4601	233	366	IHYLPDAVAHACNPSTLRGQGGRTSR DRDYPGQHGETPFLK
4572	18473	A	4602	182	325	LFVFCLFLRQCSVAQAGVQWHDHCSLY PQPPSLKQSSRLGLPSSWDY
4573	18474	A	4603	202	2	GGSSSGLLRPCAVLGLKQSSYLSLVRRW DHNSWLKRSTHLGLPKGWDYRREPPLA CILKFSINLV
4574	18475	A	4604	317	2	FRLGPQVFFSPPGAGFFFCGPVWGPGFF SRSLQLLTFGAKFFCLSLPESFGAPLR GPPSGFMAHCFFFLVLLFFFFFRDSVL LCCPGWSAVAIHRRDPTTARA
4575	18476	A	4605	233	71	FFVLLVETEDQLNEKKQEGKIRKKRKM RNKQSLQKIWDYVERPNLAGHSGSRL
4576	18477	A	4606	114	1	HPRPARVSSCCPNWSAMVWSRLAATSAS RVQAILQSRA
4577	18478	A	4607	348	3	LKFQNFQGVVHGARCPSFFGGLGRGIPF TPEVEVLVNLGPAPALPFWPPSQTLFSQ NQKKNQKKQERKEKERKEERKKKER KKKEKERERKEGRKKGQEKRRKITAKSL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LG
4578	18479	A	4608	174	3	TVVMVVOQCQVFCVLLKQGLALSPRLECT GIIIAHCNKLKLLGSPDPPTSVEKTKKLV
4579	18480	A	4609	171	334	DEHSSLNIRFSSRSVAQAGVQWCNLSLQ PPPPGFQRFCLFSLPSSWDYRCAPP
4580	18481	A	4610	2	164	ARGSRGHIWSAFCHVGQAGLELLTSRPA LASQSAGITGISHRAQPPPLNTLYSMS
4581	18482	A	4611	2	164	AREPRGHIWSSFCVVGQAGLELLTSRPA LASQSAGITGISHRAQPPPLSTLDSMS
4582	18483	A	4612	180	334	CCLMGSSYLLPRKPNTLRTAGFLQQRKS LIRPGMVVHACNPSTLGGQGGWI
4583	18484	A	4613	189	1	SGFSRVVENGLKCKGQKGGQSLVLLPIR VFFFFFFEMKSHSFAQARVQWGNLGSLLQ PLPLGFK
4584	18485	A	4614	216	358	KSTPRLGTVAHTCNPSTLGGQGKRITRS GDRDHSGLHKGTPLRSKNI
4585	18486	A	4615	179	393	EKQEEGSGWAKTEDGVALMLSEAIGS CWIKAFLTDAETFTFHADICTLSEKERQ IKKQ TALVELVKHKP
4586	18487	A	4616	2	126	ARVQRYLFLFFTLDGPLDPDSMIRGSVP NQMPRITPQSGK
4587	18488	A	4617	338	181	RVGEAGLELLALSDDLPAQSDQSAGITDI SHHTRPGSPFLEHHLYPRYRISGK
4588	18489	A	4618	3	197	HEKRPEVQNSTVEFIASSDYMLRPPPLPL PFCFFLFFFKIKMGVSPCCPGSCQTPSL KQSSCLNV
4589	18490	A	4619	1	339	GTRTFGSGNGPTKPDLLQELRVATERGL VIVNCTHCLQGAVTDDYAAGMAMAGAGV ISGFDMTSEAALAKLSYVLGQPLSLDV RKELLTKDLRGEMTPPSVEERRPSLQGN T
4590	18491	A	4620	3	306	LEPGDGGCSELKSCHTPAWVTERDSIS KKKKKKKKGGPLKGTLLGGPKFNGGWQRK IFSQKGGQKPNLGLGRNLNFGGEKNW NKFLTKIKVLREKKNF
4591	18492	A	4621	397	29	NTKEKILSARKNNQVFPHTQKKNFFPK KRKNFREGIPPFPKPPKSPQKNHPPQ KKKPPKEKKTIARPPKRAPPGAFKKK PPPPFFLSSLCISYSFIYFFSLINLFFF FFFFHDSTVY
4592	18493	A	4622	2	235	VSLCHPGGTISTHYNFCLPGSRDPPTSA SAYALLIFVFFVETGFLVAQAGPKLQG TNSIPASASQSAGITGMNHCT
4593	18494	A	4623	209	324	ILRVLWSGTVAHACNPSTLGARGRQIMR SGVRDQPGQY
4594	18495	A	4624	52	287	NPFSFLFFSFLSFFLFFFLFKGPRRGA RAQKGKPHPKKKKKKKRGGGKKNKTQKP FSPLKGRGPPRGKGQTTPKGP
4595	18496	A	4625	102	1	THSFVVSISLSLSHTHTHTHTHTHTIY RVREIR
4596	18497	A	4626	125	1	DRHVPQHTANFFVVLITEMGFLHVGAGL KLLTSGNPLVPLV
4597	18498	A	4627	3	167	ERLRQONCTNPRSEGCSEPGSPHCTPAA WATEQDSVSKKEKEKRKKEKKKIVV
4598	18499	A	4628	135	3	AASTLSRGTITTAQGNLCLPVSSNSPASA SRVAGITGARHDTWL
4599	18500	A	4629	320	210	WFLGIIFRRVENAESVNIDLTIDYIQSFT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						DTGKTPSS
4600	18501	A	4630	98	326	SSPTLAFQFYFFSCATKEAVKLSFPKS LLGTGSRSAQPGEQWHNHSLOPQPAQ LRLSSCLTLVSGWDHRCAPP
4601	18502	A	4631	275	2	RVKLLLFYMRQSCSVIQVESSSTVNGSL QPQPPGPRQSSHVSLLSRWDHKRMPPCL ANFFLFFWRAGLAILPVHSNLVNTESP LISIKSN
4602	18503	A	4632	180	1	KGLTLYFYFFIFKMRRLGLAMLADWSQTP ELNQFSCGLPCKWDFRHEPPHPVKEFK PFHR
4603	18504	A	4633	234	5	KPLRDKPLRSFSNLPPKKNLFFWFPPFPQ KIWGGFFFFFETESHCVQAGVQWLDLS SLQPPSPGLRQFLCLSLSSS
4604	18505	A	4634	171	2	GRVDILTPOHFETLFSFFSFFWQGLSV TRLECSGVIMAYCSLDLLGSGNPPTSAS
4605	18506	A	4635	324	211	LRNIIFMPVTMNPGRMYTGGCMVCVCVC VCVCLCVCVC
4606	18507	A	4636	95	1	MRQSINLSPRLECSGTIPAHCNLCPLGS SNS
4607	18508	A	4637	234	1	KKGHDTLTEKAMPVTLSSRMLSLNVCKC IYKVVKNSPNYSSLTHHNNIKPSFTRE NTLMFIHLSPIILLSLNPDIIT
4608	18509	A	4638	2	243	WGKVNVDVGGGALGRLLVVPWTHMYF EFFGAFYISFCLFFLIFPHLFFVSSIHI VSSFYLLFYNFPIIFFTLFCHFFL
4609	18510	A	4639	118	2	GRVDLQCSGAISAHCKLHLQRSRHSAS ASQVGAHATT
4610	18511	A	4640	50	168	NKINKMHLITFLKKKKKKKKKKKKKKKK KKKKKKKKKK
4611	18512	A	4641	315	87	GIFLRDRNLALLPRLECSGTIIAQCNLE LLSPKDSPASPPVARTTGVQPRPDTLT LFELIYIRYKGMIFSQDC
4612	18513	A	4642	383	2	KPKKKKFKAGKAPARLSPPLWGPKGKGGP PRAGVLSPPGPPGETPFLKPNKFPCHG GGPRKSPFFGGLKGNSLTREKGGPINP NLAPPAPPPKQNPFPKPKKKKKKNRS SPAWNWDWIGTNAGK
4613	18514	A	4643	3	205	LKRFFCFSLGGQGCSEPRSCQCI PAWET QRDSISKKKKKKTRPGGLTLEPPPPGG VKPKGPLGAGI
4614	18515	A	4644	149	1	FFPIKADLVFFFFFLRRNLADSQGAQW HDLGSLQAPPPGFMPPLSCLSL
4615	18516	A	4645	474	344	ATHEHYLPSSASGDCDEDLQAACILV NALMDFHQRLAHTV
4616	18517	A	4646	165	357	LCNALSHLLPQCTPTPLISILCIIDTIS LLIQPIHAVRLSANITACHLLMHLILL STLSICTL
4617	18518	A	4647	2	339	ARGENDLSPGGGGCSELRHLHCTPTWAT RVNCVSQKKKNQPKPNQTKPNQTRK GSPGFLLNLKVISPEKSLNPNILKTAP KVTFRNWLTPEIIPFWKMEKGSFDPRI
4618	18519	A	4648	313	187	LTSGDPPASASQSAGITGVSHHALPPLV QFPSSSLTPTPLFC
4619	18520	A	4649	236	324	GQVMWPGMMAHACNPSTLGGRSRWIVRS R
4620	18521	A	4650	225	313	GQVMWPGMMAHACNPSTLGGRGRWIVRS R

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4621	18522	A	4651	240	76	FCVHAHTHTHTPSFQASGSSEHMHTYTH PSGSPEHTHTYTHTTFLASRSAEPQLP
4622	18523	A	4652	273	379	KQLAAQCVRPLSPSQATASPVTCTYMPR WPEVTEE
4623	18524	A	4653	369	189	GTVKQAGACRNLGSLQPTPPPGFKQFS CKSLYSIMICYSKDCMTSTLGRANNR LHL
4624	18525	A	4654	168	346	DRICRASSYTIHLMLYFVFLIFLFYWI YFLFFVLFFHTIFILFYFIIILLLLLY FYN
4625	18526	A	4655	56	354	WKRTFPFFFFLETGSGFASRPCTLLFL YSLGPNPRVLIRVFLFLSSSRCYYYLF LGLSLLFLFFYIMYLLFIRLFFFLSGL LLLLSSYYRFIIFFF
4626	18527	A	4656	50	186	SACGLPKCWDYRHEALRPAMYLTLTGSS YVAQAGLNLGSDPPE
4627	18528	A	4657	131	366	DHFVASSESVKEEGLFFVVFVFFFI FFILYICFFYFKFIFIILLYIIIFIFI FYFFLYLYLILIFFLIFIFIG
4628	18529	A	4658	290	155	LEYIVEKGFHQDDKASPELLTSRYLSDS ASQSAGITGHRAWPTKG
4629	18530	A	4659	163	372	LRLFALFAFLFMFFFLFLLYVFCFVF FLFFFFTFLLYFFFLYFLYFLCSLVFL FFICFIFFWFFVFF
4630	18531	A	4660	227	378	PIFFSNCTSTALVHPLFYLSRLVLSKNR NKFIGRARWLTPVFPALWEAEA
4631	18532	A	4661	3	141	RSRHCTPAWQQSEILSQERKKERKKK ERKKEKERKKERKKKKK
4632	18533	A	4662	346	3	TFKFLGGVCPFFSPPKKRVFSKNSPGGF FLPPFLGENFFFPVNFPGPGGPFKGG PPFFFFFFF DSFDNLGIFVPIPKIQDDFSSMSNATS ILIKIAL
4633	18534	A	4663	302	3	GDINRRSHSPFVWSKPFAPCFMSSLDVF YKSSDFFYFFFEFTEPHSCCPGGISAYCN LCLPGSSNSPASASQVAGITGVRHHTQL IFASVVETFKITYKN
4634	18535	A	4664	2	76	RLAPTPQLGGHWPPTGITPLNPLEV
4635	18536	A	4665	1	210	SPTRSPKPTPPYQTTAKPFTKKKKKK KKKKKKKKKKKKRGAPLKKSPGGPKI NRGKKKKFFLKG
4636	18537	A	4666	2	356	GSRPGGKRTARRWTRPWRLRGACLTG MAFAFHQVIYKIKSLRKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKPRG GGFLKKLWGGKFFMGGGKIFFFFIRGGK KKMWGG
4637	18538	A	4667	1	323	RTRGIFCYDVCVESGCADIQLLLCLKK KKKKKKKKKKKKKKGAPLKKNPGGAQN NPGKKKKNFSPKRGPKKTPPGNFEEKPF FGGGPNGAPPPQKNKTPKEKKKF
4638	18539	A	4668	167	446	ELNKGGLCKPKKKKKGGGRSQPKPTRPK KKKKKKKKKKKKKKKKKKKKKKKKK KS
4639	18540	A	4669	321	52	GVFSPFSPKKFFSPKGLNFWGGFAPIF SPPKKRFFSKNPQGGFKYPPLRGKILIW GPRENWGPFGGFLKGAPLFFFFFFF FFFFWG
4640	18541	A	4670	82	359	NAYGIILIKGNEDTKTVKWKSSCQLANT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						WEFHIRALLGFNCFFLIFKRRGLTLLPR LDCNGVII IHNNLESLGLSNPPMLASQV ARTTGLCY
4641	18542	A	4671	249	60	LLIFYYYFFFLFFFLFFFFFFFFFFFFFF LFVQVHLPHVHLPCYDLSPLYKCVGVLVK CPFKYT
4642	18543	A	4672	2	319	AAASTLVFVFSFFVWLGFLLLLLLLLFWG PPKKILKKKGGGGGGGGGGPRGGPRGGG KRNPGGQKKGIGGANGGQKKERNFQGGG PPRGEKRGGGGPGNPKGGGLK
4643	18544	A	4673	3	451	HESFNPTVITSQLERGEDPWVLDRLKGA KKSQGLWSDYSDNLKYDHTTACTQDLSL SC PWECETKGESQNTDLSPKPLISEQTVIL GKTPLGRIDQENNETKQSFCLSPNSVDH REVQVLSQSMPLTPHQAVPSGERPYMCV ECGKCFGRS
4644	18545	A	4674	446	189	SISLSTLVNVQCILISLSDPASGFVDHVC CIFTFFYSINFALILIFLFLGVLVWAAI INYHRLHGLNTKHLIMIMWVGSPRLSC G
4645	18546	A	4675	26	170	HLVVFVLVIVAHWASSRQITISHWKNC TRH DCPVCLPLKNASDKRNQQSK
4646	18547	A	4676	3	378	HEDEFDKMGNQHQALLLEAMQQQSTSL AK AGVVCILPARTSIIA VAHSFAGLYLI FN TVSVVFFFFSNFIFLILSLFNYFCIS IY ILFLIIFIFIFISSLIVFFCLISFRFL L FIFFSALSRIFY
4647	18548	A	4677	18	242	PIGLALSRLRCESGVITAHLLGSNNPPT SGRVAGTTGIHHAQPHCFNCIFPMSS EVECLFICLLLIHILSRA
4648	18549	A	4678	288	2	PKYRWVPEKPTTASENAEIPSERQKEGI KLTRISSRKKPDSPPKVLEPETKQEK PEKEEEKTNVGRTRLRRSPRISRPPAKVA QIRDPKAHKKK
4649	18550	A	4679	340	208	SVGQAGLELLTSGDPPATASQSAGITGL SQCYPPDSVPETFLPL
4650	18551	A	4680	4	379	EENTGINLHDLGFGNGFLDPAKQAATT AKKKKKKKKKIKIKSFLFLGGLFKKGKK TPKKGEKNFGNFKFWGGDLTPKIFGDPG ASTKKKKPFLKGGRGLKKTFFKKKKKRG PHPLESPPFSVF
4651	18552	A	4681	1	350	SRFSGAKEAKMEKKITGYTTVDISQWHR KEHFEAFQSVAQCTYNQTVQLDITAF LK TVKKNKHKFYPAFIHILARLMNAHPEFR MAMKDGELVTWDSVHPCYTVFHEQTET F SSLW
4652	18553	A	4682	365	45	SPKWFVASYDYPAGPGRPTRPDNSRDET GSHSVSESSSGSDSKRESTSSDREANE P SHRASPEPEPPPTNKWQLDNWLNKVN
4653	18554	A	4683	238	372	SATPLISSFSFLFFFFFFFFREGVWLCHP GWSAVSRDCTTAAVWPG
4654	18555	A	4684	3	462	KTESREAVEKEFEPLLNMKDRA LKDK IEKAVVSQRLTESPCALVASQYGSNGM ERIMKAQAYQTGKDISTNYYSQKKT FE INPRHPLIRDLMLRIKEDEDDKTVDLA VGLFETATLRSGYLLPDTKAYGDRIERM LRLSLNIDPDARG
4655	18556	A	4686	410	0	FFFFFFFFFFFFLLGKGGFGIITKFL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4656	18557	A	4687	151	2	IFFFFFDREVQWHKLGSLQPLPPRFQQFS CLSLPSSWEYRHPVRPRV
4657	18558	A	4688	342	183	FFFLRWSEFALVPOAGVQWCDLGSGLQPL SPGFKRFSWAEVGGHLHEPRSQRLQ
4658	18559	A	4689	126	404	NCQVWPLRFTGHSVFSVHPQWFIIFYCF ALYFIFLEMGYSYVTQAGVQWHSLSGLQ PPQWSYVLTFLWHPSSWGYFVQNHLP FDGKVPWV
4659	18560	A	4690	2	128	GESLFYIVSPRDVVAKERDQDDHIDWL LEKKKYEVLILL
4660	18561	A	4691	407	2	YFFFLPRMKIFFFPHQKGGFFGGCPII SPPNEVFFSPKEGGFFSPKKRVFFH NPPEGFFPPFFMSPPPPFFFFFSLF FFFFFFFFFFFFFFFFFFFFFFFFSFR ILLNQKKNLACVELRSCCTFM
4661	18562	A	4692	1	176	SRRLNPGGRGCSEPRSHCTSTWSTERD SVSKKKKKRFFALKFLGEANVKPTIGGQ KN
4662	18563	A	4693	1	403	SKAEIGRRLGLLRQTVSQVNAKEKFLK EVKSATPMNTRMIRKRNLIADMEKVLV VWIEDQTSRNIPLSQSLIQNKALTLFNS MKAERGVEAAEEKFEASRGWFMRFKERS HFHNKAQGBAASADVEAAS
4663	18564	A	4694	343	425	HCFLSLQLNSFEQLCINYNTEKLQQLF
4664	18565	A	4695	395	2	KNKGLFFFFFLRWSFTLVQASNVTTAV CNVTILAHCNLHLPSSNSPASASRVAG ITGSCHQG
4665	18566	A	4696	429	0	VTKWICYITKKKKKKKKKKKKKKKKKK KKARG
4666	18567	A	4697	371	217	IPVFKQSSCLSFPRSDYRHMPPCVTQK KKIEYQHISLYKKPSKRCAFLI
4667	18568	A	4698	415	59	LQQQCECFISELTKKKKKKKKKKKKKK KRGGLLEKKKKKGFFAPYPPH
4668	18569	A	4699	431	0	LKKIFPPGGRVLSPPPPPPPPPPPPPP P
4669	18570	A	4700	371	245	TLGDPPASASQSAGITGVSHHAQPLFGI FIYKFTYICRTRT
4670	18571	A	4701	410	0	RQCWFTQKKKKKKKKKKKKKKKKKKKK DRG
4671	18572	A	4702	340	402	PFAGGGYRLGAAPPEESAYVA
4672	18573	A	4703	188	2	TSLPKCWEYRHHPPCPAHTLLIFLFFIF VDMGSCHVAQVALELLGSSDPPTSASQS AGIIGM
4673	18574	A	4704	423	34	LKKKKKKKKKKKKKKKKKKKKKKQDL KKMVGNGNYKNVGAQILGYKKLCFSFF YRVF
4674	18575	A	4705	2	297	PRVREREKEMASMKEEFTRLKEALEKSE ARRKELEKMSVLLQEKNDLQLVQAEQ DNLADAEERCQLIKNKIQLEAKVKEMN ERLEDEEEMNRLP
4675	18576	A	4706	2	179	QENGMNPGGRACCEPRLYCTSSWATER DSVSKKNEKKRSASLRRFDILFGALTGR KAS
4676	18577	A	4707	432	578	PRIVCFQELRKPSYAEICQRTSKEPPSS PLQPSSSSSSSS
4677	18578	A	4708	419	35	GSFFFFFLKDQPKKGRKKEGCPPPPKK IYPPPATKWGGGGGKPPPPKRGPPK KNRGRKKKPPKKKKKKFPKPPKRAPQK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KKKKPPPPPIFFYLYFFKNFIFFFFFFFFY FFFFFKKFIFFNLKKF
4678	18579	A	4709	147	31	NFFFFFFFFFXFXFFFXKXKFLFFF *FFFLKLIFF
4679	18580	A	4710	3	229	HASAHASDQPERLNAGTYFLFYTLVGSL PLLIALIYTHNTLGSLNILLTLTAQEL SKKKKKGGAVLKNPWGAQS
4680	18581	A	4711	1	158	PTRPPTPRSCSELRSRHCTPAWVTERL CLKKKKKKFPNLSVGFILGILKG
4681	18582	A	4712	163	404	KKKKKKKKKKKKKKKKKKKKKKKKKKP KKKKKKKKKKKKKKKKKKKKPSRGGAKK KKGGGAQNRAGGKRRPSRGGEKQN
4682	18583	A	4713	3	378	FEFPVYIKSRQKRKESNPKLVSSQPHK LHDFFKKKKKKKKKKKKKKDGGLPK KPPGAKNKPGEKKNFELKGGGKKNPW GFFKKKTFFGGGKIGAKPPKKKSLKKK KKFLRGKGKKT
4683	18584	A	4714	2	208	VSNPAVSVPHLPFSVYKSSPMASMTFSK KKKKKTKKKKKKKKKKKKKKKKGGPQ KKKPWGAQNKPG
4684	18585	A	4715	290	56	SAPPPIFFLFFFLFLFIFFIFFFFKQI LEKKGPPFFLFFFFIFFFFYRMGC DRWWFILIQTFRKQKPVLVK
4685	18586	A	4716	50	424	GGFKIKFLFTQFLFLFSPSMFLISKSP AYLWQSSPKQVPMVVGKTNFLVSIECK KEGIYFFCIPFVFPFGPHPKILCSLLPF LAFLRRSLALLPRLECSGAILTHCNPC PGSSNSHAWA
4686	18587	A	4717	161	2	GRPGPADFRVRPQLLQRFIYLFTEME SCSVTQAGVQWCNLSLQPLPPGLQ
4687	18588	A	4718	2	115	VYTTAMAEIPEYPAWGSVEVLVSVLVG LAMEVGSTRP
4688	18589	A	4719	1	416	GNQGGGYGGYDNYGGGNYGSGNPSSSS SSSSSSSSSSSSSSSSSSSSSSSSSSSS SSSSSSSSSSSSSSSSSSSSSSSSSSSS
4689	18590	A	4720	1	454	QPDSGISSIRSFKTILPAAQDVYYRDE IGNVSTSHLLILDSDVMEIRPRFLFG GWKTHYIVGYNLPSYELYNLGDQYALK MRFVDHVFDEQVIDSLTVKIILPEGAKN IEIDSPYEISRAPDELHYTYLDTFGRPV IVAYKKNLVEQ
4690	18591	A	4721	3	173	DAWAGFHYVQAGLELLTSSHLPASASQ SAGITDVSHRTQLDVPFSFSLSPHPQC
4691	18592	A	4722	2	201	LKPGGGGCSEPRSCHCSTPAWRQSETPS QKKKKGKGLERIGWGGSTTNGAKNQR GEKFGKKGGF
4692	18593	A	4723	2	183	LKPGGGGCSEPRSCHCSTPAWRQSETPS QKKKKGKNGLEIICWGGSTPNKRATNSP VEKF
4693	18594	A	4724	1	395	QDATSPIIEELITFDHALIIIFLICFL DLHALSLTLPSALT
4694	18595	A	4725	388	3	SFSPLEENLGNTIQDIGRGKDFSTPK AMATKAKID
4695	18596	A	4726	223	44	WLFFFXPLFFFWGGIIFLLKXLYIF FFMSKIFFFFFFFFFFFFFFFFFFFFFF FFFF
4696	18597	A	4727	41	374	KKKKKGKKKKGGGGGNPKKKKGKMEK PPGCNKRGEKKKNFLKKKGGLFKGK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KPPKKKNGGRKPKWKKKNFKKKKKKAPFF LGPKIFKKKKRGLKKLGFSSQSVGP
4697	18598	A	4728	323	69	FFFLRQSLGSASQAGAQHNLGSLQPLP AGFQLFLQPPPPGSKQFGRNLNLGNKDL WGLPVLRAHPQAPPLAFIL
4698	18599	A	4729	3	197	CLALLHLRSRQRYALPLGLPGCPHIHT HSHTHAHDHHTYTS PHAHRHAHTHTMH TLPYTTHCI
4699	18600	A	4730	309	443	VLTLSPLRECCSSMNIHYSCLKLLGSSDH PTSASQSGGIIGMSYHA
4700	18601	A	4731	3	172	DAWAFFNGPGVSLCCTGWSRTPQLKRST CLSLPKCWDYRPEPLSPAPKTLFSYVLL
4701	18602	A	4732	98	232	QTVFLLIWLLALCSPGLVQTVKRFLFR CIFSLGIVTFICLYRN
4702	18603	A	4733	238	1	LGPPPPSLGPPPPFLVIRFGFSFPKTP FFSPFFFGPPPPFFFFFFFIIRSFAL VTQAGVQWRDLGSLQPLPPGFKR
4703	18604	A	4734	121	424	LIQGHVRVVIYFSQLRKVRGRQACDSTLL GHLPKVVRMFPFLSFTVAGLEPTSHYR MFVDVVLVDQHHWRYQTGKWVQCGKAEG TMPGAR
4704	18605	A	4735	319	8	NPPQKKKKKIFPPPKKTPPKKIKNPP PFTIFFFFFFFFFFFFFFFFFFFFFFF FFYFQHVWFCFEIIHVIFFLIEVLFLAF HVGDSIADAWSTKNSNRK
4705	18606	A	4736	297	442	TQGGFFGGPRKIGFFFRGLKNGGGGNPK LRFLKPGQLVGRGKTKKNQG
4706	18607	A	4737	430	0	CVLGSKDKKKKKKKKKKKKKKKKKK KAKKKDS
4707	18608	A	4738	137	1	INYYFFLKQGFPLLPRLCEGSAITAHCS LEFPGSSDRPSASQVA
4708	18609	A	4739	188	3	ISPALKNPREVGPIFPFPKKKVPQNP PGGFFTPPHKEKNFSLPPVNLGPPKDP LKRPP
4709	18610	A	4740	188	2	TSLPKCWDYRHEPPCPAHTLLIFLFFIF VDMGSCHVAQVALELLGSSDPPTSASQS AGIIGM
4710	18611	A	4741	410	1	RRPGGGFCPPPPPKIFFSPPPPPFVGV LPQTTPPPKKFFFLNPPGFFFPKPKK KIFFFSPPFFSPPPIFFPPPPPPFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF GKDRVSLCCSDWSRTPGPKPSSL
4711	18612	A	4742	225	444	ENLKLKSFPCSHFHWLRWFNLITIGALSR SFDEAALLFFQNDTYWPGTVAHACNPST LGGRGGRITKSRDRNHS
4712	18613	A	4743	2	452	VSNPAVSVPHLPFSVYKSSPMASMTFSK KKKKKTKKKKKKKKKKKKKKSGGPQ KKKNR
4713	18614	A	4744	3	144	LAAVLLKLGYGIIIRLTILNPLTKHIA YPILLLSLNPDIITGFS
4714	18615	A	4745	206	2	IQNPQTERVNSTSKLISKDTINRAKK QPMDEWICKKHIFGKELISRMKELQL NNKKQIVPPTRP
4715	18616	A	4746	523	178	RHRRFFMDIEREQVKEQQRQKEQKDIE KIKDKREQECYAAEQRIILRMNFHEDPYS GEKLSEILAQLQLQEIKGTRKQQRKE YLRVVEALRAQIQEKMLYNITLPPLC
4716	18617	A	4747	3	518	ENRLNLEGGGCGEPRSRHCTPTWAT

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4717	18618	A	4748	491	145	LCHVGQAGLELLTSSDLPTLASRSAGIA GVSHRTRPHSHFYFYFLYSSSFFFFFLL AQRGNRAPRGKKTFFGLATLNKSNGGV FWFLFLGFGFLKREPTFALGLKDRGNNL V
4718	18619	A	4749	6	362	NKLENGTEFLSSLPVNTFFFSFLFFFFF FFFFFWGKGPPRGGGAKFYPLEFPPPG VPPPPKGGKKGPPPTNFFLFFKKEGGS PFGPGGVKTPGPKGFPSPQORGKKKGQ WAQKPP
4719	18620	A	4750	380	3	SLLLAFALLCLPWLQEAGAVQTVPLSRL FDHAMLQAHRAHHLAIDTYQEFEEYIP KDQKYSFVHDSQTSFCFSDSIPTPSNME EPQHKSNELELLRISLLLIBSWLEPVRFL RSMFANNLVYDPS
4720	18621	A	4751	1	345	LFYIFKKTWSLFLCFLWMMCVFIFFFFL LFVFFFLCLGGIILVSFIPPGGEKREKKR RGGEKKKKKKNVVFKKKKKNPWGGGGGL KKQRARGGKKKKKKGGGSGGGKKKQSP LRG
4721	18622	A	4752	1	407	QEFEETYIPKDQKYSFLHDSQTSFCFSD SIPTPSNMEETQQKSNLELLRISLLIE SWLEPVRFLRSMFANNLVYDTSDDYH LLKDLEEGIQTLMGVRVAPGVTNPGTPL ASRAGGEKYCCPLFSNKARDQEN
4722	18623	A	4753	357	1	PLFFFKRNLFFFFFFFKKEKKAPVFFF FPPPSREWGFFFFFRVGGVNTQFLHPFFF SQNTSVFFSTLFFFFFFFIFFFFFFFF FFFFFFFIFFFFLFYCFIYFSR DRGLTLL
4723	18624	A	4754	1	207	LGLAGVEEVEASRLNAGRGCSKPRSHD WTPAWAMEQDSMSKKTNEYQRRQLIHL QSSTSGFLYVHEQ
4724	18625	A	4755	2	336	HEERERERERERERERERERERERES RAQFRARKNSQAPHPRVCETLWTEEGGS FYPLTEKDFACERAHFCVLGVSHPPGW GLCKKMNPECERATHSLHGDADISGVL
4725	18626	A	4756	230	446	VGFSSLFSTRYCTILISASSLTKEKCEKK RSFLFCFAFWLLGLRQSLALSRLLEYN GAISAHCNLHLPSSD
4726	18627	A	4757	3	390	QTSFCFSDSGPTPFNMEETQQKSNLELL RISLLLIBSWLEPVRFLRSMFANNLVYD TSDSDDYHLLKDLEEGIQTLMGLEDGS RRTGQILKQTYSKFDTNSHNHDALLKNY GLLYCFRKDMDKVETFL
4727	18628	A	4758	234	387	LAKIFLSFSSATGWIENRPQSPATGRTP VFVSPIPPPLPPPPFPAFVT
4728	18629	A	4759	396	0	IYTHTHTHTHTYIYMYVFMI
4729	18630	A	4760	176	384	MVIPLEFNKDTQHILFWGVLIFFFLKR NFVFVAQAGGQGRYFGSLKPPPPRLKPF SCLSLLGTDYRR
4730	18631	A	4761	419	208	IYPPPPPWEPKGSFLKKKKKKKPGPG VPPFIPPLGGQAGGFPSKIQIPPAQ GKPLFFQKNQNYLA
4731	18632	A	4762	158	2	GNQLNPPPPSGSAFCFLFLRRSLALVT QARVQWDLGSLQSPSGFKRFSC
4732	18633	A	4763	489	398	AGFELLTSSDPPASASQSVGITGMSHCT QP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4733	18634	A	4764	420	1	FFFFFLGEIFPPGGKGGVFPPLKKFF FSPRGLFFLGGGPNFPFKRVFFKKP RAGFFPPPGVLKRGPGPGFLTPPQKEKN FFPPPGVLGPPKGGFFKGGPPFFFFF FFFLGKKKKKKALFFTCKKGGGGTVRKA
4734	18635	A	4765	167	3	IYFFFLKKIFFYKKKINKLKKKKKKKK KKKKKKKKKKKKRAARDLELAHAS
4735	18636	A	4766	424	222	FQNIHKKNFSPPLKLTGPAPLFKKPPK KKKKYFFPPPEKLGPPREFLKGPPPPFF FFFFFFFFF
4736	18637	A	4767	254	423	VIKSWARNKNKWDWPGAVALS CNPSTL GGPGQANPLRSGVQDHPGQGETLSLLK
4737	18638	A	4768	363	0	KTTSQARGPTSVIPAAQTEAGDSSNP SGYGSYSSSSSSSP
4738	18639	A	4769	51	169	YTHTHPRTGFVKKKKKKKKKKKKKK KKKKKKRGGGF
4739	18640	A	4770	188	3	ISPKALNPRREVGPFPFPKKKVPPQNP PGGFFTPPQKEKNFTLPPVNLGPPRDP LKRPP
4740	18641	A	4771	1	131	KLDKENALDRAEQAEADKAAARGQLE DELGSLQKKKKGGPF
4741	18642	A	4772	363	452	RLECSGMIIXHCSLNLPGSSDSPTSASQ LA
4742	18643	A	4773	121	1	RPRRPVAQAGVQWHNLSLQPLPPGFKQ FFHLSLLSSWDY
4743	18644	A	4774	31	226	MISSQLSIITPTQEQGLKKKKKKKKKK KKKKKKKKKKKKKKKKGGGLLKKILG GAKFLGGEKKNFFFF
4744	18645	A	4775	161	1	KPPPPPPPPPPPPPPPPPPPPPPPPPP FFFFFFFFFFFFFFFFFLFFFLKKSWRP WGLKSAPAL
4745	18646	A	4776	394	67	SPPRGEGGVAPPPPPKNFFFPRAVFFLG GGGGPMPPPKRGFFPKTPGGVFKPPPK GGKFFPPPGGGPPPEFFKGPPPPPPFF FFFFFFFFFFFFFFFFCFEEEEEE
4746	18647	A	4777	2	409	GVCIFSGHKHNKAPLPFVLYSIQYINS LEKKKKKKKKKKKKKKKKKKKKKKKK KKT
4747	18648	A	4778	456	0	PFYKKKKKKKKKKKKKKKKKKKSSS
4748	18649	A	4779	438	0	LLKIDKKKKKKKKKKKKKKKKKRTSKR GG
4749	18650	A	4780	58	330	SEFYQLKKKKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKK GKKKCGGGVVLVGKPHKEKKRGGGKKKN FSG
4750	18651	A	4781	435	73	FFPPPPRGKFFFKKPPGGKLFSPPELGV FFPPFPLKIFFPSTPFFWGGFPFSP PPKKVFPKFPFGFFPPPLKKKFFFS PPFFLPPPGFFFSPPPPPPPPPPPPPP FFFFFFFFF
4751	18652	A	4782	420	109	LFKKFFSPTEREGVFPQPPKNFFFSNP PLFFGGGGAQNFPQKNFFPKNPFGFF FSPPKKKKFFSPPGKILAPPGYFFKGP PPPPPPPPPPPPPPPPPPPPPPPPPP PPPPPPPPPPPPPPPPPPPPPPPPPP
4752	18653	A	4783	230	2	LGLVVGALYSPFLGGLGGRKFLLPWRPR VPLTPISPPSRLGGPPKKKKKSQAWWHA PVVPTTREAEAGGSLEPRRL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4753	18654	A	4784	271	440	VLYSKRDNNKSFKNNTYTGTGPGVAHAH CGESTLGGRGQIMRSGVRDCKPYRHGET
4754	18655	A	4785	2	266	KKYGIIIFCSFFLSLFLKDQGLAPLRL ECSVVFAAHRGLGLLGWSDPPKSAFLVA GITGMHHHAWLIFKVQFSNLMGPWSYTW SAVD
4755	18656	A	4786	216	435	HRSGDSSLKKKKKKKKKKKKKKKKKKKK KKKKKIWEFWKGPFLWGGKKRKSGGG
4756	18657	A	4787	249	437	MNNEVVPLKTETSRPDVVAHACNPSTLG GRGGQITRLGVQDQPCQHGAEPSLPENR KYLAWSV
4757	18658	A	4788	107	368	AHGSLDLFLPGGPKKSHQWFPKPKDGKPP PFSKKPLKKKTPGKKGGHPTPGARSKK GGYPRGGDPGGPFFFKKPGQKKKTPFLL RRD
4758	18659	A	4789	1	225	PTRPFITNNIFPASPFQTTIPLYLKLTA LAVTFLGLLTTLDLNLYLNKLIKSPKC AKKKKKKKKKKKKKKNEG
4759	18660	A	4790	2	216	SGRNSRVDRQEAAACRDYQSSLEDLTFN SKPHINMLTLAEENLPFAKEIVSLIEA QTAKVFIHPAASYF
4760	18661	A	4791	389	30	EKKSPQKKKKKFFPPPPQKKFFSPPNQ KTCGGGGPKKPPPKKKGSPQKNPKGVKK PPPKKKKKIFFFFPQKKGPPPKILKKEPP PFFFFFFFFFFFFFFFFFYFSLFFSGG FSYKIFL
4761	18662	A	4792	164	3	LFPGFNPGVKGEKGISFPFFFFFFETES HSVIQARGQWRRGLSLHPLPPGFKR
4762	18663	A	4793	550	413	AEMGFHHVQGAGLELLTSSDPPALASQS AGITGISHRAQPHRPIC
4763	18664	A	4794	456	352	RSQDGLYLLTSSFACLGPKCWDYRREP PCLAVFF
4764	18665	A	4795	242	3	KPFSGGGGAFTAFFITFGKKFVVSRLG LLKKKVFLKFLPQAFFFFFFETESHVA QAGVQWRLGSMQSPPGFKRLS
4765	18666	A	4796	218	346	GFSCFVFETVSLCRPGWSAVVRSRLTAT SASRVQAILPQPPE
4766	18667	A	4797	383	80	KFFFNQIGIGFFPPPPKNNFFSLKPPF FLGGFSPFFPPPKKIFFSKIPGFFFSF PLKKKIFFFPRLILAPPRFFFKAPPPF FFFFFFFFFFFFFRPI
4767	18668	A	4798	1	126	ILIKLSSTWEGIQAGKELEEQHGHCNM TLLFSFAQAVACAE
4768	18669	A	4799	81	356	ILFFFFFFFFGGGTPKKSQVFFKNPQNP GKPTRMGKGEKPPPPRGKKKKGGPPTL GKNKNPVPGWPGAFLPLEBKPKPFGP PPLKKK
4769	18670	A	4800	1	99	GCSEPRSRHCTLSWATRKLHLIKKKKK KKKGA
4770	18671	A	4801	238	5	NHQNSVQNYFKNLRIFQLIYSLSMNLP SSFKLKSMTHSISFSFLSFEEIQSHSV AQDRIKWHDLGSLQPQPGLK
4771	18672	A	4802	166	62	IFLFSFFLFLRDRVLLCYVGWSVMVQST QTPGLK
4772	18673	A	4803	102	6	AASTTESPSVAHAGVQWCDLGLSKPGSR RFQ
4773	18674	A	4804	17	374	FGSRAATLFFFFFFFFLGRGGFFLGRGPK KKTPGGEGFTRFFDPGWGKGPEKTPPP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						WGGKGGPKKMNWLGAGKIKFLEIKGKSF PRGTTNPFPGPPLFFSPKKTQGPNGFLD FSFKLKN
4774	18675	A	4805	59	175	SFYFFFLMMKKKKKKKKKKKKKKRGA LKKKTGGGPN
4775	18676	A	4806	406	300	SSGVLYSRAPTYFCGQTLTFRQVDIKTS HLPQEA
4776	18677	A	4807	123	1	KSTAWLGTMAHSCNPSTLGGQDQGTTRS GVRDQPGKHGETP
4777	18678	A	4808	319	406	LYKSYSSWPNVVAHTCNPNTLGGQGGQI I
4778	18679	A	4809	236	351	GFWPAPGVHACNPSILGGQGGRTGPKL GNLLGQHGETI
4779	18680	A	4810	173	2	EVLFLGFRSILISLLQMNLYLLIAKFA FVAQAGVQWHLSSLLPPPPRFKRFSCL R
4780	18681	A	4811	2	94	TRILKVWQKRKCSVKNGFLTISHGTVSI LF
4781	18682	A	4812	358	2	FFFFFFSETESCSVAQAGVQWRDLGSL
4782	18683	A	4813	362	3	YSEVCIISLQQAHDLSLVINFHLAECVI QLPVNLRRLPGAVAHSPGLSELCSFSDSG SVPSHTRSFPAKAIRLTANHRRGCTESG WPFSLVFLFERCMWPGTVAHTCNPSTLG AQQGGIT
4783	18684	A	4814	341	1	WNQKRAHITKSILSQKNAGGIMLPDFK LYYKATVTKTAWYWYQNRDIDQWNRTEP SEIMPHIYNYLIFDKPDKNKKWGDLSL NKCWENWLATCRKLELDPFLTPYTKIN S
4784	18685	A	4815	2	283	VYTGEIILQKKEITTRDQEAPLYLRNLS DHTVAISSSTTLDCCHANGVPEPQITWFK NNHKIQEPELYTSTSPSSSSSSPLSSS SSSSSSSSS
4785	18686	A	4816	266	3	AASTLQAHRAHQLAIDTYQEFEEYIPK DQKYSFLHDSQSLRQLHTHTGSGVTRT LAASLSSGRTAHTRTHMHTQHTKRRTAH TNA
4786	18687	A	4817	365	1	SFFFFFFSETESRSIGRLEFSGTISAHCN LRLPDSSNSPASA
4787	18688	A	4818	87	372	ASYKKDKYCMIPILIRVIKFPQTERKKWL SGLGEGNKELLFNGCNMAVFLVLGGGF ETEPSPVTQAGEQWCDLSSLKPLPHRLE RVSCSLPSGW
4788	18689	A	4819	5	175	FAFLTIPLSRLFDNAMLRRRLVQLAYD TYQEFEEAYILKEQDQDQSLQNPQTS LCS
4789	18690	A	4820	235	351	FFXFFFXFFXFFXFFXFFXFFXFFXFF XFFXFFXFFX
4790	18691	A	4821	2	155	IFLLLESWLEPVRFKSMFANNLVYDT SDSDDYHLLKDLEEGIQTLMGRL
4791	18692	A	4822	90	2	LEFFFFETESPSVTQAGVQWHDLSLQ P
4792	18693	A	4823	247	3	KVKGSPSHRRAMVAKGNLSLHERMKSPG ISNYMGNSKILFSYFKNCWPGTVAQAYN PSTLGRGGWITRSGVRDQPGQYSET
4793	18694	A	4824	93	407	QHPKKKKKWGGRGPLNKEKVFKHKT FFSRQKKKKKKKKKKKKKKKKKKGGG GLKKFWGGPKFPGGKKKFFFGGKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						NPPGVFLKKNFFWGGEKKKKK
4794	18695	A	4826	2	129	TTAHCSLNLPGSSDPPTSRSLVAGTTHVCHNAWVNFVFCRRG
4795	18696	A	4827	342	140	GGFFFFPPPPFFFFKFPLFLPPPPPPGPS CVGGVQKFTFPPPPQLSRSLFFLFFFPAP PPETDNPPFFS
4796	18697	A	4828	1	259	GGGCSEPRSCHCTPAWVTEYDKKKKKKG RGKGGKKIGKGGFQRKFGPNPHGRFLR ESHNSPKKGFPPKFFGNPPPGTSKKVPL PH
4797	18698	A	4830	125	1	KGTRTFETESRSVAQAGVQWHDLSLQPLPPGFRRLTCLSL
4798	18699	A	4831	1	323	ARGEREREREREREREREREREPPPI SRGGSSEYLKSAWRERLLERDPLFFFG GKMGNLFPPPPPPVGRGYTGGGLITGGP FWWGEVSHHTHTHTHTYMSV
4799	18700	A	4832	3	297	TRRERERERERERERERTL
4800	18701	A	4833	1	150	AREREREREREREREREREKKKKN HSRGGGPGPQFPLGGGVKKFGGGV
4801	18702	A	4834	1	98	ARGERERERERERERERERERE RERGAGGGPT
4802	18703	A	4835	2	66	HEERERERERERERERERERAAAR
4803	18704	A	4836	2	73	PEERERERERERERERERETAR
4804	18705	A	4837	146	2	FGLVYSISQFCLFFVRRSLALVTQGVQ WRNLGSLQALPPGFTAFSCL
4805	18706	A	4838	354	0	PPPPPPSPPPPPPPPPSSPPPPSPSP SSSP
4806	18707	A	4839	62	358	GLVHDKHSHPHGGCGSHHVLPSLNPSFPT FSTKSPSPPARALWPPDSRWALQVGH GLTPTTRQESAQAPRRKLALLEGSFQGG AQWLTPVIPALWEAE
4807	18708	A	4840	121	13	RPGRPPPEFTPFSCLSLEGSWDCRRPP RPANLLYF
4808	18709	A	4841	3	221	LVMGFVGFSSKSPSTYGGIALIVSGVVG CVIILNFGGGMGLIVFLIYLGMMVGF GCILDFSLNFNVLNF
4809	18710	A	4842	3	84	CHCTPAWTANLDSIKKKKKRKKFKN
4810	18711	A	4843	33	230	LTVTISKAAEVLKHKKKKKKKKKKKP KKKTPKKNPNPPPPQKGELGKKIFFFWE RFLPQKKRP
4811	18712	A	4844	3	368	HELNPRGRSCGEPRPCHCTPAWATRAKV HITKKKKKKKGFNLFKPGGSLSNFFPKK KETPWSQNFEEKGPRRFSRGNPPLA LRGKKKGKSLSGKIFPPFPRGKTPPWA FMGTQKGEYS
4812	18713	A	4845	163	2	HHGHSISKFLLTVSSPKSFNQLRPDAVA HACNASTLGGRGWITRSGVQDQLV
4813	18714	A	4846	387	234	KGCGEPRSCHCPPAWATIALLFKKKKT KPKKNPKKQEKTFPYNLNRVCY
4814	18715	A	4847	189	349	KFSRFSGQKALLKDLRLGTAAHTCNP STLGGQGRWIMRCQVFKTSLAKMVK
4815	18716	A	4848	3	95	HENFYCPGSALGRNEGNIFPNPEATFVK EM
4816	18717	A	4849	2	325	DSHTIIMGDFNTPLAILDRSTRQKVNE IQDLNSALHQADLIDYKILHPKSTEY FFSAPHRTYSKIDHKIYSQGNHETDCRY GKKGGGWKDERFPDVCCKFKSQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4817	18718	A	4850	241	348	SFFSQTQASEQLTKSKQGLALRTLPPVQ FPPPPRP
4818	18719	A	4851	2	176	LVETGFCHVGQAGLELLTSGECWDYRCE PSPAYCFLHTIVTIYPLLCLAFFSYLC DC
4819	18720	A	4852	2	191	VGRVGLELLASSDLPTSGSPSAGITGMS HCPWPNFLLIFIGYFFTULTPEYYSGG MTVPLWL
4820	18721	A	4853	67	376	IKCTTFNIKKKKKKKKKKKKKKKKKKGG ALKKKPWGGQKKTGEKKKKFFSKRGGKK KRGPGRVLKKGEREKIFWNFLKKNFFW GGGNLGQPPPKLRLALGKK
4821	18722	A	4854	278	363	IWPDVVAHTCNPSTLGGQGRWTRMSGRV RGCSEPRRLRYCTPAWATEQDSASKKKKK KKTQIFWEGPGGGVSPFKPHFFKGPQGGK KPWGQKFKNPPQWEKPLFFFKKKKTKF SPGGGGPP
4823	18724	A	4857	382	224	PVIQLIGGVRQEKNFNLGVKGFNEPKSP PCPPTWVAKQNSLSKKKKKIGKK
4824	18725	A	4858	392	102	FFFFFFLRLQGLSVVQARVQWCFCSNLGL LGSSNPPTSASLSCFLNKKEYRWENVTN KV
4825	18726	A	4859	3	111	PHRISQEGLLILLTLGSAHLGLPECWDYR REPPRPA
4826	18727	A	4860	282	83	AQIYKVQNWGSSGNKICVCVCVCVCVC VCIYIYMLCMSRFKYKCIIVGCMNIDSYV VYIPNIQCYI
4827	18728	A	4861	3	417	NHSNLGGRGCSDPDSRHCTPAWVTERDS ISKKKKKKKKKIFFGLREKKLTLPFPLG KKNENSGFPLNPNFFFGKGGKATLGLPL GLVLRGVPPFRGGETQNGENQKPGTTLE KFEKHFWVGPPPLEKISPHKGKQTQK
4828	18729	A	4862	1	88	MEEMYKKAHAAILNPVYEKKPKKKKKK K
4829	18730	A	4863	274	369	VSLCCAGWRAAVRSQITAALISRAQAIL PPQP
4830	18731	A	4864	37	444	DPVRSEKKIPFKILLIDNAPSHPKAL MEIYEEINVIFMPANTTSILQPMQGV STFKSYLRLNTFHKALAMDSDVSDGSG QSKLKTFWKGFTILDAIKNIRDSWEEVK LSTLTGVWKKLIPTLIDDYEGFKT
4831	18732	A	4865	341	210	VYMCHVGLLYHQPVYIYRNRIEASEITP HIYNYLIFDKPSHQF
4832	18733	A	4866	206	412	QLCLSQACTLARGNAKGLKYIHRNNVS MPSVAGHTWGPDLVKGQGETCPATIH SDSPSLKYTMYPM
4833	18734	A	4867	248	78	SHFEAGLAAQLTVSWFPQGTVPFVHAGP FANIAHGNSIIADRIALKLVGPEGFVG
4834	18735	A	4868	637	2	EFDGRWPRQIVSSIGLCRYGGRIDCCWG WARQSWGQCQVPCQPRCKHGECIGPNKC KCHPGYAGKTCNQDEHLPAPLDQGSQPP LFQPLDHQATSLPSRDLNECGLKPRPCK HRCMNTYGSYKCYCLNGYMLMPDGSCSS ALTCSMANCQYGCDEVKQIRQCPCSPG LQLAPDGRTCVDVDECATGRASCPFRQ CVNTFGSYICKCHKG
4835	18736	A	4869	276	426	VSFFLFFFWGANPPFVPOAGGQGGFLG SLNPLPPLGKHFFCLTPPSSGN

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
4836	18737	A	4870	100	485	EERNREMTERTCSVTQAGVQWHDLGSLQP SPPGFKRFSCLSLPSSWDYRLECDGMNL AHGKLRLPGSSSPASASRVAGITGMCH HAPLARLVSNLTLPQVILPPLGLQQAEL PRRQVEHNTPLVPI
4837	18738	A	4871	718	408	EVLTQLLAHFPGLGAHWNQDAAALGR ATDSKEPPEELCPDVLRTARTLHGQET YTPRLILMDLHYDVSLGALVLTAAGYRA SSCSQSVAVCTGSLVLEA
4838	18739	A	4872	392	246	RGGCELSRCHCTPAWATRVKLHLKKKE KRCKIRPEGNEILVNNAKG
4839	18740	A	4873	1	156	GGGGYSEPRSCHSTPAWITRAKLRLKK KKKKKGVCVFGVFLGPRPKGGFF
4840	18741	A	4874	246	2	AHGTSIYASMLAMSISSRNVSFRAGQ VKAVFPVSVVFGPLHRHLGEHFLFLR QSFTLVAQAGVQWCHLGSQPLPPA
4841	18742	A	4875	72	2	CEPAAPDEDSTTNITKKQKWIVE
4842	18743	A	4876	375	221	GRLRQENRLNPAGGGCGEPRSHYCTPAW VTEQDSISNICIYINIFSVVHGQ
4843	18744	A	4877	151	2	RAPFFFFFFFFFVAQAGVQWRVLGSLQAP PPGFTPFSCLSLPSSWDYRRP
4844	18745	A	4878	401	70	PHRREGGCVPPPPKNNFFSPGGYFFWG GGQNPPPPKGGFFPKTPPGFFFSPPQK KKIFFPPPPERGGPPGFLRPPPPFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFF
4845	18746	A	4879	4	152	LPYSTPSTPFRAKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKRGNFK KR
4846	18747	A	4880	267	1	TPPKKKKKKIIPPPKNGPPPHIFKKTTP PLFFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFRTGRTRGRTRGR RGR
4847	18748	A	4881	2	408	LQDATSPIIEELITFDHALIIIFLICF LVLYALFLTLTTKKKKKKKKKKKKKK KKKKKKKKKKKKKKGGGPKKKNRGG PKKLGGEKKIFFFKGGKKKTRGGVGKK KIFLGGGNFGPPPKKKKPRGKI
4848	18749	A	4882	413	69	LPPPPPGFKHFWAPPDPGRVPGPPPP RVNFVFLGKKGVSPFGPGGPRPLFPNPG GVGAGDPLDPRGQGFHGFMPCCPARG TKREPPPKKKKKEKEKKEPERKEKKK EI
4849	18750	A	4883	46	394	KQYQVSVKLLFVTQNLGTTKKKKKKKK KKKKKGALKKKPGGGQKKPGGKKNNF LKRGGKKPPGIFEKTLFGGGENWGTP PQKKKPPGKKKKILKGEGGKKTLYFGRG KNFS
4850	18751	A	4884	399	3	FFFKKFFSPNEFWFFPPPLKIFFPPP RLFFFWGGLAQFSPPKVFFSKFPRGF FFPPPLGKNFFPPPGYFWPPPGFFLRA DPLFFFFFFFFFFFFFSVSIRNAIAI RMGTMRSRRLAMGMLRRG
4851	18752	A	4885	391	47	PHFFWGGVFPPPPKKKKFFFLPQKGGG GGAPKKKKKKKFLPPNFGGGFFFSPP GGPRRFFFFIFFFFFFFFFFFFFFFFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=/possible nucleotide insertion)
						FFFFFFFFFFFFLSKMFTFILKYTLKQNEFY
4852	18753	A	4886	32	379	LLPVKKKKKEKKGEKKKKKRKKKKKKKK KKQKKKGGPSIKIIIGGHLSSGGRKNN SFSHRGGLKKPLFFLGRTYFLGGGLWP HPPPKKIAGGAKNIIIRGWGEQKP LLFP PGEK
4853	18754	A	4887	178	33	IFKRKVVFRRFFFFFFFLLYYFFKF F FF F FFFFFFFNICHHPKLY
4854	18755	A	4888	238	3	KPFNPFKKKIGPQQKKKKFPFCLKNP PKYKTQNINIIYKIKIFFFFFFVRGSDS VAEAEVQWHHLGSLKPASPGFK
4855	18756	A	4889	93	1	DGILLSPRLKCSGTISAHCNLCPPGSS NSR
4856	18757	A	4890	6	219	I EKAKALGTVPGSTFVRVHHYHHHNHY HHHCHHHHPHQDNSEWEKAQSLEPDCLF LNPGFATSQLRGLR
4857	18758	A	4891	1	364	TSSRSRAGRPMDFGFFFKKKGHREPFGG VEKKKNWGSRKTPPSGVKNFPGFDPK MWNKGPPPTPPNVFSGFKKKRGFHKLK PPPPEIAPLNPQGGEKKGGPPPPPTPF LGGKFQGR
4858	18759	A	4892	387	81	GVSFPPRGGPPEGKTPPFPRGGPFPCG PGGRGPIFPPLSHKFFFSPPPPLLGGG GGPKSAPPKGVFKEFPENFWGAFIKK SFFLKGGFGPPRGFF
4859	18760	A	4893	213	14	KTPPFFFFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFF FFFFMLEVMFLVNRRGKICRVPTTFNL SL
4860	18761	A	4894	384	10	PLPFPIPPPPPPPPLFGGVCVPYSPPP HLGSPSPPPGGRPSPPPPPRSTPPPP PPFFPPPPFVSGAPPPPRSCLAPFF FFFFPPPPPPPPFFLPFFFLKSD FI F S L QMXYFM L I
4861	18762	A	4895	240	355	LIITPALFFKIFVLWLGAHAACNPSTL GGQGGQIMRS
4862	18763	A	4896	339	3	GVGWHLFPFPQKKFFFFQVTGASCAAK SSKESHKGLHLNIYLPKIFFYRPPPPFF FFFFFFFFFLEFFFFFFFFFFFFFFFF FFFLVREGYNQHFRMGPIGRVGGRV
4863	18764	A	4897	56	335	TCFLYKLLLLLLLLLLLLLLLLLLLL KKRGGPLKKNLGGPKNRGGKKKIPFFK GGEKKNLWGFFEKKPFGGGKICTPPQ KKKPPGEKK
4864	18765	A	4898	7	206	LCLQPDNRWDDQSKSF L EKKKKKKKK KKKKKKKKKKGGGPLKKNPGGAPNN PGGEKKNSPP
4865	18766	A	4899	74	250	INTCSEKLPKKKKKKKKKKKKKKKK KKKGGKIKRGLNSQTSLKKREKKKRG KI
4866	18767	A	4900	151	312	KYHFHKNYFFSLLYFSQNVSQLSPDGPL PQLPLPYINSSATRVPFGHDRPADG
4867	18768	A	4901	1	364	LNLGGRGCSEPRLRYCTPAWATEQDSAS QKKKKKKPNF
4868	18769	A	4902	1	96	GGGCGELKSCHCTPAWVAEQDVS K KK KRG
4869	18770	A	4903	3	225	GFHRVGDGFDLPTSWTARLGLPRGWDW

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						RREPPRPAVWAGLQLLTSSDPPASDSQR AGITHLSHLTLFCHLRF
4870	18771	A	4904	384	194	HWVGRPFNNLWGQKNPPPPPPKRLVYQG WGPPPPPPPPFFFKKTPIFSQVFNPPPPF FFFFFFFG
4871	18772	A	4905	3	387	TIITPILTLFLITQLKILNTNYHLPLP AQYPLPQKKKKKKKKKKKK
4872	18773	A	4906	1	327	PTRPTEPIPENPKFSVPPITPHPKKKKK KKKKKKKKKKKKKKKKKKKKGGALKK KTWGGPKRGGGKKIFFFLRGGKKKPRG EFLKKTSEWGGENLATTTPKKKKKARKKK KNF
4873	18774	A	4907	134	2	ALYSLKVKWPGAVAHACNPNTLGGQGEW IRRSQVDRDQPGQHSET
4874	18775	A	4908	59	449	ATRHYYTIMLAYTSVGIPITAVVLGKQAI KGARFQVRRRTTENYDKQQLIHKGGGRPP GCHSTHTVLLPPTVWKTGTGNSTVANFV LILVCLSFLLLVYRCIQQLQSDSNQREG AMMMVVVLSKRKGGYAGK
4875	18776	A	4909	337	3	LKTAWATRGNNPLYKKNQISGARGE PIPLIGGGLSQKNFFTPGGENSINDDPP PSPPPGAKKETPPPGKKKKKKPTTKELG KDWTELEWSDSQRAGKLAEPGESSP
4876	18777	A	4910	14	162	AESGAKRETAFFAPQQGATDKRLNIY AAKHKMTCLPSLAIREMQIK
4877	18778	A	4911	331	2	LELLAPKEGQGGKILGYKKPPPPGLPPFF GSTPPRNKEKGGPPPPRGNFVVFKNNG FERLGGRGPPPGPKPPPRPPQKGGKQG GNPAAGPFFFFFETEFHSCCPGWSA
4878	18779	A	4912	116	316	ACAHATLFFFFFLKKKPPFVPLLGGKG GNLGYLKLWLPGLKKVCLTPRTGNYYG APPHRIIFCFL
4879	18780	A	4913	93	16	SPPGWPPTVAHACHPSTLGGRGGRIT
4880	18781	A	4914	316	2	KPRPGNPLRARVFNPPGPPGETPFFPKN PKFTRGGRGPIYNPPFGRVRPKNFLYP RGSRFHWPNSIPCFAWGTKNFFSKKK KKRKKKKKELCFASVDAQ
4881	18782	A	4915	3	289	TSCNPSTLGGRGGRITRVGVRGQPDQHG ETPSLLKNYIYIYICVDVLYVCMYVGA YIYICICGYIYIWRVLSLTSEHTHTRAP QYRVYIYFFCG
4882	18783	A	4916	1	222	ARGERERERERERERERESRHQGGGAGP PHTLWGEVGLSSPQTGVREKNAPIWG CAAPVLAPRVGRTPPFGVD
4883	18784	A	4918	1	281	ARGERERERERERERERERERERERE RERERERERGAPPPPPRGVRERGTPCP SARGARALSPTISCGDPRHGPKIYRGVG VHTQRYFSVGSSLCINTHT
4884	18785	A	4919	1	259	ARGERERERERERERERERERERERER MVTLPAGIYHRFGGGEKKYTKAVRVCVR KPGWRAHNRPADHFGARGPHVKFLAQTV YE
4885	18786	A	4920	797	910	NTMQPGVVHTCNPSTLGGQGGGRITGSG VQDQPGQHGE
4886	18787	A	4921	2	67	LEERERERERERERERERERERSS
4887	18788	A	4922	1	698	TLLLAELGTICDPYRSCSISEDGLSTA FTIAHELGHVFNMPHDDNNKKKKRGGPF KGNFNSPPVRASKNFFFGPPNLNSWARF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LTPGEGKTPGVPPFPNPFATKAEL
4888	18789	A	4923	323	2	LVCGRGTIHKFRCPVPHLTGRRFEHGVTDCTYTLFRDAYHLAGIEMPDHFHREDDWWRNGQNLVLDNLEATGLYQVPLSAAQPGDVLLCCFGSSVPHNHAATYCGDGELLHH
4889	18790	A	4924	3	225	HEEALHLFQTLMECMKRRELITVFHIGSDEHQDIDVAILTALLKGKPLRTFLFVRPFILCMYMCVVVICVCI
4890	18791	A	4925	371	169	HTQSISVVLVERRFHHSQENPLNPGGRGCGELRLCHCTPAWATRAKSRLKKTQTKKDAIKCSLCN
4891	18792	A	4926	2	352	ARAARAGRIIKELFFFFFFGNLKKKKGLFWWPGGVKNPDLGNPPWPWKGGGITGLTPRPGPMGVIFKKFGKKGSPSPTGPKSLGEREFFGLALQRGDDLGLNHRGPPFFFGVLETM
4892	18793	A	4927	2	379	ARANMEETQQKSNLELVIRISLLIKTGLBPVIRILSRMFTNNLVYDTSDDYHLLKDLQEGIQITLMGRLENGRRRTGQILTQTSKFDNTSDNHDALLKNYRLLYCFTKDMDKVETFLRMEQCRSV
4893	18794	A	4928	175	31	ILGDLFPPAWLHPFLFLLPFPSRPSLAVTEVAVQWRNLGLKQPLPPGF
4894	18795	A	4929	368	247	VDRLFPPCCPGWSPSLELNQSACLSFLKCWDYRCEPLCSVS
4895	18796	A	4930	2	110	ARGEPRSHHCTPAWAMSETVSKKKKSGGLFFLPRLV
4896	18797	A	4931	150	1	KYVAPCRPLFLVLSPCRSFCFPFFCHDKFPESFSEATMFFLQPAEPRA
4897	18798	A	4932	2	155	ARDDLNPGGGCSELSRHCTPAWATERDSISKKKKNPQNIWGNLKKKWNLK
4898	18799	A	4933	144	249	ETLYPQPQSLNASCVVCVCVCVCVCVCLCVCV
4899	18800	A	4934	2	153	ARESFEKGRHVGVGLKLLASGNPPNLATQSAGIISISHCTQWRQGL
4900	18801	A	4935	1	355	GTSQEFEGRKDRLASPLETGNAAGRERLAEVSTCPSGASKPLQTPRPGQEGTPGLGRRMRHSAGSPNPAPWESIRDPSLTSALLVACSI FHIHEDPILHDVLI SRCMSIKTSHR
4901	18802	A	4936	112	358	NIKFSKAFFFSFYIFILINSVGLASTFMWGGELKFSTSGILIIQPFFKIKGHPQRGILRTGTFKBDPDDPEGKNKVSSLLQ
4902	18803	A	4937	1	258	GTSPYVTQFFSGWGRQGLTSLPKLEHSELRLCHCTPSWVTERDSISKKKKKLIFYLAGPTFFPFGGNFNLAGRLLRGGEKK
4903	18804	A	4938	380	1	FFFFFSETPEYSVAQAGVQWC
4904	18805	A	4940	255	1	LGNNLAGYKIRGLYSISLRNNRHPSPIVSLCGNLFYVIRFFDMESCSVTQAGVLWCNIGSSQALTPGIAPFSFISLPSTRQNSRP
4905	18806	A	4941	10	173	KYIEYDTNKWKHNSCSQIGRINFVKMSLPPKAIYTFSVFPIKIPSVYLPVHLSI
4906	18807	A	4942	144	3	DKCIRRPQTVTHTCNSTLGDQGGVRMSGVRDQQGQHSETPSVRV
4907	18808	A	4944	484	274	PSSQSRSPRTARMIALSTFPTTRSMKFCHVAQAGLKLGLSSDLPASASQNVGISGVS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						HHTWPRFYLS
4908	18809	A	4945	103	412	KKKKKKKKKKKKKKKKKKKKGGGPKKN PGGAKKKRGRKKKIFFFKRGEKKNPGGI FEKKPFFGGGKNWAPPKKNKPFGEKKK FLRGKGGKNPPIPPGKKKL
4909	18810	A	4946	309	81	KFFFFLKLIFLGGFCPIFFPPKKIFFF KIPPGVFFSPPFKKNFFFPPLIFGPP RVFFKGPPFFFFFFFFFFF
4910	18811	A	4947	18	264	NYTQRFKVEYLNNIINQLDLTDIYRILY PTVEYTFKPNPHGTLCRTDHMLGHNTGL NKFKRTECTQSMSSDHNGIKYHSAP
4911	18812	A	4948	418	293	QLLRRVRQENCFNPGGGGCSEPRSPPCP PTWVTQVFFSKP
4912	18813	A	4949	3	252	DSAKHLGLKHVVYCGLENVKRLTDGKLE VPHFDSKGEVEEYFWSIGIPMTSVRVAA YFENFLAAWRPVKASDGDYVTLGKTK
4913	18814	A	4950	434	270	KRGFFPKTTPPGFKKPPKKKKKIFPPPP KIGPPQKILKKPPPPPPPPPPPPPPPP
4914	18815	A	4951	399	1	VGFSLFPPPPQKKGFSKPPRGFLFPPPK GKKKIFPPPGKIGPPQGFFKRPPLFFFF FFFFFFFFFFFFFFFFGPPSVTLFLVLTIL LQIQTTALGRKSWGKGFRIKPVCPVPA QOTKQGAHLLGQVVEINCA
4915	18816	A	4952	235	56	FTVVPPPKKKKKKNPPGGGGPVPPWGGK NKKIFLPKFKGPFSGAPLPFPFGQKK KPL
4916	18817	A	4953	13	194	SILISLQISLIITFTATELIIFYIFFET TLIPTLAIITKKKKKKKKKKKKKKKKKG GGAF
4917	18818	A	4954	177	1	PPQKKKKNIFSPPGKIGPPQGFFKRGPP LFFFFFFFFFFFFFFFFFRFEGECSDLG RV
4918	18819	A	4955	450	0	LPNKADKKKKKKKKKKKKKKKKKKAR
4919	18820	A	4956	29	158	AMIVPLYSSLGDFKKKEKKKKKKKKKK KKKKKKKKKKGGGGF
4920	18821	A	4957	397	0	PSSPPPPSPPPSPPPPPPPPPPPPPPS SPPAPPPPPPPSPPP
4921	18822	A	4958	257	397	FFFLSFTFVAQAGXQGXYSGLDPPPPG FNLFSCLPRIWNYTAPP
4922	18823	A	4959	419	266	RFHHDGQDGLELLTSSDLPASASQSAGI IGVSHRAQSISLAPQYWYFSPF
4923	18824	A	4960	300	190	FFFFFFFFFIVAFFFLFCFLFFFFFFF FFXIFNNIF
4924	18825	A	4961	3	179	DAWVLPFIIAALALHLLFLHETGSNNP LGITSHSDKITFHPYYTIKDALGLLFL LS
4925	18826	A	4962	2	182	RVNAKDSKWLTPHRAVASCSEAVQVL LKHSADVNRDKNWQTPHIAAANKAVK CAKL
4926	18827	A	4963	273	440	KIHIQHCWWEYKLLQSLWKAAWHFLKEL KAELPFNPAILPLDIYPEEYKSVYKDT
4927	18828	A	4964	179	3	SLPFCCNLTPKKKLFKFCRKNGFFFFFK MESHSVTQAGVQWCNLSLQPCPHGLKQ FS
4928	18829	A	4965	268	364	TVCVIELLTSGDRPASASQSARITGLSH HAQP
4929	18830	A	4966	374	2	QNFFLKKKKKKRVGPGVPPFNPPFFWGQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GGGFPRSLGNPIKPLFFLNSPKISPPPLWPGPFFPLPWGVWAGKNLPRGGGFPLTKFPPLPSSLGKKKKFRFKKKKKKKQARWLTPAIPTPREA
4930	18831	A	4967	79	346	DKIFSNISCGIVIDLLAIYNWDAYATRLGIYKHWFIIIDKDTSSCRLSFSSYPRLFESLDDFYILSSGLILLQTNSVFNKTL LKQVI
4931	18832	A	4968	3	93	FLHVGQAGLGLPTSGDPPASASQSVGLQ A
4932	18833	A	4969	158	1	SKSNFAYIFPIKDNGLTGKKTINRVVTKNWANDLNRHFSKVN IQMAKRYMKK
4933	18834	A	4970	2	266	VGQAGVELSSSDPPASAYEGAGIPGVS HHTWPKHFFPALFVACISSLVNCLFQLF ACISIGLSFFFFFREGDLGNLLKIAGL TFLG
4934	18835	A	4971	3	96	GVRHHAHLIFVFLVETGFHHVGDGLNLF L
4935	18836	A	4972	253	348	NFIFLLFIYFEMESHVAEAGLQWHCLSLQ P
4936	18837	A	4973	326	2	PMEIPQHKLSLWPGFAISVS YFERKLLF SADVS YKVL RNETVLEFMTALCQRTGLS CFTQTCEKQLIGLIVLTRYNNRTYSIDD IDSVKPTHTFLKRDGTEITYVDY
4937	18838	A	4974	3	244	DASLVFKVAETANEEVKKMCMYKYPGN KCGREGGREKKREERREGRKEGREGLR EGETDEEREEGEGLSYSPFKNSI
4938	18839	A	4975	6	79	THFSLTITSLQPEDIGTYCQQYD
4939	18840	A	4976	15	339	PGEAGNCLNPGGSCSEFSRHCPTAWA TERNVS KKKKKKKKKKKKIPRGRGLPPV SHPFWKAGGADWFDLGTLEPPWPTGETP VFKKKKKLTGGGGAPLVAPTWGGG
4940	18841	A	4977	204	275	ITEVDPDTKEMKLKLDGSLSNLQ
4941	18842	A	4978	3	352	RRSPHGLVGAVSVGGAGVMAVETLSPD WEFDRVDDGSQKIHAEVQLKNYGFLEE YTSQLRRIEDALDDSIGDAWDSNLEPMA WRLPYEQSSVLELIK TENKVLNRVVTG YAGL
4942	18843	A	4979	219	3	AASTMAMSFEPWPQYRFPPFFTLQPNVD TRQKQLAAWCSSLVLSFSRLHKQSSMTLM KSLTSLSTVMLDC
4943	18844	A	4980	142	3	FQGFFFLRDKVLLCCPGWSRTPELKRSS CLGLPKCWDYRRELPLA
4944	18845	A	4981	351	2	FFFFFSETESRSVAQAGVQWRDL D
4945	18846	A	4982	133	3	SFFFFLFETECCSV PQAGVQWCDLHPLQ PLPPGFRRFSCLSLP
4946	18847	A	4983	3	161	LGSLHDTANTLWPRLESRRTIMAHYSLD LPGSSDPPTSASHVRGTTGMRSTRP
4947	18848	A	4984	363	3	GPSNKKRGRSKAHVLAASVEQATENFL EKGDKIAKESQFLKEELVAAVEDVRKQG DLMKAAAGEFADDDPCSSV KRGNMVRAAR ALLSAVTRLLILAD MADVYKLLVLQKV V EDGILKL
4948	18849	A	4985	101	1	LQVCYGRRVVMNSREYGAWKQQVESKNM PFQDA
4949	18850	A	4986	341	1	PPPMSPPDVLKTS PVADAAGVVDVKET LQHORYPNVFGIGDCTNLHTSKTAAAVA AQSGILDRPISVIMKNQTPSKKYDGYTS

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						CPLVTGYNRVILAEFDYKAEPLTFPFDQ
4950	18851	A	4987	86	1	KCSGTISAHCNVRLLGSSNSGSPASRAI
4951	18852	A	4988	124	3	LPWLCSKFETKTFQFQIYYKAKGVKTVWYSHKDRNIDQWN
4952	18853	A	4989	305	150	WLLNRYRSHSAEVQVCQFLTWFVSTLGSPDHFSKFFNQYFFKICFDYWK
4953	18854	A	4990	64	340	KKKKKKKLLKFPQGQREKPLSPNFGGLGGKNGPPGKPSRDPWPPIKPGKKKNPLKKKKKKKKKPLSKGGGKKTPKKKKKPPPKGF
4954	18855	A	4991	3	158	PSLVQTRLRHAGQAGLKLTTSTDSPASASQAGTTGVSHHAMPKDCSLNSN
4955	18856	A	4992	116	66	FFFFFFFFFFFFFFFXE
4956	18857	A	4993	3	107	GQAQWLTPVIAALWEAKVGGSFVRSRPAWPTQ
4957	18858	A	4994	1	105	KLDRLARHGLYEKKKTSRKQRKERKNRMKKVRGTW
4958	18859	A	4995	110	3	RRIGRYKTVFLCTQLEILMARYPLPPSPKPIKIKN
4959	18860	A	4996	109	3	DEVSLCPRLECNGTILAHCNRRLPSSDSPALAP
4960	18861	A	4997	1	148	ACCPFCTIYLLPMFMIKAPLMGTSKKKKKKKKKKKKKKKKKKKKKKKKKKKKK
4961	18862	A	4998	3	110	VILQGSNDVELVAEGNSRFTYTVLVDGCSKKTSTRP
4962	18863	A	4999	3	330	PIADRGAEYVSAREWMTICFELLQLLKAHKKAIRRATVNTFGYIAQAIGHDVLATLLNNLKGHERQNRVCTTVAIAIGAETCSPTALPALMNEYRVPELVQNGVLK
4963	18864	A	5000	3	110	VILQGSNDVELVAEGNSRFTYTVLVDGCSKKTSTRP
4964	18865	A	5001	25	329	NSRRRRNDQGSPNLCQFTFTMLTPYLPEHRSLLLKIRSCAERETKKDDIPEEDKGNIKQCEINYVKKFQSFQDHKLKISKEESKILKKAQKDGFLHETLLN
4965	18866	A	5002	278	345	EDEEGYNDGEVDDEEDELGG
4966	18867	A	5003	101	3	VRITISGTGKKKKKKGLPKNYDPKVTPDPER
4967	18868	A	5004	18	350	VSHECLIFHIQNVLTGLVISLSCPSVPSHTHKHTHIHTHTHTHTHTHTFS
4968	18869	A	5005	26	147	KEEVRMALFANDMIVLENPFVSAPYVLKLISCFCGRIG
4969	18870	A	5006	85	1	SASRVAGIIGKHHHTRLIFVFLVETGQS
4970	18871	A	5007	370	3	RARKPLLWVLKKIWSPIWYKKKTRINFQKEKKSFFSRPFFFLFKGGFLPPGVFFSRGFLKKIPPPFFFFFETESRSVTQFGVWSVQWCNGLLLQPEPPGSKQLLCRGLPSSWDYRCLSTRP
4971	18872	A	5008	1	85	IRILSKIKNALTHFLPQGTPTPLIPILF
4972	18873	A	5009	218	93	FFFFFFFFFFFFFFFFFFFFFFFFFFFFF
4973	18874	A	5010	3	250	RPRRRRLRQENHLNLGGEGCSESRSRHC TLTWATEQDSVSKKKKRVFPFPHPRGKFFWAGGPTFFPPLKTVFPFGGKPNF
4974	18875	A	5011	336	0	SSSSPPSSSSSPPPPPPPPPPPPPPP

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4975	18876	A	5012	2	80	SNQNGTGGESIYGEKFEDENFHYKVK
4976	18877	A	5013	53	324	FLVFFVPENSEKISLQLHLALTSNSSWV QSPSHLELMNLCRHINIRVDPTGLREGM HYTEVCGYDIASPNARSLFRGPITAVIA AQVNES
4977	18878	A	5014	329	1	FFFFFSETESRSVAQAGVQWRYLGSLQA PPPGFM
4978	18879	A	5015	193	32	PLILCSERLCHCTPAWAIERDSVSKTN KTKQQQQQQNQGTCKMFLALLGQI
4979	18880	A	5016	354	235	CGEIGMLLHCWWECKLVRPLWTLNLFRLD GSTLTVGSKSSF
4980	18881	A	5017	348	2	RLLVGKLMELHGESSSGKATGDE
4981	18882	A	5018	76	1	IFFLSQVSPLSKEDAGEYECHASNS
4982	18883	A	5019	68	356	YFGGVGGFFFFFFFFFFWFGPSGGVFFVG VQAIFFFFFFFFFLGGFFFLVRDYFFVAVF WWGLLFFFVFFVFCVFFFFFGWKRK NIFYGWVFLFCW
4983	18884	A	5020	1	288	FFLNLEKNIKMLSSYTONGIVVATAEDF MQNFKNLVGYHNSITEENLPQLGANENL ESQSGNFSVVFIFFNADRKRGMLVLLPN NEMTILKPRTSV
4984	18885	A	5021	133	1	VVATETMWSTPKMWPGTGAHTCNPSTL GGGGQITSPQKFKTS
4985	18886	A	5022	2	337	RRSDPNFKNRLRERRKKQKLAKERAGLS KLPLDKDAEAAQKFFLEKIQLGEKLLAQ GEYEKGV DHLTNAIACVGPQQILHVLQ QTLPPPVFQMLLTCLPTISQRIVSAHSL
4986	18887	A	5023	1	325	VDGCPANLLSSHRSLVLAETISLGEHP CDRGEQVTLFLFNDCLEIARKRRKVI GT FRSPHGQTRPPASLKHILMPLSQIKKA LDI IETEDCHNAFALLVRPTEQA
4987	18888	A	5024	135	2	ATMFLNSKSVSKSYGYLLGFHECREKGWM TWDGERDPSPGILQLQ
4988	18889	A	5025	2	94	KTATKLIGGXHYDSXNIKAIRDGLLARR HAL
4989	18890	A	5026	2	362	QELERSMAQRVCVIALVAMLLLVFPTV SRSMGPRSGEHQASRIPSQFSKEERVA MKEALKVFPTVVSTSFQHEVVEEYSHL FTIQGSDPSLQPYLLMAHFDVVPAPBEG WEVPPFSG
4990	18891	A	5027	222	84	AASTFCHVSQAGLELLTSDDPPASASQS AGITGMSHRTQPMVHLY
4991	18892	A	5028	366	0	SGRSKKKKKKKKKKKKKKKKKKKKKKKK KKKKKKRGR
4992	18893	A	5029	231	68	AGMGSRALPKPLLMSSHSLKAVELPDSF SPELRSLLLEGLLQRDVNRRLGCLGRG
4993	18894	A	5030	2	366	LNLGGRGCSELRSCHCTPAWVTETPFKK KKKVPHGGYFVAQLLPPRKMRTHRRPQA QGERTGPGWGAPVHTGLLPRRGQAF TQP PSAFKGFHPTNKSSSEAKKKKKKPRVG RKNVGYIL
4994	18895	A	5031	241	368	QVERNFKSQSGAEAHICDLSTLGGCGGQ ITRSGVHDQPCQHG
4995	18896	A	5032	279	396	DGGMWPGTVAHACNPGTLGGQGRWITRS GVRDQPGQHGE
4996	18897	A	5033	173	398	SNESSLRVNPPFFFFFLKTNFSFCPPGG RQGNFSLLDPPPPKVKEIFCLTPPKRW

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						EYRPAPPPPRNFGFLIKTG
4997	18898	A	5034	2	143	SNPPALTSQSMGITSMTTRHALPIACFLV FVFLFFEMESHSLAQAEVQ
4998	18899	A	5035	350	2	QEISSVQTSQTLFNGMTVKARATTREVM ATYTIEDIVIELIIQLPSNYPLGSIIVE SGKRVGVAVRLFIFITQKSFIFLFSFLT LCLCLQHFHNDFLLLVIPILIAMAFIML TERK
4999	18900	A	5036	1	100	HECGSSSQRTLSVQEAAYLKVSNEIRI LIAIF
5000	18901	A	5037	247	334	LQIDISAVVAYTTIAVKEDGELNLMKKA S
5001	18902	A	5038	2	296	DKAPMLKVI VNSLKNMINTFVPSGKVMQ VVDEKLPGLLGNFPGPFEEMKGIAAVT DIPLGKVHLEALKKKVIKFFYKFPPLRCD IHTAKCTGLRYTAQ
5002	18903	A	5039	152	335	RPIWSYVLLFFFLFWGLVLDVNKRIFTF ILSEKYFDMKKNQCKEGLDIYKKFLTRM TRISE
5003	18904	A	5040	336	1	GGLTISSLLKEKEGSEVAKFTLEQLCLI CNIMSTAEYCVAATQQLEKLEKVDVS LFDRINLSGDMGTFSVVISSSIHLLVQD VDAACDPAMVAMSKMQCQNVQHVGVKSS
5004	18905	A	5041	3	204	LNLGGGGCSEPRSCHCTPSWVTARLHLK KKKKKKRGNPLKNGGKENFKFLQILVN PKNSLENLAV
5005	18906	A	5042	382	148	WCNHRGPRSRKKRSEGSTKSRRLGATIR MVTPTHTRTCARDPELTSKEKCVIEEH THTHTHIYIHTHTHTCIYVKTH
5006	18907	A	5043	137	1	RPRRRYMKKFSTSLIIKKMKIKITMKYH LSHLIPVKMAITKKTKD
5007	18908	A	5044	198	34	KPASRFCHVGQADLELLTSSDLPASASQ SAGITGVSHCSQPNFTLCLVVDHFF
5008	18909	A	5045	11	357	LLTYFIIMFKILEIYEKEEQLIITQISE GQEKVKELRQFKEHRKAKDSALQSI ESKMLELTNRLRESQEEIQIMRKKRKN AARGPYWKFKYSQRWKSPPGPFQWGW PRKNFFV
5009	18910	A	5046	2	193	GLQLLTSSDPPASASQSAGIAGMSHCTQ PQVHLMPSLYHFRFLQVDTKDLLRASAD LIHRGIT
5010	18911	A	5047	1	196	KLCLVMNSPMKAAPRNFSCAPSLSLPF SFRKTTTTLTSNTADDFAYFDLCKMEPC SMVLFFVFC
5011	18912	A	5048	386	276	AQAVLELLDSSDLPPSASQSAGISGVSH CTQPSIF
5012	18913	A	5049	1	324	VDAAAEKLEASTGWLMRFKERSCLHNIK MHGEATVADTEAAAGYPEDLAKITDKGV YTQQIILNGDEIAFCWQKIPCRIFLARE QAVPGCNASKARLT'VLLWANAAGD
5013	18914	A	5050	1	129	PRSCHCFPAWVTEQDSVSQKKKKKKKE KEKKKNPVEKSAKVI
5014	18915	A	5051	193	356	RSFIPASASASTLCLKCSQNGQPGAVA HACNPSTLGGQSRQLTRSGVQDQSGQY
5015	18916	A	5052	192	341	AKRVKRNFFFLKQFCSPVQAGGRGP DPGSLKPLPPGLKGFSCPTPLN
5016	18917	A	5053	340	1	KRIPDKPKELRRLATKLIREAPEKGQA QGKEIHKSIQEAKEIFKAIDRIKKSQF

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						DRQEALDILVLMQNALESLSNRIFQVBE RNSELEDKVFDLTRSSKAKGKRIRNYDHS
5017	18918	A	5054	2	383	VVKVATQPADNPLDVLRSRKLHLGPNVGR DVPRLSLPGKLVFPSSSTGSHFFMLGIGD IVMPGLLLCFVLRDNYKKQASGDS CGA PGPANISGRMQKVSFYHCTLIGYFVGLL TATVASRIHRAA QPC
5018	18919	A	5055	2	383	GSVLSKKGDYLYHYNASLLDGTLLDST WNLGKTYNIVLGSGQVVLGMDMGLKEMC VGEKRTVIIIPPHLGYGEAGVDGEVPGSA VLMFDIELLELVAGLPEGYMFIWNGEVS PNLFEEIDKDGNGEV
5019	18920	A	5056	2	383	AVIDEVRTGTYRQLFHPEQLITGKEDAA NNYARGHYTIGKENIDLVDLRIRKLADQ CTGLQGFLVFHFSFGGGTSGGFTSLLMER LSVDYGKKSLEFSIYPAPQVFTAVVEP YNFILTTHTTLEHSD
5020	18921	A	5057	26	452	KLMSLRRLRQAWHEAAIDEFRTGTYRQLF HPEQLITGQEDAANNYARGHYTIGKENI DLGVDRIIRKLADQSTGLQGFLVFHFSFGG GTGSGFTSLLMERLSVDYGKKSLEFFI YPAPHVFTAVVEPYNFILTTHTTLEHSD CA
5021	18922	A	5058	2	385	AVIDEVRTGTYRQLFHPEQLITGKEDAA NNYARGHYTIGKEIIDLVLDRIPLADQ CTGLQGFLVFHFSFGGGTSGGFTSLLMER LSVDYGKKSLEFYIYPEPHVCTAVVEP YNFILTTHTNLEHSDC
5022	18923	A	5059	3	390	GDAANNYARGHYTIGKEIIDLVLDRIIRK LADQCTGLQGFLVFHFSFGGGTSGGFTSL LMERLSVDYGKKSLEFSIYPAPQVSTA VVEPYNSILTTHTTLEHSDCAFMVDNEA IYDICRRNLDIERPTYT
5023	18924	A	5060	103	3	KIFFFLRWSFALITQAGVQWRGLGSLQP LPRAT
5024	18925	A	5061	262	412	KASPFRTGTAFGNGKTSYLLLNFGYTT FGGITGCLKAGLETSYWTWFTH
5025	18926	A	5062	293	406	VIIGSIFEVIWAVIKPGTSFGISVLRAL RLLRIFKVTK
5026	18927	A	5063	419	15	WEEEGPLPKKKKGGFSNKRGNIIIMPFL KRPPEKKPPPPPRKINPFFFFFKRGPP PPRVKGKGAIGSRNPPLFGSRDFFSPA POKSGAPGGPPPPVKNQFFFFFVLVE TGFHHVTQAGPELLSSSSPPTI
5027	18928	A	5064	2	216	GLTNLFIFCRDRILLCCPGWSQTPSLKQ SSHLSLPKPDWYMEPLCLYFLYPWFCL SLSLSFPLSHTYFFG
5028	18929	A	5065	259	36	SQPHWDYRASRAEEIATFLEVWLQAI FV CCLFLRQSPFIAQAGVQWHYLYLKS LQPPP PGLKQFSCFSLLLVPRLA
5029	18930	A	5066	2	404	GKGAPTTSLISVAVTKIIAKVLEDNKL P GAICSLTCGGANIGTAMAKDERVNLLSF TGSTQVGKQVGLMVQERFGRSLELGGN NAIIAFEDADLSLIVPSALFAAVGTAGQ RCTTARRLF IHESI HDEVNRL
5030	18931	A	5067	1	400	GENMITGTSQADCAVLNVAAGVGEFEAG ISKNGR TREHALLAYTLGVKQLIDGVNK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						MDSTEPYPYSQKRYEETVKEVSTYIKKIG YDEPTIAFVPISGWNGDNMLEPRANIP VTGWKATPIDCDASGTTLLDA
5031	18932	A	5068	41	392	GSPHHPCAHTERKKKPYNSNIGFYTKRN ALRVAEVWDDYKSHVYIAWNLPLENPG IDIGDVSERRALRKRLCKNFQWYLDHV YPEMRRYNNVTAYGELRNNAKADVCLDQ GPLEN
5032	18933	A	5069	3	395	GTPTRPHILLQALFIRAMLPCPDYDITD KTGLDQALKICQAMLDEAANQGWLVTVL NNTNLIQMAIQGRWVKDSSLLTLPYIEN HHLHLFKKRPIMKGPHAKSRTSIECLP ELIHACGGKDHVFRSLVQQ
5033	18934	A	5070	3	405	PRASEVCGFSCHITCVNKAPTTCVPPE QTKGPLGIDPQKGIGTAYBGHVRIPKPA GVKKGWQRALAIVCDFKFLYDIAEGKA SQPSVVISQVIDMRDEFSVSSVLASDV IHASRKDIPICIFRVTSASQLSAS
5034	18935	A	5071	3	393	ITRQEFIDGILASNFPPTTIEMTVGADI FDREGDGYIDYEFGAALHPNKDAYRPT SDAPKTFHQGTRQVAQCICAKRFLVEHI GENKYRFFLCNHFGDSHQMLRVLRIILST VMVLDGGGWMALDQFLT
5035	18936	A	5072	3	394	ITRHEFIDGILASKFPPTTKIKMTVGADI FDRDGDGYIDYEFVAALHPNKDAYRPT SDAYKIEDEVTRQVAQCKAKRLLAEHI GENKYRFFLGNGFGDSHQRLRLVRIILST VMVPVGGGWMALDEFLVND
5036	18937	A	5073	1	393	GEDAANNYSRGHYTTIGKEIDLGLDRIC KLADQCTGLQGFLVFHREGGGTGSGVTS LMEHLSPDYGPKSKLEFSIYPAPQVFT AVHEPYNSMLTTHTTLEHSDCAFMGDNE AIYDICRTNLDIERTTYTN
5037	18938	A	5074	39	482	LGLHSAWRDDKIGYNPDTVSFVPISGWN GDNMLEPSANMPWFKGWKVRNDGNASG TTLLEALDCILPPTRATDKPLRLPLQDV YKIGGIGTVPVGRVETGVLKPGMVATFA PVNDTTEVKSVEMHHEALSEALPGDNVG FNVKNVSV
5038	18939	A	5075	1	390	GVSMVSLVITTYQYVVRNMPDPHNLPV AGWKYPLFFGTAVFAFEGIRVVLPLEN QMKESKRFPQALNIGMGIGTTLVTLAT LGYMCFHDEIKGSITLNLQPDVWVYQSV KILYSFGIFVTYSIQFVV
5039	18940	A	5076	330	462	VNEFFREGGTESPSIAQARVPWCSLNSL QPLPPGFKRFSCLSLP
5040	18941	A	5077	1	403	GGWGEAEDEFYAPDVEPLEPTLSNIE ORSLKWIFLGGKGGVGKTTCSCLAVQL SKGRESVLIIFTDPAHNISHAFDQKVS VPTKVKGYNLFAFAMEIDPSLGVAEPLDK FFEEDNMLSMGKKMMQAMSAF
5041	18942	A	5078	348	1	RPQGNNIERWQGGEVLIQLLRIAKSVK NVQLLWKTFQFLIKHLHLLFYDPRIPFVS NYPKEKKTYVHKKTAYAQIFISLPRTFL LRQSLNMLPRQDLSS
5042	18943	A	5079	248	3	PGQVLEREHTCRPPWAVVNVICLAGPA KPNREDVSSSQEESLQNSIPTPTLTS TAVKSRQPLWGLKEMEEDGSELDF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5043	18944	A	5080	3	192	GDGSELRSCHCTPAWLTERDTSSQKKKK KEKKTWNPAPELFFFLLEKKGQNGKPNM NMKKVL
5044	18945	A	5081	10	171	CFCLGPVGVCRSLKPKQLCFLGFPWLQD ARQKFRSVLVEATVKLDELVTSTRP
5045	18946	A	5082	94	1	DFWPGKVAHACNPSTLGGRGGWITRSGV QDT
5046	18947	A	5083	142	3	AASTGSHSVAQAGVQWHDLSLQPLPPG FKRFSFLSLPSSWGRKIA
5047	18948	A	5084	257	177	ISLGEVAHACNPSTLGGRGQITRPG
5048	18949	A	5085	143	1	GGESHSDTQAGVQWCYLGSTQPPLTLTF KQFSCNLPLSSWNYRCVPP
5049	18950	A	5086	3	87	HVGQAGLVLLASCDPPSLASQSDGITV
5050	18951	A	5087	375	220	LHSLSQHIATRSKKPAFNLFAFGTSLSPV STNWVGFPNISFEGMLLIIFFFFF
5051	18952	A	5088	40	203	IFLPLLLVSPFFFYILTWGFTFFWGLTLI NDLLNFFFGNSGISFSWFGSRAGELG
5052	18953	A	5089	1	145	MDMRVPAQLLGLLLLLWLSGARCDIQMTQ SPSSLSASVGDREDGDVDA
5053	18954	A	5090	146	328	FMPFPLLESLEIFSSKLFNPPNLFFFFE TESCSVAQDGVQWYDLGSLQPPSPGFKR LSCLS
5054	18955	A	5091	338	1	PNLPSVQLPPTTCTPLIGDLLVARAHF AGWKHQGINSPSLPMAPREGMEAPRNP HPHIFLCILHGFHLAVSKLYSLFYIIII YFSRWSFTLVAQAGVPWRDLGSLQPLPP
5055	18956	A	5092	2	327	PPLTPPIFFSSPKNKNPPPHYNPPPPP FRTPPPPPYPLSPPKSPPPPPRPVDPPL PYSIFPRPNLISPPPYSPFYLLPQLQAF P
5056	18957	A	5093	133	3	AQTCTPSTQINSKWITDLNVKGGTKIKLL KDNIREKLDLDLGCGE
5057	18958	A	5094	170	350	AGGQGGNFYSLQPNPPWIRESSHTLPK FWNYRHTPTGPPNFGFFFLKMGFGLVAQ TIFN
5058	18959	A	5095	133	274	RDIIIFLESIGIKGYFLFFSDKITSELVS KIGDKNWKIRKEGLDEVAG
5059	18960	A	5096	2	188	REMQIKTTVRYHLTTARMVLIKKSEKNR CWHGCSEKGTLLHCWWECKLLQPLWKIG WRVDA
5060	18961	A	5097	235	81	FPKKKKAQIKKPQAAQSLNLSLSLYIYA FTYTHTRHRTHTQTHTHTYIHIS
5061	18962	A	5098	355	169	KILLITDSCAHISCRFSECMKYFNPPFF HPHSVYVTDKIRLLEEQLPHVFSNKME PFKVCN
5062	18963	A	5099	160	1	FSASYFNSKKKLIIFLLKLKRWNFVCF GMESHVAQAGVQWCHLGSLLQPLPS
5063	18964	A	5100	364	151	QMGFCHIGQADLELLTSSDPSASASQSA GITGVSHYASQEFLLKKEFHSAHLIPLQG TCVQGKTAQPYSEAL
5064	18965	A	5101	205	3	AASPGVQWPDRLQLQPRFFGVKQFFFLS FPSSWGYRGAAPPFGHFFFFFSPSRDEIS VCLPGWSPTE
5065	18966	A	5102	349	207	DGASLCCPDWGLELLSSSGLPALALQNP BITGVGHHTQPWTLSLLIY
5066	18967	A	5103	425	0	CEFFKNKDFCLSKKKKKKKKKKKKKKK KKKQSSQTSYS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5067	18968	A	5104	437	184	LFLEFFPPPPKKVFSQKTPRSVVSPPPKK KKKNSPPPLKLGPPQEIFKTPPPPIFFF FFEMFFFSFFFFFKGHRPRFISLWSPPL
5068	18969	A	5105	401	10	MFSPFFGGPRGGVPLRPGFKNPPGPKGK TFPFLKNQNYLGPPLYSPFLERLNKKKA FTLEAKGPNPNSSRSPPPGAQKNPPF KKKKKKKKRIIFMPQAHPAVVVCSGNQ LPITFPYSIISGPLSSFT
5069	18970	A	5106	413	2	PNKKPSPPFPSPPHKTPSSPSPPPPPNK PTPTPPPPNKNFPPQPPPKKNPPQT PPDQKKTTPPPKKKKHPPPHKKTTPPP HTKNPPPPPLPPSLIPPLFPLYINSP FFIPFFFFFKIFFYLGRVGGRV
5070	18971	A	5107	269	115	GFFFFFSSFFFFFSSFFFFFSSFFFFF FFFFFIKKCHFIFKYIGSTSN
5071	18972	A	5108	238	4	QWLPLVDRIWVILLFFDSLNLKMFQYQ IGLQKIKVKNNTTFYFLFSFFLRWSFTL VTQAGVQWCDLGPLQPPPPRFK
5072	18973	A	5109	496	0	STPSRASPKKKKKKKKKKKKKKKKKK KKKKKKKKSSK
5073	18974	A	5110	1	243	DHLSLGGRGCSEQRSCHCTPAWVTERDS VSKKKKSFRALDIFFFNGKKILGTLRGK NQKPPREVSSGNYFHFKGLFGPCYK
5074	18975	A	5111	78	4	LGMVAHACNPSTLGGRGRITRSGV
5075	18976	A	5112	2	96	AGVQWRDLGSLQPPPPGFEQFSCLSTMP NFL
5076	18977	A	5113	128	6	IYKDVLEPGVLRLLDNDNRVVLPIEAPI RIIIPSQDVLHS
5077	18978	A	5114	132	2	DDLSSLQPLPPRFKRFCCSLSDSWDYR RPPLRPAIQEAEEAE
5078	18979	A	5115	1	146	AVETGFCHVAKAALELLHSNDPLASASQ SAGITGMSHRAWPSLFSILS
5079	18980	A	5116	213	3	GAVGFSSGCFLLYLYALGLGPPPLPLQ LKFICWPGAVAHVCNPSTLGGRGGRITR SGVRDQPDQHDET
5080	18981	A	5117	407	0	LGWAWWFTPIPTLREVKAGGSPEVRS
5081	18982	A	5118	215	414	KTRPKETIRNNGSQQRKAQLGKLEQTN PVLNFKAPFFGEQGDYYSFFKTCLDNL PRRGKGVFFF
5082	18983	A	5119	40	326	KKKKKKKKKKKKFKKTGGAKWAPFLNLK KKGIKPQKKKGFFQKKKRGKKKIPKI LIQGGFQKKKNFSKKKISQKKKNGFWP LGKGFPCPKKT
5083	18984	A	5120	99	2	GRSTRHSPAHTHTHTLRHTGTLHHTSH RHSP
5084	18985	A	5121	3	219	ELRLCHCTPTWATRVLRSQKKKREKKKK NFVGKKKGKKGKKPPNPKKKGSLGFGK FLFSKFFKTRGTTII
5085	18986	A	5122	262	351	TRPGTLAHACNPSTLGGRGGWIMRSGVQ DQ
5086	18987	A	5123	340	0	KKKKISQAWWWVPVVPATWEAEVG
5087	18988	A	5124	94	2	LMPIIPALWEAEVGGAPGQEFQTSANM VK
5088	18989	A	5125	310	68	LSPFYKLGFWGRVIYPPPPPKVSPVFG APPPPEKKKKPPPPPKSSIKKPTKKI CLAASGKLEVCFCCKPLIQSYFL
5089	18990	A	5126	343	131	SRPRRPGLELLTSDDLPAPATQSAGITG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						VSNHTQIWPISVGDLMNTGVVIPENRIV SELLREIHFLRICL
5090	18991	A	5127	2	145	FSLLGSSVGRLEGTTGTISTHCTLPASRD SPASNYRLTPPCPADFLYF
5091	18992	A	5128	1	130	SRSVTRLECSGTISAHCNLPGSSDSPAS DYRLTPPCPADFLYF
5092	18993	A	5129	1	338	VVRKEGIRFEKEKSKDFKNHVIKYLETL LYSQQQVCKLWVTFI
5093	18994	A	5130	346	3	DFFFFFFHPIILFFFFFFKTLFFSPPEGNGG HTLFLKNTPPRGRIFFFLPPLLLWGGWA PPPPPKKNFFFFFFFFFFFFFFFFFFFFF FFFFFFFFMPPTQSLFKDQEGPVQGGERA PV
5094	18995	A	5131	3	114	FLHIGQAGLELLTSDDPPASASQSAGIT GMSHHAQP
5095	18996	A	5132	292	180	AASTDSTEGHGASLPSKKTTPSEEDFETI KLISNGAYG
5096	18997	A	5133	338	216	RGENRLPPGGRGFGSPKSHFCPPAWATE RDSLKSKKNPV
5097	18998	A	5134	337	3	IVVLGNGKGIIRNNQIFSNKEAGIYILY HGPNVVSNGNHIFKGRAAGIAVNENGKGL ITENVIRENQWGGVDIRGGIPVLRSTL ICFGYSDGVVVGDEGKGLIEGNPISAN
5098	18999	A	5135	227	343	NYVKEKLIPTWNWVMSIMDSTEALPYG SALTSSVDPGQ
5099	19000	A	5136	166	375	ATFVSLGVFCSAVILLYFKNMMKLDLSL TPHTTINSKWIKRLHTRPEAIKFLEVNI GKKFFDIGHEIIL
5100	19001	A	5137	90	2	KTTLWPGAVAHACNPSILGGRGRITRS G
5101	19002	A	5138	213	379	PTFQSVGETGSLLKMHLGPGAVAHACN PSTLGGGRGRITRSGVQDQPGQYGETP
5102	19003	A	5139	384	2	FFFFFFFFLSVMESCSATQAGVQWCDLSS
5103	19004	A	5140	41	317	TMSRDRPSDKTWTYNRSNVVMPDGGAPF RYSFSALKDRHNAVEVNWIDPNNGWETA TELVEDTQAIARYGRNVTKMDAFGCTSR GQAHRAGL
5104	19005	A	5141	29	523	VKAEEAAYKKADDIWNLRKDDYFVNDEAR ARYWDDREKARLALEAARKKAEQQTQQD KNAQQQSDTEASRLKYTEEAQKAYERLQ TPLEKYTARQEELNKALKDGKILQADYN TLMAAAXKDYEATLKKPKQSSSVKVSAGD RQEDSAHAALLTLQAEIARTLEKHAG
5105	19006	A	5142	432	144	GGFLPKAFLPPKKKKGAFFPPPGKGATP PLFWGGWTVFLIPEKNPPRGFPFPPKRGE KPVGGPFPRIFAPPPQKKIGGGGFFLER FFFWDWGTGP
5106	19007	A	5143	403	6	FFFFFFKQIGPRGGGPPQKSPPLGGGGRG GSPRPGVLTPLGPQGNLFFLKKKKKLG GGGGPRNPFLGGGPGKSLYPGGQRFQG PKILPFFPFRGKKKKIFFPKKKKKKSHR KLIQTLILQTGKLMKMLWRT
5107	19008	A	5144	115	427	KKKKKKKKKKKKKKGGGPKKKKNFSPG GGKKKFFNGAKKKKPRAPVKKTGEKKK GGKKKKKCFEKNPFFGGGKKKKKCSSS YPCPKQ
5108	19009	A	5145	2	79	GCSEPRSCHCTPAWVTEGDSISKKK
5109	19010	A	5146	317	444	IHQPVCAHAYNPSTLGGRGGHITRSGD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						RDHPGQHGETPYPL
5110	19011	A	5147	3	413	SFYRGFIPVLQTVTVLTIIGDPSLHGDAW SWMEFFLTVIFIALWMLPLIGLTIIVNA IWFQDIADLAFEVSWTKPHFPFVSQII ADMLFPLLQALFLIQGIAVSLFPIHLV GQLDSLHMTLLYSLYCSEYRLVIN
5111	19012	A	5148	409	247	QTKFRHVAQAGPHFLGSSDVPTSASQSV GITGMSLHAQHQHFFFTASMGRAFGEN
5112	19013	A	5149	284	1	AEASRAHMEAHARTQGTGSKAEGVGPV EEYRIWRRPGPDRAHASDSEESGEGGP PPHPANFVFLVETGFFRVGOAGLEFFTS GDPAASASPV
5113	19014	A	5150	439	120	FGSPRLCSGVISAHCNLRLLGSSDSPA SASHVAGITARPNAIRIKAFGAPSTCTV VWERHEQQTCTIQRSDLPAGRQKKTGPKN RPGLVAFPFNASPLGGPGGRIA
5114	19015	A	5151	415	0	FFFFFFFFFFFFLPPFVQSFYIYIYMI
5115	19016	A	5152	67	179	ICLSLFLT VHVCVCVCVCVCVCCEM VFGVSI PCN
5116	19017	A	5153	280	2	KTPFFLNLEKTRAPFFLKKTFFKKKPF KIFFSKKRNFFPPPPGKRPTLFKKKF FFFFQKKKNFFFSPPKKKKKKKKGRRS RSRTSPRV
5117	19018	A	5154	296	406	DRVLLCHSSCSEVAESRLTAASTSWAQA ILLPQPPEW
5118	19019	A	5155	114	402	VWRIKASVEKKKKKKKKKKQKKKKKKR
5119	19020	A	5156	110	1	QRFLTLKSLILRLGAVAHACNPSTLGG QGGIRMS
5120	19021	A	5157	382	95	SSSSPHFLTSPQLRLFFPPFPLKIFFFP KAFNFCGGVFPPIFSPPKKFFQNSQVG FKNPPQKEKNFSFPPPVKFGPPKGFKR PPPPPPPPPP
5121	19022	A	5158	2	350	TLQPGRQSETPFQKKKKKKKKKKKKK KKKKKKRGGGFLKNLGGGPKIWVEKFF FFFFGGGYKKPLGFFLEKIFFLGGGIWA PPPPKKISFWGKKKFWGGGGKTPLFFC GGKK
5122	19023	A	5159	1	208	PTRTLVYLKGLMGPBIFLSSFQEIRL IDYDKMVDHRGVRVVAFGQWAGVAGKYA RAYITHFLNLGE
5123	19024	A	5160	1	208	PTRPLYLLKLSLMGPVEIFLSSFQEIRL IDYEKMVDHRGVRVVAFGQWAGVAGKYA RAYITHFLNLGE
5124	19025	A	5161	419	25	AQKKKKKKKKKKKKGGGGLKKNFGGGK NKRGGKKKNFFLKRGGKKKTGGILEKKN FFGGGKKGEKPPQKKKALKEKKKFLRGK GGKKPLNWGGKKKK
5125	19026	A	5162	475	150	KPRTSGTARVPGDPPPRCLDDKRLPSRP VIFVFLAETCDRVGQDGLQLLTSGDHP HLTFPNCYNRREPPRPTSSGFQHDIE LHYRRGKADRFKAHLPK
5126	19027	A	5163	237	409	FHNQKTYLDSALCTLVYFVFLVLRDGI LLPQLECSGTVMACNLKLLGSRSPAL A
5127	19028	A	5164	373	476	LGFILLSFLETRSHSVAQAEVQWCDHGL LQPQTP
5128	19029	A	5165	374	132	IFYSPFLYYHMLGKYHKIKNLKIKHMWL DAVAHACNPSTLGGRGGRITRLGDRDHP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GQHDETPSLLFLWTFASSLSGFPL
5129	19030	A	5166	332	2	RPQGLANCFPGALPPTKSEGFPGQSPGF QIWGGKAFFLRGFPFFPQVESKGAVSPP CKVPPGLRPFSAPTPPKNGDKRGPPPG RATGFFFFFVFLVETGFHVSNDGLY
5130	19031	A	5167	238	1	GGFTGTGGKYEPAGIVHRGEFVFTKEAT SRIGVGNLYRLMRGYATGGYVGTGPGSMA DSRSQASGTPEQNNHGSAGESRG
5131	19032	A	5168	1	89	FFFFKTESRSVAQAGVQWCTLGSLQPPL P
5132	19033	A	5169	3	127	DEDFSDFDEKADDEDVFPDASPPKTKT SEPKQVSYLIWVLS
5133	19034	A	5170	20	254	IAPPARIRHEERERERERERERERERER ERERERERDTRAERARLEFFFFFLPA DQCFFIKPSGQRFLPPGGGGVP
5134	19035	A	5171	36	479	TXGXDNNKDLLISVGDLVDRGAENAECL ELITFPWFRAVRGNHEQMMDGLSERGN VNHLLNGGWFVFNLDYDKEILAKALAH TADELPLIIELVSGDKKYVICHADYPFD EYFEGKPDVHHQVIWNRERISNSQDGIV KEIKGADT
5135	19036	A	5172	278	448	RFLCPLLHPFFSSETKSLTLPLRLGCSG VIAHCSLKLGLSSNPPTSASRVAGMTG S
5136	19037	A	5173	205	1	HARLIFVFLVETGFHCVGQAGLELLTSG DPPSASQSETPSPLKILKSAGCGGANST ALASGLLFLSLGP
5137	19038	A	5174	409	194	FFFLRWSLALSARLVQWRDLGSRQAPPP GFTPFSCSLLSISFQPSATYMRFLNTI TIVEYSFAYFPISQP
5138	19039	A	5176	339	472	AKFTCISSNIKLSNTRPGTVAHACGPST LGGRGGQITGSGDGDH
5139	19040	A	5177	426	148	GGRGPPPLSHPPFGGGGGGGLRAGGQKN PGPKGETPFGQTQKKNRGGATPPFSQK LGGEKHKNSFTPGKENSIFDFPPAPPT WGEKNFFF
5140	19041	A	5178	328	474	NNTEYNKNRLGAVAHACNPSTLGGRGRW ITRSRDRISP
5141	19042	A	5179	448	330	ETGFCHVGQAGLELLGSSDLPASASQSA GIIGVSPHAWQ
5142	19043	A	5180	259	14	LRKAILCSWIRTTNIVKMAELPKVIYI FNAIPIFKIPDMFCRIARFILKCMWNVK VSTIDKTIFFKENRVGIPPRVLMVV
5143	19044	A	5181	2	423	KFYATLVRYVGDRKNLVCREMSMALLSN LAQGDALAAIAVQKGSIGNLISFLED GVTMAQYQQSQHNLMHMQFPPLPPSVD MMCRAAKALLAMARVDENRSEFLLHEGR LLDISISAVLNSLVASVICDVLFIQGL
5144	19045	A	5182	182	312	FFIQVGFHHVAQAGLKLPSSSSPPHLAS QSAGITGVSHCAQPG
5145	19046	A	5183	301	472	GIPFFFFFLRRSFALVAQDGVQWRDLGS PQPPPPGLKQFFRNSTAWTKGLQFPRL
5146	19047	A	5184	216	413	KPXXXXXXXKKKKKKKKKKKKXGAVK KKGPKQTPVKPPGGFFFAPPLGVSPPPG VFFAGGGAPP
5147	19048	A	5185	357	465	IKPTKILAPGPGAVAHACNPSTLGQGG WITRSGD
5148	19049	A	5186	467	0	FFFFFFFFFRFLFFFFSEKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5149	19050	A	5187	346	3	RFLPLGQGGVEILTFRSTCLGPPKWWDY KGEPLRPAQKCFFFKKRRRKKVQNSVA VYMVYHSMCGENKLRWRWGI FTHTHTH THTHTQKKQNILSRTHKKLVIT TGSEEG TL
5150	19051	A	5188	11	109	GETPSLLKVQNIKXAWWHMPVIPAMWEA EARES
5151	19052	A	5189	3	151	QLLRPRQENHLNPGSRGCSEPRLHHCT PAWATVQDSISNTNNNNKCP
5152	19053	A	5190	2	373	AVAADKGVPLYRHIANLAGNPDILPVP AFSVINGGSHAGNKLAMQEFMILPVGAS SFKEAMRIGAEVYHHLRGVIKAKYKDA TNVGDEGGFGPIILDNDAL ELVKTAIQ AAGYPDKGAIGR
5153	19054	A	5191	55	421	ARVADVCESMKEHLLVLVERAKYIPGFC ELPLDDQGALVTAHAGEHLLLGATKRSM VFKDVL L LGNDYIVPSHCP ELAEMSRVS IRILDELVLFPQELHIDDNEYAYLKAI I FFDPDKETEA
5154	19055	A	5192	163	466	TCFLGSQSAGITSVSHCP SREVFFLKI HWRQGGQVALLVATPHSPCCPQYRLAPI PRARHDFACASLIFACILLVHVLMPRV SAGRGVGV RPAGIQAGR
5155	19056	A	5193	470	0	ECLWPGTVAHASNPTTLGGRGGRIMK
5156	19057	A	5194	491	281	RGLALLPMGQC SGMMLAGSLDLLSSD PFASASQSVGIMGVSHHAWPSLVNISFV CLIHRSPKTKPEGR
5157	19058	A	5195	3	222	LSFHS LHRCLYMLGTTSENVSPFSLLEL LSRLATLLGDYCGSLSEGTISRNVALVY ELLDEVLRLESRCVAQA
5158	19059	A	5196	20	191	STWWNSSRGGGCSEPRSHCTPAWVTER DSVSKTKKKINNKPALALPAVHPTSHPG S
5159	19060	A	5197	460	350	RRLRRENHLNPGGGGCSELRSSHCTPAW VTERGPSD
5160	19061	A	5198	174	41	SLGELLTECLFETKSHSVTQAGVQRHP GSLQPPPPQGFKRIPPH
5161	19062	A	5199	131	454	FYFKNRK PFFFFFFFFGKGVSFCA PGGK AGDPFKLREPPPPRVKGFFGPPPPSGGN NGPPPPPRVFFWFFKKRGGSPFWGGVL TPGGGPPPPAPQRRGGINGLDPPAR
5162	19063	A	5200	168	51	TVKTPIRPGAVAHACNLSTLGGGRMWIT RSGARAQPNR
5163	19064	A	5201	414	497	LLFXXXXDNGSIYNPEVLDITEETLHSR
5164	19065	A	5202	381	614	VQPGAPPEWVALSTCPSAAPEGSQQFYI PPTFCFFPVKLLSVTWLYLFIYFLSWI SVAQAGVQWCNHGSLQPRPSRL
5165	19066	A	5203	377	485	PKEPGQPQCAPQPQPAPQPQPAPQPQ PCAPQPQ
5166	19067	A	5204	54	434	MRTPENLELTNPQEF GSSWAAVECPDTL DPRDMCVLNPLREPF AKKECSILLSEVF EICHVVDVTFYSNCLTDTCGCSQGGD CEFCASVSAYAHQCCQHGVAVDWRTPR LCRECPRQSP EGTE
5167	19068	A	5205	201	418	GDAGAHAVLRLLPGHPGTSHLPFSSLT T SPLGLKRV TGGFNSKNRCDARTYCYLLP TFFAHKDRDVQDETY
5168	19069	A	5206	27	177	NSFHHAGQSGLELLTSSDPPASASQSAG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						ITGVSHRAQPKAGTFLSPFHR
5169	19070	A	5207	6	1175	DLGPHTPAWTRPKREDLVYQSTVRLPEV RISDNGPYECHVGIYDRATREKVVLASG NIFLNVMAPPTSIEVVAADTPAPFSRYQ AQNFTLVCIIVSGGKPAPMVYFKRDGEPI DAVPLSEPPAASSGPIQDSRPFRSLHR DLDDTKMQKSLSLDAENRGRPYTERP SRGLTPDPNILLQPTTENIPETVVSREF PRWVHSABPTYFLRHSRTPSSDGTVEVR ALLTWTLPIDNEALFSCVKEHPALSM PMQAEVTLVAPKGPVKIVMTPSRARVGD VRILVHGFQNEVFPEPMFTWTRVGSRL DGSAEFDGKELVLERVPAELNGSMYRCT AQNPLGSTDTHTRLVFENPNIPRTED SNGSIGPTGARLTVLALTVILELT
5170	19071	A	5208	401	3	FFFFFSETESHVAQAGVQVHHGLGSLQG PPPGF
5171	19072	A	5209	402	229	GFFKKGPPFFFFFFFFFFFFFFFFKMWL RLSGSKVEVWVWSQKLYMNGCCGRSW FT
5172	19073	A	5210	198	2	PPQAKILSSSSPPIRPPPKGFFPKNPQ VGFYSAPHKEKTFTLPAPVKFGPPKDP KRPPP
5173	19074	A	5211	516	222	GSTLRLTQRSMPASSSTMAPSSKRLLP RPERSVPAAAGTAGHHEASRNCGRGGAG ADEGPATKGDSPKPGYCRAHPSAAPW PPGPEKNFMRVG
5174	19075	A	5212	103	203	DKVSLRCPGWPQTPGLKQSSCLSLPKW DYKCE
5175	19076	A	5213	409	249	RRNQVGGPRQLNPGKRIKSPGIDPYIYG QLIFDKAVRAIWRKGSFLQKALE
5176	19077	A	5214	2	170	ERKILGYIQLRKGNVVGPLYGLLPFAD AIKLFTEKPLKPATSPYPLQSPAPPLKP
5177	19078	A	5215	270	464	GQLNKNVWGDGKVTFRDGSVLYCLHW NAVAIHGHRHSVPQPTPGFKQSCRLP SSWDYMPLY
5178	19079	A	5216	156	248	PDKSYIICVCVCVCVCVCVLCVWCMC CP
5179	19080	A	5217	412	2	PPPQIFFFSPPHFFSPPPKGFFPPPPP KIFFFPPLFFFWGFFPPFSPPKKFFF PKSPFFFPFPKPKKFFFPPLFFFP PGFLLTPPPFFFPFFFPFFFPFFFP FRMGCDRWHGEFWILRDGFD
5180	19081	A	5218	165	1	QVKYHNKKTHTNPRIKGRSEQTFHEKDT QMANKYMKRSPTSLRIKGIQIKTIMRY
5181	19082	A	5219	408	88	PSSSPHFFSPPPLGGVFPPFPKIFFFP PGLFFFWGVFLFSPPPKRVFPNSPPG FFFPPLFGKKFFSPPFPFPFPFPFLS PPPLFFFPFFFPFFFPFFFP
5182	19083	A	5220	3	259	NLLLLIVPILIAMAFMLTERKILGYIQ LKKKKKKKKKKKKKKKKKKRGAPKKK PRGGQNFPGEKKKKFFFLREVKKPRGN F
5183	19084	A	5221	10	479	KLMPAESDGRHRERERERERERERER ESSARARCVSLSDRYKNRVYMKVAEA LCECRLLAYISQAPTQMFFLLRLINIIH AHTLTQENDMCLHTTLEILTARQRRV PLYLRVLQRMHEKKKHGPFVLNNSHNLV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						RLWQQLYLHRDRDSIC
5184	19085	A	5222	142	56	KFQPGAVAHTCNPSALGGWGGQIKRSGV
5185	19086	A	5223	14	471	LEMRSSEIDSONYCNC DAGRNEWTS D T I V LSQKEHLPTVQIVMTDAGRPHSEAYTL GPLLCRGDQSFWNSASFNTETSYLHFFA FHGELTADVCFFFKTTVSSGVFMENLGI TDFIRIELRGKLATLDKSQGTHYLAIKA LTQKKKKKKTRG
5186	19087	A	5224	480	0	FFFFFFFFFLLIVAQFYFL
5187	19088	A	5225	16	422	VRTARIRHEGKPYECNACGKAFNRS L TEHQRTHTGEKPYVCKEKGKTF SRSTH L TEHLKIHSCVKPYQCNECQKLF CYRTS LIRHQRTHTGEKPYQCNECQKSFSLSSA LTKHKRIHTRERPYQCKKKKKKK
5188	19089	A	5226	99	436	GHPSFEIPATMTAAPAGFPQPVEDVR YLFEIMYGGHITDDGCKLCRVYLEEF MNPSLLAALSGTHACGKPRLPANSHVS EPSWKWILQPQSSLOMTAALANILTATS
5189	19090	A	5227	473	9	FQITATPHLAVYDPTVQFEFFWFSEKQIA DIRQVEASTRYLGTALYWIAASINIKPG HDYFFYIRSVNTVGKSAFVEAVGRASDD AEGYLDFFKGKIAESHLGKELLEKVELT EDIASRLEEFSEKWKDASDKWNAMWAVK IEQTKVGERDVTSG
5190	19091	A	5228	1	473	PPPIDRLPNCTACRNSARVMTDAGQPHS EADYTLGPLLCCGDKSFWNSASFNTETS YLHFFAFHGGELTADVCFFFKTTVSSGVF MENLGITDFIRIELRGRLATLDKSQGTH YLAIKALTQKKKKKTRGGAGPPFPLIGS RITIHGPPFNNAAMREK
5191	19092	A	5229	170	25	KTPLLGPGTVAHACNLSTLGDQSGCIMR SGVRDQLRQHDPTPSLLKRI
5192	19093	A	5230	465	0	VVLYPPQKAQKKKKKKKKKKKKKKKTK ARG
5193	19094	A	5231	419	56	CVLLRSTKKKKKKKKKKKKKKK
5194	19095	A	5232	79	451	AGSNLQEHRLRPESFPNPGGGCREPR RRHCPPAWAKRAKRLKKKKHGRNQEVA QGRHGPFPGGLGPEGFLPRRPGSRKRRK GRNVPGPGLKGPAGVLFSSRRRRGGADLR PPRKGPGRGGGG
5195	19096	A	5233	39	467	VQQQQRAQEQQQQHPVLHLQPQQIMQLQ QQQQRQISQQPYPPQPPHFFSQQQQQQQ QAHPHQFSQQQLQFPQQQLHPPQQLHRP QQQLQPFQQQHALQQQFHQLQQHQLQQQ QLAQLQQQHSLLQQQQQQQIQQQQLQRM HQQ
5196	19097	A	5234	194	45	MILKFFNFKIHFFFFLRLQSLALVAQAG VKWCNVGSQQPPPPGFKRNST
5197	19098	A	5235	204	475	ASITVHLWYVEKCSQSTSEKVTMPSSS WFGPQPDALQKHGLRPGAVAHACNPSTM GGRGGRITSSGDRAHP
5198	19099	A	5236	59	357	NHWRKIYCKVYNRKKIKHNTTNTTKNYQ NFQRNRKSSFTIFRIQSHYNKHKKH QRKRQSIETDLEMTQMLELVWIFKVIV ILTKIKTPKTLKING
5199	19100	A	5237	447	166	ELLAFWQTQYNNMNAVNLFFFWIKAPGI PTPSFASRRTHSPFFSFLFFLFFFLGKK GFPLCGPGPKSLNLKTPPLGPPKGGK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5200	19101	A	5238	34	296	LSVAEFLAFWQTQYNNMNAVNLFFAWIK VPGIPTPSFASRRTHSPFFSFLFFLFFF LGKNGFSPCGPEGPKFLNLITPPLGPPK GWE
5201	19102	A	5239	340	472	SLNETHVRSPAHRPGATAHACNPITLG GRDGLIMRSGDQDHPG
5202	19103	A	5240	460	0	PKKKIIFTIYFFYFFFFFFFFFFF
5203	19104	A	5241	161	46	SFYSTHRKPCHWPGSVAHACNPSTLGGR GGRI TRSRDR
5204	19105	A	5242	175	36	LKYYLIFIYLLSFFFLRQSRVSGQAGVQ WRDLSSLQPPNSTALQYR
5205	19106	A	5243	11	442	DTIRWGLPTLGSKSTTNEKKREKRKKK EQQQSEANELRNLAFFKIPQKSSHAVCN AQHDLPLSNPVQKDSREENWQEWQRDE QLTSEMFEADLEKALLSKLEYEEHKKE YEDAENTSTQSKVMNKKDKRKNHQKDR PLTV
5206	19107	A	5244	459	333	FLRV TQAGLKLSSSDPPTLASPKCWDY RHEPLCPAQWSVS
5207	19108	A	5245	229	436	FNSTVVRKRGLGGFIHLNLIQTSTFFAHL VVS LTYVLCVSFFVCLFLRQSHFVTQAG VQWHNLGSLQPLP
5208	19109	A	5246	227	30	VFFARWVFLRQDLDLSSRLCSDVILVH CNVRLAGSRGTPSSSVKVGTTGMLYHT WVFFYEFHR
5209	19110	A	5247	173	442	FLGSSSKAAITLYYCQYMEFFFFFFFPE KNFFFSPGGGEGPNFILLEFPPLGLKK ISCPTPPRGWDYGVAPPLVNFVFFKKN GVPPPW
5210	19111	A	5248	255	358	TGPGTVAHTCDPSTSGGRGGQITMSGDR DHFGQH
5211	19112	A	5249	3	130	QPQLAAPSISWAPTSASQVAGTTGVCHH AWLIFLFWVESRRG
5212	19113	A	5250	90	1	STRLENNGTMSAQCNLRLTGSSNSPNSA SR
5213	19114	A	5251	358	447	SFISYRRRSPSPYYSRYSRYSRYSRSTP
5214	19115	A	5252	55	202	CWNTSMRGPWEAEAGESLEPGGRSCG EARTCHCIPAWVVRACLVDAA
5215	19116	A	5253	330	3	EEMGFSHVGQGGFKILASGDTPAWAFQK GGISGVSPRAWAGFIIFWNFSGGPQTG FPFYPPFRGIFFPRAKINYIRVLNPKGLC QKGVFFFFFFSGFPHYRCRLCQISV
5216	19117	A	5255	175	3	MYLRFPLGLSLSERPGMVAHACNPCTYW ESKAGGSLSLGVQDQPREHGGTLCCLQKS K
5217	19118	A	5256	263	1	RPRRRFNDRKTALLQEMPFTFTALGKL ISDFKDSKDGLTYFVETASRSVVLGAL ELLTSSDPPTSASQSTGITGVSHFSQPG LAF
5218	19119	A	5257	1	103	CHVSQAGLELLASSDPPASASQSVGITG VSHRTW
5219	19120	A	5258	128	2	THKWRDCKMVQPLWKRAWQFLMNLNTHL SCDPTVLLLDILTQ
5220	19121	A	5259	381	2	FFFFFFSEMESPVAQAGVQWCGLSLQA PSPGFT
5221	19122	A	5260	2	173	ENYLNMGGGGCSEPSLHHCSPALAIERD SVSTTTT TTKQQQNNQLGLFSYPNPL I

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5222	19123	A	5261	1	175	TKGNQIGKKEVKLFLETTDDMILYMENPK DSAKNYYKQSKTFCLPVVLGRSCKRTCP LA
5223	19124	A	5262	2	145	QVSLKLLGSSDPPALTSQGAGIMGVSHR TRPRNTDFKNNTQKSKNTQ
5224	19125	A	5263	182	3	STTSFLNFFLTEMVSHVVSQAGLKVLS SDPPSSASHSAGITGMSHHTRPQQPLLN LKV
5225	19126	A	5264	183	369	WNSLDDFFFPSPFFRGYSSMGKVQDAFI FYRRFIDKSKPRANTWGSIGGLYQQQIH PMDALR
5226	19127	A	5265	329	207	RGCSELSRSHCTPVWVTEQDSVSQKRKK KSPCHLQLGTSQ
5227	19128	A	5266	177	13	TLTILLNFFFLRQSYSAQAGVQWHNLN SLKPPPPGFKRFSCLSLPEFQQGHNR
5228	19129	A	5267	474	122	FTCSPPHGGFLTGLGPKNLGLGPSQLFP LRGGSKKQGIFFYSYKIKGPPGAGPPGS ARYSNPFGYGGRVLPPEFPDPPGEHK PRFFLKKKKKGHVPTSKYLPYLFAYY NASLE
5229	19130	A	5268	55	311	GIQTFGKNVVVAGRSKNVGMPIAMLHHT DGEHERPGGDATVTIAHRYTPKEQLKIH TOLADIIIVAAGSLISHSAGVQWRNHGS L
5230	19131	A	5269	238	133	NKNIWVQKKCVFYIYLPICVVCVCVCV VCVCVCV
5231	19132	A	5270	336	517	PVLYILEHSPYNASIYQLALKKYQSRPG AVAHACDPNTLGGRGRITRSGDRDHG QRGE
5232	19133	A	5271	262	467	VLSMRPRIHGSAAREEDEHPYELLLTAE TKKVVLVDGKTGTFTTPGRNTSKGIF KVCDPPEWKGKMS
5233	19134	A	5272	213	2	MKIYINVYILLFSLKKRQGPSTLSPRLEC SGMIIVHRSCLKLVGSSDPPALTSRIAWL IGARHTPDCSVCKF
5234	19135	A	5273	284	105	YSCSYSYFDEPVELNSSFRRWNHSSDS YWKKSCKDTEPVLKPPGYSARYECKTV GSS
5235	19136	A	5274	290	449	IFYFSGRVRAKLSAPLAGMGNKADSRG RSRTKMVSQSQRMYCLSALLYSLC
5236	19137	A	5275	248	423	NKVNITLMTKLEKDTTKENYRPIISLLN IDMKILSKILQNIQQYIQSIHHQDQVK LL
5237	19138	A	5276	425	30	TRRGMPHRQGSPPKAPVSVRRQRVREEC GREPLLWFLQSOLLGRLRQETHLNWGG GCSEPRSCHCIPAWATRANSIFCNFQAS SVEVRRSARKKLFSDILKRHNITITWRVS GLLLVDSYFGLRATPVRTQ
5238	19139	A	5277	25	185	SLFSVAEFANAYKVQTEKEEKEEARSK YKEAKESFQRFLENHEKMTSTTRYK
5239	19140	A	5278	263	483	VFTVVFQFLFCVYKLI FSLTECRSVAQ AAHAGAHWNHLSLQPPLSGFKQFSCLS LPEFFRMYSVLSPSP
5240	19141	A	5279	25	252	LETTLGLMTLVQCGGTPGFCHVGQAGLKL LTSGDLPASASQGAGIAGMSHHTRPILL HFIYFILLYHPPCLAYFIIF
5241	19142	A	5280	326	203	IETESCYVAQDGLLELLGSSNPPTSASQS AGITGVSHHTWTT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5242	19143	A	5281	210	459	NKNNKKFNKKKKKNYKKWARELYRHFSK DDIHVANRYMKRYPTSLIRKIQIKTSM RYHLTPIRIATIPR
5243	19144	A	5282	262	454	LLFTDYHEGMLHSVKLLFCFLGWSFTLA IQAGGHWRDLGSLCPLLPRLKQSSCLNL LSSWDYKR
5244	19145	A	5283	451	303	GTEFHHVAGLELLGSSDLPVLASKSAG IIGMGHHAQPKQYSFVILTVO
5245	19146	A	5284	217	489	PVSIISIILRCLSLPTFGSRVLCMLEGMD GISLGWVPLPSLPVPLHPLDLSLPVCRQ VGGTKTGVRVYVGETDFAKGEWCGVELD KPLGKND
5246	19147	A	5285	247	99	FFFFFFFFFLYGFFFFCFFFFFFFFFFFFF FFFLKNKTQPYFIYKRNILSM
5247	19148	A	5286	2	117	PRVRPRVRPRVRPRVRPRVRPRVRKKKK KKKKKKKKKGGGF
5248	19149	A	5287	121	3	KFWPGAVAHACNPSPGLGRRGGWITRSGD RDHPGQHSETP
5249	19150	A	5288	416	48	IGKPGSFFPPPPSPRGAPPPPKIFFLP PPPPFFRAGFPLFPFPPIFFFPKIDPP FFFTPLKKKFFFPPIFESPLGLFFF PPPPSLFSFFFFFFFFFFFFFFFFFFFFF FFFFFFFFLGV
5250	19151	A	5289	503	0	FFFFFFFFSPFFFFFFFFSSFFFFFFFFFFFF
5251	19152	A	5290	70	236	IFCNSQLTSPHKHQKKKKKKKKKKKKK KKKKKKKKKKKKKGGDFKKKIGGAK
5252	19153	A	5291	443	287	QFTKKKKKKKKKKKKKKKKKTQKKTI IPKPPLF
5253	19154	A	5292	334	115	KNENALFFFFFFFFVDRISLLPRQWHNIGS LQPLPPGFTQFSCLSLPSNWDYRCEPLR PALLFFSSKSKIHIKPL
5254	19155	A	5293	413	3	SSSPPIFFFPQKKKIFSPPPPKIFFFP KTFFFLRGFFQIFPPPKNFFPKKPQNF FFYPPKKKKIFFFPPIFFPPKIFLKT PPPPPPPPPPPPPPPPPPPPPPPPPPPP LEKGFDDAWADAWADAW
5255	19156	A	5294	291	11	IQPYIKRLMQHDRVGLSSEKQSWFRIYT YINVPGFQNGFIIIGSSQAQKMIFFF LDRVLLCHPGRSTVVQSQPTAALKNWAQ KTLPPQPSE
5256	19157	A	5295	2	401	NPRSTEAAIKYFLTQATASIIILLIATLF NNILSGQKKKKKKKKKKKKKKGGGPK KKKIGGGKKKPGGKKKIFFFIRGEKKNP RGEFEKKTFFWGGEKRANPPPKKTLGE KKKILGGGGKKKFFFPVGKKK
5257	19158	A	5296	49	363	RLQKNKEKKKKKKKKKKKKKKKKK KKKKKKKKRRNGGGKLLWKGGGQILTKE KILILVAVSYTCNINNLRQRKWIIGGG KSEPNYEFKRNIGAGRGSLL
5258	19159	A	5297	100	323	EYLNCTVRICHSHAHFLPPSYVSFALLP RFLFKVLLYMVQVFGEATEAVKKSLEGI FDDIVPDGKVKINVCFLF
5259	19160	A	5298	595	0	VCVCVCMCACICIC
5260	19161	A	5299	412	141	TVDTSYSEKKILFQILLIDNGPGLHRA LMEYKEINVVSMPANTTSIMQLMNQGV ISIFKSSYLRNAFCKAIAAIHSDSPDES GQSNLL
5261	19162	A	5300	216	2	SQDWLRKFCYHPRVFQRQPIQKLMGLFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FCLPNMVKNGVFFFFFEMEGRSVVQAEVQ WHDNSPLQPKPPGLK
5262	19163	A	5301	368	3	TFFFFPQKKEGGGLFYIFFPPKKKGGFFFK KKIFFFYPPPPKKKKKIIRAAEKRGPPPLF FLKKTRPNFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFFFFFLVREK VENSTISTQ
5263	19164	A	5302	389	2	AMAAQASGSCSLCSRLLDGFIPIWGVFRYF IVEAGSCYVDQGGGLAILASSYPTTLVSQ SAGMTGLSHRARPPPLNGPPPLTPSLSM VPKANVFSLLEKPTGLTQALRITLANVS NAPGQTRSGLEGWGCFF
5264	19165	A	5303	84	333	FHDCCRPERSRILRNFLSSAGIQSIAD AYRLALPQGLLYGPTNFAP IINHVARFA AHAAHQGTASVRVVGSGSGGNQGLP
5265	19166	A	5304	485	93	PPLFRFRFSPPPPPKFFFSRAFFFGGGF FSFFSPPKKSFFFKNPPGFFFPPLKKK KIFFLPLPLAPPKDSFLAPPFFFFF FFFFFFFFFFFFFFFFFFFFSRENIFPI IIFIYLFDRDRFLFCCLG
5266	19167	A	5305	157	2	PPPPPPPPPPPPVWVITLNVELEPSF SPNTESQIGPEAMERLQENRVE
5267	19168	A	5306	1	133	TQESIMDLENDKQQLDERLKKKKRPAV LKNPWGGQSLPGMARE
5268	19169	A	5307	239	2	PERNWGFFSPLSPLKSSSPPKAFNFWGG VGPNFPPPKKRFFSKNPPGGFFYPPLKE KNIFSLPPVNLGPPRVFFKGPPP
5269	19170	A	5308	454	116	FRLPSSSNSPAPASRVAGISGFRVCVGRA GLQLLTASDPPASASQGAGIADGVSTQ CSMVPRLECSGMISACYNLHLPAACLGP PKCRDCSLCLAATPSGK
5270	19171	A	5309	123	1	CSVSKWYPIAFLKNIIMLWEAEAGSGRG QEIKTILANTVKP
5271	19172	A	5310	153	33	WPGVVAHTCNPPPLGGRSGLITRSGVQP QPGQHSESPSI
5272	19173	A	5311	350	3	NSRNLILTQEHSPPEEKNEFLFSLPLQSV SMNTTHSPLLSNSLPHFIISFLPTRFLV GPSPTRSFPPAQSPDRISFSSRLECSGT ITAHRSNLLEGSSDPLISVSQVAGTTCM CHH
5273	19174	A	5312	1	392	RTRGRTRGICKSITIIHHINRTNEKKNH MIISVDAESAPLQIHSKLLK
5274	19175	A	5313	1	239	LKTSFHHVGVQAVLEFLASSDLPALASQS AGITCMASHCAQPYISINFIPAAETQQSS PELVPLPASQKTPSFSTPLFSLP
5275	19176	A	5314	345	237	LYFYIYFLKSACVILSTLCVCVCVCVC VCVCLCM
5276	19177	A	5315	268	412	GMISSNNSDSFGNCLNPGGKGCCPEGS YHYPPAWATDTFSKKKKKL
5277	19178	A	5316	112	224	PWMLLENELGLHASYLAMSTPLSPVEIEC ASKKIFTFC
5278	19179	A	5317	377	139	KPPPRIFYLGPQKKKLFYPPPPFKNCFF LGPPPPPLFMIFFFFFFFFFFFFFFFFFF PQWVMFLFLLSASNQNSPSWSP
5279	19180	A	5318	216	385	RGVLLCCPAWSQTPGLKGSSCLSLPKCW DYKHELPRPATSCNSILFFNLQGAEMYH
5280	19181	A	5319	376	3	RIDFGGPKKKILLPPPPAVKIVSLKGPP LFFFFFFLNSFFAPAGQWGVFQLISSGDP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PEPAPESVRIPGVSFCAQVPGQFFFFFL NSSVAQAGVQWRDLGSLQPLPPRSKRVS CLSHPSWDVSH
5281	19182	A	5320	377	287	ELLTSSDLPALASQSAGITSMSSHHTQPG SF
5282	19183	A	5321	381	65	SSSPSSRTSGPFFFFSPKKKKNFQKKK NFLYPFFFFPPFYKNPPKKKLKGPKKK KKISPPPPKKNLSLKNPPFFFFFFFFFF FFFFF
5283	19184	A	5322	132	396	EGGFVLKIITREGIGPHFLGLEEEGSKFH EHIFWEKHRESFPPKQGPPIPHFMEGLTGW LSKNPYFRVKQQRVEHIEGFKNFFNEKKD FLKE
5284	19185	A	5323	366	1	GFLKKGVPFFPPGKRGGNQTPPKPFVL GKQPPPPPLKKKNPKGGPPQKKIFF FLTRGGVSLFGPGGGFFFFQPPKKPPP GGFFFFFLKKPPPPPLFFFFFFFETGF CSCRPGRTRG
5285	19186	A	5324	131	1	DGALSPRLEWCSGTILAHCSLRLPGSSA SCVSASRVAGITGVC
5286	19187	A	5325	112	1	DGILLLLPRLESNGAISAHCNLHLPSTS ESTASAFLS
5287	19188	A	5326	404	18	PVSPHGXNHEKHTVTCVGSTSGAFLHGE EHCHGNTHHPFEPSPNPQTACQSQANRIR HGNSFKNLWRSWAWWRTPVVSATQDAEM GRPLEPRGLSLAWATQDDPSLKQKQKQK KPTHLWSYILGHHQLP
5288	19189	A	5327	109	3	KCVLTPVIRALWEAETGSGRGQDIETIL SDTVKPR
5289	19190	A	5328	1	117	ETGFCCVAQSGQLQLDSSNLLALVSQSA GVTGMSHRSRP
5290	19191	A	5329	3	120	DAWVAEAEQGNDTIEEPNKVQKRKRG INDNVPAGQAH
5291	19192	A	5330	105	2	RSGVVAHICNPSTLGGQGRWITRSGVQD QSVQDG
5292	19193	A	5331	204	411	SKKKQKKKKKKKKKKKKKKKKKKQDKK
5293	19194	A	5332	185	2	FFFETESHITQAGVQWRDLSSLQPLPP GFKSLPSSWDYRCLPPCANFCIFSRDR VSLCW
5294	19195	A	5333	561	325	WSTLHSFPIWLLNTGYFYKELTGFFFFL TVALSPRLCSDTIIAHYSLRLGSRDP PTLVFQSTKITSVSHCTQPSVRF
5295	19196	A	5334	3	96	EGKAAFSQEKSRVKEENPEIAVSASTI PE
5296	19197	A	5335	375	228	LSPWLECSGTILAHCNLRPLGSSNSPFGV FGFYFFLTLLLGSGVHVQLC
5297	19198	A	5336	403	0	NISVPASKHISPPPKKKKKKKKKKKKK KKSQKKKSRG
5298	19199	A	5337	397	80	IIITSKKKKKKKKKKKKKKKKKK
5299	19200	A	5338	406	34	KRTLKDSKKRKEKKKKKKKKKKKKKNR EKKKKPKKKKKKKKRGGAQKKNNHPAG GKAYFFFLGGTKKKRGGGDTKPLGEKNS PAQTKKLGGNNPPFVERGKKKKTPGI
5300	19201	A	5339	410	0	KKQKKKKKKDAPGGGGGGKKKKGGPQKK KKGSHLKTPEKKTGGA
5301	19202	A	5340	306	392	IQYKILPQKENDWDKIQQLAIPVSSLN F

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5302	19203	A	5341	3	173	TFTATELIIIFYIFFETLIPTLAIITRG GNQPERLNAGTYFLFYTLVGEGLLARS R
5303	19204	A	5342	247	426	GRAWWFTPVITPLWEAEAGVQWRDLSSL QPLLPGFKRFSCRLPNNWDYRHPVPRP ANFL
5304	19205	A	5343	3	149	SWFLHFGEAGLELLTSGDPPALALPKCW DYRLVNSWPEVILQPQPPK
5305	19206	A	5344	464	147	LRRLRWENRLRPGGGGCEPSRSHRCTLA RVTESLSRVQCQRDPRLAQTSRRPGAS SFPFAGPAFSAVNSTYQRALPPAQGAPW TPRLPLGPHGTTSSSTSYLPV
5306	19207	A	5345	228	1	VIRLEETYFLFFVFLFLFFRQTRSGS FAQAGVQSSHLSLPSSWDHRYTPHLANF CIFLQKQSLAMLPRLVNTK
5307	19208	A	5346	2	106	FVLELLGSNNSPSSASESAGITGVSHCG QPLFNF
5308	19209	A	5347	140	436	FLCDMRVLYVTFFFGKGVSFPPGWRA GGEFGLIENPPPGFNPFLLNLPKKGEL RAPPAPIFFFFFFEKRGFTRLTQEGLN FWTWEPPPLTLPRGG
5309	19210	A	5348	1	465	LESRRFEDGTRVPGSTISWDPPEEAVCP FSDLQLRAGRTTTTLFKAVRQGHSSLQRI LLPFVWQCPAPRGGVYRGRQASLSCSGL HPVRASWLLCFPSEAWAMSGTPPPASLP PCNLISDCCASNEQGSVGIGPSEPGVEY NLLLRHLLKPEEKRS
5310	19211	A	5349	183	58	ERDYEEGPGAVACACIPSTLGGRGGWIT RSGDRDHPDEIVDP
5311	19212	A	5350	288	404	IEXNGMILAHCNFQLPGSSNSPASASPV AVITGMNHYAR
5312	19213	A	5351	413	305	AEAGLKPLSSTYLRSASQSAGITGVSH HTQPLLFF
5313	19214	A	5352	91	356	TVPKRNTFSPKMVAITTAGTVSTSVLAL GNRESALPTRLGWALCCFIFWGGRGHRV PLCHPGWSTVARSRLTATSTSQVAILL PQPP
5314	19215	A	5353	2	410	FVQWQFLKTGSDRSRKAVESLGVEKVEK AMTVNYSFRSLNTKGLELLGKISVNLV AKWKHFREKGRRYTNLTGPTATAAFYST EKTEFLPVVEQTCKPFIDSFNKYLLPGA ADHACNPSTLGGRGGKITRSGDRD
5315	19216	A	5354	3	288	SLDDDLKLLPLMLQYSDEFVQSAVLS RRLAYFCARRLSLLSDSPNLLAAHSPH MMIGPNSSIGAPSPGPPGPGMSPVQLA FSDFLSCAQH
5316	19217	A	5355	187	3	KKILWQTPGVNLFSEFKGAPLFFFLRRV LLCCPGWSAVARSPLTATSASRVQAILL PQPPK
5317	19218	A	5356	383	261	GYKINGQKSQAFLYTNNRQTESRLWYCY DSPQRLIHLSIK
5318	19219	A	5357	367	241	FFFRHVAQAGLQLLGSNNPPASPSQSVR VTGVSHCTQPLCFV
5319	19220	A	5358	217	1	SCDRENTGLKLLSILLIHCETDTRISL LCISLSIKREIWLGAVARACNPSTLGGR GGRI TRSED RDPGETP
5320	19221	A	5359	255	412	TQLCRKRNAFFFLATNHSQKGQSRWGT AHACNPSTLGGRGGRI TRSGDGDH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5321	19222	A	5360	391	271	RSCHIAQAGLKLASSNPPASASQNAEITGVSHHLTPICC
5322	19223	A	5361	232	397	EGLKEPAGLFTMEYYTARKRNKIMPFVV TWMQLEAILLGESTQEQTCKFCMFSPV
5323	19224	A	5362	213	392	LFIKVEGKFFLRSLINILNESLLFLSSNG PGLLKKLGVWPGVVAHACNPSTLRGQGG RTA
5324	19225	A	5363	306	418	SDGITGTLPLASQESAVVEDLLYVLVGV DGRYVSAQP
5325	19226	A	5364	347	48	KKRWLKPGGGKNPPKKGKGGTTPPFQ KKGFFFPFPPFFLEKRDLSPOAGGKGEK KKPPQPWKAEGKKNPWGNPPQRRGYKGN PTRPPPQGGFFFFFL
5326	19227	A	5365	412	172	PDSNLSFGAHYQASLLGSFSLMPLLLYS KCSGQWDVARSAECTSKSSQNKERKKER KKERKKERKKERKKTRQKKNPLT
5327	19228	A	5366	400	296	LVEGGFHHVGRAGLELPTSSDPPTSASQ NLGLQA
5328	19229	A	5367	162	1	APSSLDETPTLLKKTFLFGPGLVAGICNP STLRGRGGRITRSGVRDQPDQHGETP
5329	19230	A	5368	152	403	TTVLCKLVQPLWKTVMRFLKELEVDLPF NPAVPLLLGIYPTKEKSYEKGCTHVFIA AQFQIARIWNQSKCPPINEQKKKGAPV
5330	19231	A	5369	170	367	IVFEILVISYFKSFQKTTEWNTFFHHP FKVFNWNPSTVAHACNPSTLGGRGRQITR SGDRDHPAR
5331	19232	A	5370	396	1	QMCVRAHTFAGGRARTHHTHTHTHTHS VVATPRVSHNHCVCVCVCVCVCVCVC
5332	19233	A	5371	139	3	PKLECGASIIAHCSLELLGSKDPPPSAF QVAETTGCAAPCLAFF
5333	19234	A	5372	1	341	PLINILSHLILLCRNYSFVKFCIRHTS LLYVVVISLHFVLLCVVSFLTDRRAHNAS VTYGFVLPVTFKNSPLPGAVAHACNPST LGGRGGQIMRSGVQDQPGQARSSRPALP T
5334	19235	A	5373	280	449	ICHNLQLCPSKDTIEKVKRQPIEWKIF ANHISHKGLSS
5335	19236	A	5374	170	1	QKRGFSMGTPMVSI FRPQDLTPLGFPKA WDPVNPWPWPWCPLFFKGNPQLFQAPG
5336	19237	A	5375	462	165	PPTRFLHVVTGLELPTSGDLPASASQG AGITGVSHHAQPRGHVFDVLEYSQQGV FTLLSFLGFSVFFEPFC
5337	19238	A	5376	3	451	PRAKLGTRRGLRNLDTIGVAVDLILLFR ELRVEQESLLTAFPCGLQFLRNIASRHE DSQSIGWVHAFFPPVWPCLSLPPHTGS SSSITLPPLLPHRPHPPPHSHPPMATLS RPPYFPFPPHPPHPLPPSLSPPALSPPP PPPPPPPSL
5338	19239	A	5377	460	300	KVLLCCPRLECRGAIMAHHSLELLGSSN PPTSASQSAGVTGVSHCRSPVVEFL
5339	19240	A	5378	452	191	DSRFHHVVQADLEHPTSSDLHASASQSA VITGVSHRTRPDIAFAPSISYFSCVAE ISLLHLSSESFPKQFL
5340	19241	A	5379	240	395	LATSSVANLRNTFYLLKSSVLGVEAHS CNPSTLGQGGVRIKSGVRDQPGQ
5341	19242	A	5380	210	411	TSVNSAPNSGQKASVEECFGQVTKVKIQ NVFLGWAQWLTPVIPALWEAGAGGSRDQ EIDTILANTVR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5342	19243	A	5381	406	300	FHYVGQPGLELLTLGSTCLGLSKCWDYR REPPHQA
5343	19244	A	5382	364	479	INDGISKISLFLSHLKDQAGQVWMLTPV IPALWEAEAG
5344	19245	A	5383	182	395	HHLRGSAAFLKSAQEPTDFRHTGFKRF SCLSLPSSWDYRCPPPRGGVLCPLGW RTVVQSWLTTSISQ
5345	19246	A	5384	37	478	GGIHSYPVICLFILMGSSVSLPFSSVAC LLAWLLPSFLPSLLPSFLPSFLPSLTGR AFL
5346	19247	A	5385	201	458	WNPPFLSPRKWAARADTEWVGKTAQEP GLSSRLQAYEERQRHWQREAREALREDCA AYAQAQRAQQLLQLQVFLQOQEKRLQ DD
5347	19248	A	5386	206	407	FFSPGGRAGEKFGFMEPPPPGFKTLWL NPPGKWKQRAPPPIPVYFLEFKKGGWP NMVQVGLNPRP
5348	19249	A	5387	468	0	NFFPPRPAPPPPPPPFVAQAGVQWRVL GSLQAPPPGFTPFSCSLSPSSWDYRRPA RVSPHC
5349	19250	A	5388	136	2	LEFFFLFETGFCVSRLECSGTIIAHCS LKLPGSCNSPTSVSQV
5350	19251	A	5389	397	0	TLYPSQKKKKKKKKKKKKKKKKKKKQ
5351	19252	A	5390	299	3	AQPLAPFPGSFILMYFFMLLLFGIPLLY MEVIMGQWLHVDNIRVWKQLVPWLCSMS YAHSLVNEGSPSPSPISLGLQVSAHR VHPQVCASVSLYS
5352	19253	A	5391	264	202	FFFFFFFFFFFFFFFFFSENKI
5353	19254	A	5392	2	150	PRVRFLIETEFCHVGAGLKLTSVDPP TSASQSAGITGVCHLVRPEKS
5354	19255	A	5393	382	0	NSRAQAWLMPVISPHWEAEVGGSLPT S
5355	19256	A	5394	395	239	SLPSSWDYRHAPQCWANFIFLVETGFSS VILCSFRLGGFGLSLNILCSLKS
5356	19257	A	5395	24	265	LLPHRKSRYRTRPTRSLRQKNGMNLGG GACSESRSHCTPVWATERDSVSKKLF TIELVYVFLKNSKGEPLPKVLGL
5357	19258	A	5396	174	118	FFFFFFFFFFFFFFFFFRSS
5358	19259	A	5397	406	134	PSAPSSPPPPPLIWGPPGFPPPLFKNP PPKFFFGAPKKKIYLPPLALNFVLLKG PPPPPPPPPPPSFF
5359	19260	A	5398	294	64	IFFFFFFFFFFFFFFFFFFELHILWGALF LLKSRIPPCKKNTCKIFLCTPLTGYIP LLKCFQKQNKKSQSQNTLKS
5360	19261	A	5399	1	211	LLLPTPYHHINQDSSNKYHETKKKKKKK KKKKKKKKKKKKKKKKKKKKRGEKKK KKKKGGGGGYKKKR
5361	19262	A	5400	305	1	SPRRPFLFLFLFLPSFFFKAPHTINH FFSPPLFFFFFFFFFFFFFFFFFFFFF FFFFFFFFFLKLYLFYKMRINYSNI LKINIFVSSPGSGRR
5362	19263	A	5401	416	3	ENTERDRGRQRREDRSRAETQETNRAGQ QUESTPPPKKNTYSIPSSSSSSPTPQK GKKGGPPGPPPPAGEKGGPKKKRGPQ KKKIRPPPGKKKPPKTPPLFFFFF FFFFFHKPQTFIVGVNTYILLRSVS
5363	19264	A	5402	154	416	KKKKKKKKKKKKKKKKKKKKKKKKKK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KKKKKKKKDSGGGAF
5364	19265	A	5403	327	2	PPPQKFFLGGVFFFPFFYNPPPPFFFF SPKKKKYFSPPRGKIFFFPFPFPFPF FFFFFFFFFFFFFFFFFFFFFFFFFFFF LRWSLALVAQAGVWWLNLHGSLQSL
5365	19266	A	5404	372	181	YKGLAHTRCsirNFLNFIliEMGSRFV AQAGLEPLGSSDPPTSASQSDGITGVS RTRPINIC
5366	19267	A	5405	110	1	PVPVSSTEVKKLVLWPGTVVHACNPKTS GGOGGRIT
5367	19268	A	5406	2	401	GFHLTTYGNRKQMQRHVREASARPLQGT PPPGHALEWTLNVLAAAPRPRKAQVLF AIVASETSSWDREKLWLSLEAKCKGIT LFVIALGPGVGTHELAELVLSAPSEQ HLRLQGVSKEPVNYAQGFTR
5368	19269	A	5407	3	181	QLILFHDKLSPKLLSWGNDILINFFLS HCSPEARARLQAKMMTNLVMADRLQLL GIN
5369	19270	A	5408	371	222	SVEMGFHHVAQPSLEPLGSSDPPASASQ SAEITGVCHCARPNHDSYRRS
5370	19271	A	5409	204	416	NQVGEWLVRKGTGLDLMFMLFHLVVR SKDEKNTKIWPGAHTCNPSTLGGRRGG QITRSGVRDQPRHG
5371	19272	A	5410	236	308	AGRPGTVTHTCNPSTLGGQGGRIT
5372	19273	A	5411	375	216	GCSEPRWCHCTTPAWVTQDSPPKKEKK RKEKKKKLLTENSCKALKRNGYL
5373	19274	A	5412	1	381	RFHHVAQAGLNLLGSNDLSASASQSAGI TGMSPRTQP
5374	19275	A	5413	144	3	RPPPIFFFLAKKLALFFFFHSHVIQAGV QWRNLGSLQLPPGFQKF
5375	19276	A	5414	412	32	LFSKKKKKKKKKKKKKKKKKK
5376	19277	A	5415	414	2	NNNSFVFFSKPIFLKTGVGAPPPSPIYN PIPIFLYIYPPHKWGGVYIPTHMYGGGD IWGYMYTPPPPLFIYFFPPPFYIEKK KKTVFCFFAQGGVRLCLKKKKNKDRGWG DTMTMGHGRLEMVANVCGLKRYVV
5377	19278	A	5416	1	240	GGEGCSEPRSCHCTPAWATERDSISKKK KKKGPPFKRTHFSSPGLPSFFFFGAPK FNSRARFLTPREGKNPGLPPFYPA
5378	19279	A	5417	2	63	LCLKNNNNNNNNNNNNNNND
5379	19280	A	5418	322	1	WPLCFSRCCKRGSPGLFPFSPPLGQSK KFVRFACKTPSAFKPFPSLSFFQWAGP PPFLQGLGELPKGLFFQCCFFFLRW SLTLVAQAGVQWHDPSGLQPPPL
5380	19281	A	5419	1	392	FRMAGSYPEGAPAILADKROQFGSRFLS DPARVFHHNAWDNVEWSEEQAAAAERKV QENSIQRCQEKQVDYEINAHKYWPDFY KIHENGFFKDRHWLFTFPELAPSQNQ HLKDWFLNKSEAPSQKK
5381	19282	A	5420	273	91	RWYIVLDNLIFILENICETSLKIYLG GVVARACNLSTLGGQGQITRSGVRDQ GQHGE
5382	19283	A	5421	1	149	GGGCGSEPRLRCTPAWATERDSVSKKK NLKKFFCPGLGLYQKQNTWTL
5383	19284	A	5422	381	179	SSCLGLPKSWDYRCEPLCPARTALNLKT IKKSKDNRWRGCGEKMMLHCWWECDM VWLCVPTQISC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5384	19285	A	5423	195	369	CSLSFTIKECKLHISGLQDSSISLVNLGLAIRNIRNKPGVVAHSCNPSTLGGQAGWIT
5385	19286	A	5424	253	414	KKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKXRRGGAAKKKPHSPAPAERDL
5386	19287	A	5425	160	2	NLKGSAPFSKKTSPFFFLVKENPLFFFFFFEMESLSVAQAGVQWRDLGSLQPLP
5387	19288	A	5426	53	426	ASSSFFFFFFFLGKGGSIFPPKGGGEGKNFFLWKPGAPGGGGPPPTPRGGGKKGPPPGGQKIFLGMFFEKKRFHHGGGGGFKLRGKKKPPPLAPKRVKNKGNPGGGQPLKFKKTLPKEMGLKK
5388	19289	A	5427	60	1	KWPGTVAHACNPSTLGGRRG
5389	19290	A	5428	87	247	KKKNPQKKKKKKKKKKKKKKKKKKKKKKKAPAGAGDLSLYYPRAGRNNLFFNYLP
5390	19291	A	5429	209	405	KLNLVNFSSLSLKAMISAILLKLSVPIFPMKIVILSTLNSGSWPGAVAHACDPSALGGRGRIT
5391	19292	A	5430	324	237	VMNAFVCVCVCVCSCICVCVCVCVYFLF
5392	19293	A	5431	409	3	FFFFFFSETESRSVTOAGVQWRDLGS
5393	19294	A	5432	270	402	MKIIIFHLIRITGWAQWLTPVTPALWEAETGSGRQEFETTVKPC
5394	19295	A	5433	107	277	YNFNHRYREATQKWDEALQLTPNDATLYEMKSQVIIMKNFTFLMKLCYCVCSVSEQ
5395	19296	A	5434	95	1	RNRKNNGQSGTVAHACNPSTLGGRDGWI TRS
5396	19297	A	5435	412	105	GGEGCSELRSCHCPPAWATRARLHLKIKKKERWDLAMLLRVGYSGRHQVHCTDHGTLQPQPF
5397	19298	A	5436	276	488	PLPQPNKDSRLPLLVLCGLFAPLLMLGHGPKRARLPPIFFPQEAIFYITFRLVFAEKKGYRGPLTMCLAPR
5398	19299	A	5437	179	2	GISPLKGGTPSLKKKKKAKDFNRRVSKEDIQFTNKHMKRCITLLIHKMQIKITMR YLP
5399	19300	A	5438	3	156	TPLYSQILISLRQEHYFKAEGRCNELTSYHCTPAWAKDGDSVSKNKQNT
5400	19301	A	5439	47	173	SLQLFLQTEERKDSDEKSDRNRPPWWRKRFVSAMPKGNFIKY
5401	19302	A	5440	3	122	TTLTTLTSLIPPILTTLVNPKNKNPPKLI RILVLFQTTEK
5402	19303	A	5441	390	489	KYKSYSLQPPPPKFKHFSCVTLPKHWDY RREPP
5403	19304	A	5442	86	275	RQEFETSQGETPCLLKIQKLAGRAHLNPGGRGCSEPRLCDCTAAWVTRAGLSQIK KIKKKKK
5404	19305	A	5443	424	166	CFFVSPKAKSQGVVLGSPPPPPPGLKHF SAPTRGLFLFFFFFFPRGVPPLGKGGSKSPPGVFPWPWPQKGDGSGGYPPPRAKIF LF
5405	19306	A	5444	356	3	AFFWFTNPFPFPGFKGFFCPHPLSGISKG GPPPRGNFFFFGKAHFFSPFFKFLPPIFLPFLAPQKVGFGFGPPPKPSQGVLFFF FFFFSFLFFFFFFETESSVAQAGVQWR DPDAW
5406	19307	A	5445	198	86	PWPLGAQAAILLPQSSCLNLPKCWDYRREPHTALLNS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5407	19308	A	5446	198	86	PWPLGAQAILLPQSSCLNLPKCWDYRREPPHTALLNS
5408	19309	A	5447	143	3	TMIYFYFYFFLSQSLALLPSLEGNGTISAHCNLRLPGSSDSSADAW
5409	19310	A	5448	324	1	KKNSATSFVSVEPFSTGGVLANKGALTQEKILPCFKIKKIRKRVGAVAPARNHFLFSPFFKEGLQGIVYFFFFFELESRSVTQAGVQWRNLCSPQPLPPGFKRTRG
5410	19311	A	5449	403	0	LLLLLLLLLLLLLPPKENH
5411	19312	A	5450	114	409	LNITWTLKYLTSKHLIVCLPDTILSSLC LIKYIGLQGVLIFFFKQFSAIDKLGQN IAVVGKFGFAHYSLLTKKWLFGNITQE QNMIVTGGLSWWND
5412	19313	A	5451	192	406	RNFFLGHLYVKKRFEQIGWRDFMFKTPKARATKNKMDKGDLLKLSFCPAKETTF RGTGHPTKGEKIFAT
5413	19314	A	5452	254	48	NAFGWLCVHYALQFIDKSVKNSVCWLGA VAHACNPSTLGGQGGWITRSGVRHQPGQ YGETLRTRASTR
5414	19315	A	5453	1	288	PLLFILIPSPFSFPHFPFCGPIKFILPRE KKKKKKKKKKKKKKKKKGGPFKKKKI FPRGGKKKIFFFWAQKKIRGGVLKTGG RKKPGGKKNKSG
5415	19316	A	5454	285	415	TSGCCFVFLVLKLSIFCKGKVLNAIEDN GLKNSTFTYFTSDHG
5416	19317	A	5455	372	125	ITPAFSFSPMGKKGVFPFPKFFGFPPGF PPPFFFKPPPGIIFLGPKKKKFSPPPR VYFFFKRPPPPPPPPPPPPPPPPPPPP
5417	19318	A	5456	3	159	AHASAHAYDTIKDALGLLLFILSLMTLT LFSDDLGDQKKKKKKKKKRGGP
5418	19319	A	5457	109	392	NIIIIKRSTSLFLRPFIFFPHLFPFILIYLFISLRTLLEFFFFFKREFCFLPQVGGQGF FLNSLKPLPRGLMQFSCITLLRSGNYGP PPPPPIFFF
5419	19320	A	5458	243	402	FLKIGFIHKYLKEFVWGILNIVFNRFNS HERAPHAIVFVNGTTIEGHVEKCYW
5420	19321	A	5459	394	105	IPPPSPRPGGPGAAPPGGGGSTTPPK KKPFFPKNKNQPGGGGAPPSPPRGL GPKIPLTPGTKVFKETKPPPPPPRGAP PKFLSKKKKKET
5421	19322	A	5460	56	379	VCFSPSTYGAIVLNKSPLRSHGSSSTSG WGGLPSPPFAQRLPLASQVQEHNGHVFA SYQVSI PQSCEQCLSYIWLMDKALLCSG EWLPHQAPKPSMSPTTPHCSRGLQ
5422	19323	A	5461	184	420	FFFFFLNNLFFFFFFFFFFFLLGRN
5423	19324	A	5462	295	384	LGAVAQARNPITLGRGGWITRSGVQDQ PG
5424	19325	A	5463	413	257	FLNPGGRGCSEPKSHKSTLAWVTERDLI SKKKKKEKCWIPQRMPERGQWSPD
5425	19326	A	5464	2	181	SLYCSGWSQTPGLKQSSCLSFPKCWDYR CELPRPVVLLYKTSFPKRYVFGIHLCF MSQ
5426	19327	A	5465	1	229	TGSCYVAQANLELLSSSDASTSVSQNAG TTGVSHHVQPYTSSFSQVPPLRAQSAAT ETTSILWVQKLRLOVVRCSV
5427	19328	A	5466	1	368	KERETKKEREERMRMRREGREKKEGRK ERKKEREKEREKREKRNLLGQSAGIT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GMSHHTRPKSHNVLSKFTNLCWAAFKAI LGHMWGRDLKLNVEQCFSTELSAFSII ATSHMRLWVI
5428	19329	A	5467	183	3	VSLCYGEKFSPPQMNESQLYFRPGAVAHA CNPSTLGGGRGRQITRSGDRNHPGQHG ETGRV
5429	19330	A	5468	1	128	GGAGYSELRLCHCTRAWATRAKLHLKKK KKKGPLRALKKIGG
5430	19331	A	5469	1	155	NKFPVLISNVINIIGMCHCTPAWATERD SVSKRKKKKEKRSKLARHSVLCCL
5431	19332	A	5470	113	1	FFFFFFQKTSSRLGTVAHACNPSTLGGR GGRITRSGD
5432	19333	A	5471	407	281	NGMIPGGRACSELRSRHCTPAWATEQDS ISKQNKSKNPGLK
5433	19334	A	5472	1	177	GGGCSEPRSRHCPPAWATERDSYLHKMK QSKTKGERMEVACYCIIILFMLTDALEV LMA
5434	19335	A	5473	76	267	KERREEKEKEKRKRSEKGRKKEGRRDR EKEKEERKDERREGEGBEGRKEKEKD IKRRGVVP
5435	19336	A	5474	133	2	LCRMVVVLCFEAGSHSVTQAGVQWCGLN SLQPLPPGFKQFSC
5436	19337	A	5475	5	394	YGVGTGKFRAGVKEFQALFLITVHSQ LCHIEGTRHHSRHIIIVVDFINQIENGTF FPLVLSNGCIWLLIVYLFWNIFTRQEGQ FFYGKLSHYSVFVFCFLRRSFALAQAGV RWCDLGSLQPLPPGFKRF
5437	19338	A	5476	163	2	SEKPVVVALTMTFSHFFFIYFYIIFI FQMESCSTQAGVQWRDLNSLQPLP
5438	19339	A	5477	111	2	PLFLKQDLPGAVAHACNPSTLGGGRQI TRSGDRDH
5439	19340	A	5478	232	0	HLVWRMESGSVAHAHVQWCDLSSLQPPP PRFKPFSS
5440	19341	A	5479	388	225	ALFSSKKKKKKRKRKRKKKKKKESM QRKGHLPRVCCGASMVSPGHKLSL
5441	19342	A	5480	150	2	HRVAVIYEVFPVCLFFYFLRQSLTLV TQPGVQWRNLSKLQPPHPGFK
5442	19343	A	5481	156	395	DSVCTCVLHTCHSSGLSQGRSCLHCSLG LENSNCPVCVCVCVCVCVCVCVCVFC PLHQGVVCVCVCVCVCVCVFLSAHFTKGC VCVCVCVCVCVCVCFSPPI
5443	19344	A	5482	391	115	RACPDICRVFPHTSPPCLPGPEAEPPG GPALRELVPPLPGQLQPPFGMPSPGLGA APSPAPPACAWTRPPHLHPSSFSSSVPQ ISSLFLCF
5444	19345	A	5483	392	2	FFFFFFSETQFRSCCPRLCNGAISVHCN LRLPGSNNSP
5445	19346	A	5484	381	282	PVPWQAIFLPPPPPYLGIPGPPPPFGL FLFP
5446	19347	A	5485	407	3	FFFFFFLRRSLTVAQAGVRWCDLGSLQA PPPGFT
5447	19348	A	5486	2	417	QENHLNPGGVGCSEPRSCHCTPAWVTEY DKKKKK
5448	19349	A	5487	3	413	VYLHPSLQPSLSSLVDPQALSHDIWLKK KKKKKKKKKKRGGISPPSPVGGVGP RETWGVWGPANLFRGGGVRELFSSQKKKG EKGQRNPEKKPPHKGPGGPKEKFIFFE KKKKKGGKPFKKTKPPPPRVNPGG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5449	19350	A	5488	229	411	IHGPGFKNGGRGKTLGLPNLMALKKIPFSPGGYKPKNP
5450	19351	A	5489	190	50	YHHHHHCHHHHHHCHHHHHHHHHYHGDNDYSSSHSRSTCHVAVTV
5451	19352	A	5490	615	402	RWCLTSPRLCSCGMISAHYNLHLPGSKQLSCLSLPSSWDYRCPPPGKTTFSRGIRDALKPRKPKRINLI
5452	19353	A	5491	338	53	KGPPFFFFCKKGLFCSNWFLTPGGKWFSPPTPPRSGGKRVPPPEGGKGFSLPFFVEGGSCHIAQAGLKLGLSSDLVTSASQSA GIMGKSPHAWP
5453	19354	A	5492	266	412	NPNFFERKSCSVSQAGVHRRELNSLKAA PSGYTPASCVS LPSWDYRRP
5454	19355	A	5493	285	412	RDGVSALSPGLECGMITAHCNLELLGSDPSALASQSTWNY
5455	19356	A	5494	1	1350	MGFMTGICIEDNVVGPSPESGSVLTVGGVRIQMLDRCHTAHCPVIPGLLRGQLWTE NLAERNSHDRPFPPTVVCSHFAQDLWPE QSIKDSYQKVI LRKFEKCGHGNLHFKKG CESVDECKLHKGYNGLNQCLTTTQSKI FQCGKYVKVFHQFSNSKRHRHTEKKP LKYLEGDKAFNQSSHTTHKKIDTGEKP YKCEECGKAFNRSSHLTHKITHTREKP YKCEECGKVFKYFSSFTTHKKIHSGEKP YICEECGKAFMYPYTLTHKI IHTGEQP YKCECDKAFNHPATLSSHKKIHTGEKP YTCDKCGKAFISSSILSKHEKIHTGEKP YKCEECGKAFTRSSHLTMHKI IHTGEKP YKCEECGKAF TWSAGLHKHRRTHTEGKP YKCEECGKAYTTSSNLTEHKTTHTEGKP YKCEECGKAFNWSSDLNKHRIHIGQK PRT
5456	19357	A	5495	4	146	PPTRPTCYVLSFYVSYPTGYKEDTRMVN KHMKRCSTSLVYLLWINFY
5457	19358	A	5496	5	388	CGCFFFSPPPKKKVFPDPFFFPAGGFP PPLFFTPPPQFFFWAPKKKKNSPPPPGK KIFFLKGPPPP
5458	19359	A	5497	231	163	FFFFFFFFFFFFFFFFXTNKWF
5459	19360	A	5498	163	2	SVKFTLQKVSQFLKKHTPAGWAHTVIPA LWAEAGGSRGQEIETILTNTVKPH
5460	19361	A	5499	229	388	RTHLQASSDLFCLYSLRTGSCCVAYAGV QRHDLSSLQPPPPRFKRSSCLRPPE
5461	19362	A	5500	405	289	HVAQAGLKLASSDPPTPASQSAGVTSV SHCTHPRCLFV
5462	19363	A	5501	286	375	GDFVRFSFWPGGAHSCNPSTLGGRGQ VT
5463	19364	A	5502	20	374	ILQFQNFVIVLFKNFYHFGKFLIYILNW FSGLFWYYFSELSCFSLSSKINILNLLS GILNVFFSISGVRKKIFLIKRYCWLGTV THACEPSTLGGQGRQITRSGDRDHGQR VVKIQN
5464	19365	A	5503	1	185	FHHIGQAGLILLTSSNLPASASQKAGIT GMSHCTQPIIIFLYSLFLQLSFSWQDFV MRKKF
5465	19366	A	5504	202	402	NSFSSTAKLREKYRQFLYTPIPTGTQPL PLLTFCTRPDTVAHACNHSTLGGQGGQI TRSGACNQPGQ
5466	19367	A	5505	118	7	IKKENNWPGAVAHACNP SILGGRDGRIT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						RSGDRDHPG
5467	19368	A	5506	205	422	ANHFTSIRMAIINNKKQTENNKCWQGG EVGTLVHCWWECKMVWMLRQIVWSFLKK LNIQLSRDPATLLAI
5468	19369	A	5507	3	425	RSCHCTPAWATERDSVSQKKKKKKKK
5469	19370	A	5508	3	86	EKKLQVLLNCMTETIYYQFKDKAERSK
5470	19371	A	5509	395	108	GVLECNDDTTAHCSLDLVGSSDPPTSAS QVTGTTGTCHHAQLGLPKCWDDRHEPRL PAWNKTLRRKNWHSLLPVPAIQELEVG GSLRPRSLRLE
5471	19372	A	5510	421	59	FFFFFFFFRRSLAVSQAGVQWDLGSLQA LQA
5472	19373	A	5511	168	3	EICKMCFPVFPGVFFLWIVFVFVFVFL RWRMESLSVSQAGVQCNLSSLQPPP
5473	19374	A	5512	446	149	FFFFFFFFCFEETESCSVARLESSGMISA HSSHNLCI
5474	19375	A	5513	74	398	DRIIDAGPKGNFYARFMNHCCQPNCEQK WSVNGDTRVGLFALS DIKAGKNHFRILQ LTSEFQGFCLQTASSDYNFKHFYMYRS LELSSFTFLCNHHHHPSPELFSSS
5475	19376	A	5514	73	335	BGGSLFCPGWSAGALFWLTAPSASRGWG GAPGVVPVGEVGVQKNCWNPGGGGCNELG LHHCIPPWGTGKTLSPKKKKKGATDMG GAS
5476	19377	A	5515	416	0	WLGPGAVAHTCNPTTLGGRGRWITRSD
5477	19378	A	5516	242	423	AGSPLIHQGGQAIILTONPTPGWGTMTVF QPVLRPVKGLYNANHVTS SPVASQPIIF TTAG
5478	19379	A	5517	2	151	GRVGFVGMGSHCVAQAGLELLGSGGPPT SASQSAI IAGVSHRAWPYFPS
5479	19380	A	5518	312	405	GQVRPGAVAHACSPNTLGGGRITRSGV PDQ
5480	19381	A	5519	3	387	ACSGPRSCHCTPAWATHQDSVSKKKRKK KREKPFLLLEKKRGPTLTWGEPPKGIPLG ERNGPPSHFKKGPPLAPKPPGGNLHPEI AQGPGSP TDGNKKGDLNPTPVFYKFKTP EQAINWAAPFPSEK
5481	19382	A	5520	292	140	KKGPPRARPGGGSPPLFFFFFFFFFFFF FFFFFFWESTLKKRELHRSDL CV
5482	19383	A	5521	1	399	KKWFLSSAQIPTKLSRRRRNRETWPKE RSKINLHKPILKKQRHELDPKEFKIALI KMLYELKVTMHEQENENINKETENTK KKK KKKENPPLFGTGKNQSPPEKFQMGQPP PPPPQKKKPPPNRFFVFSP
5483	19384	A	5523	316	399	MLLYWPGT VAYACNPSTLGGGRITRL
5484	19385	A	5524	400	0	FFFFFFFFCFFFFFFFS
5485	19386	A	5525	3	429	TTNIGRAMGATTISVGS DTSQAERP GGT TVVSPGASSTSQSSRP GTSVTPDSSASE SETVTTKEFSGTTAISRTSHTGT PAASG QOATGSLTATTGVAPGTTVAPGSSNTEA TTSVGEKKKDQKKKASSP
5486	19387	A	5526	135	3	GGKICTLIKQSVIQESWPGTVAHACNTS TLGGRGGWIMKSGDR
5487	19388	A	5527	105	5	KKKKKKKSGRWPGAVADACNPNI LGGQG GQITI
5488	19389	A	5528	411	31	GQRVPLSRGVAKKKKFLWNPGGGAGKNG GKNFLKKKPPGAPPPSGGPKKGP GPPPP

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						KKPLILVSPPPRKGGAHNMHFRQKSGN KGEGSTKGGKEKIFLGKFVQKNFFFFFF DPEFHSCCLGWSAMP
5489	19390	A	5529	411	142	PRFSFLFSPPRKKEVFPPPKILGGPRFF PPRFLKPPPHFFFWGPKKKKKFPPPG EKFFFFKGAPPPPPPPPPPPPPPPPP
5490	19391	A	5530	174	401	QVQPQQKKKKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKASPGGGGKKKKK ERGGGGERKNIWVPLLFPP
5491	19392	A	5531	410	0	QPQSKKKKKKKKKKKKKKKKKKKKKAS QKKKKKKKKKKKKKSSGGGFFKEV
5492	19393	A	5532	383	145	GGFFFNPPAKKGSFPQPHNLGGPPVFSP PPVFKTPPRNIFFGAPKKKKFPPPGAK KYFFKKADPPPPPPPPPPPPPPPPPP
5493	19394	A	5533	418	328	KTGFRHVQGAGLKLASSDLPALASQSA GL
5494	19395	A	5534	169	3	IILIIHPCSHVPRRETGLKACTFKNLF WPGMVAHACNPSTSGGRERRITRSGDR
5495	19396	A	5535	1	254	PTRPCKPPQTSPNSGKLSPPSSNGCMNTL HISSTNTVGEVIEALLKKFLVTESPAKF ALYKRCHREDQVYACKLSDREHPLYLHD
5496	19397	A	5536	43	404	QGGLTVLPRLVLNSWPDKRSSRLGLPEC WDYRYEP PHQAN
5497	19398	A	5538	2	212	KENHLNPGGGGCSELRSCRCTPAWATER NSVSKKKKKKFRGGGLKKGPGFYPLEK KFPGVGFFPKTNLV
5498	19399	A	5539	2	387	IFQEHKNCGEMSEIEAKVKYVKLARSIR TYGVSFFLVKEKMKGNKLVPRLLGITK DSVMRVDEKTKEVLQEWPLTTVKRWAS PKSFTLDFGEYQESYYSVQTTEGEQISQ LIAGYIDIILKKKKKKD
5499	19400	A	5540	317	407	GLSHHVFFEEGKLKKPRIKDKDKVPEP DN
5500	19401	A	5541	120	3	NFFFFFFLRRSFALSPRLCSGTISAHCN LHLPGSSDSP
5501	19402	A	5542	430	0	QKAQSNNGPEKQEKRGVIONFKRTLKSKK
5502	19403	A	5543	172	2	FIFNFLHIFSFWFITKFGCFIVLFLRQS LALLPRPGVQWRDLGSLQPPPPVRPRV
5503	19404	A	5544	149	2	EKDIQELNSALHQADLIDYRTLHRKST FFSAPHRTYSKIDHIVGSKAL
5504	19405	A	5545	84	276	TLKKRPKEIRNQGGSPQRKRAQLGKLQQ KYPVLNFKAPFFGERGDYYSFFKTCLD NLPRRGKG
5505	19406	A	5546	2	914	RPAWHEEQKSKNEPEDTEDKEGCQMDKE PSAVKKPKPTNPVEIKEELKSTSPASE KADPGAVKDKASPEPEKDFSEKAKPSPH PIKDKLKGKDETDSPVHLGLDSDSESE LVIDLGEDHSGREGRKNKKEPKESPQKQ DVVGKTPPSTTVGSHSPETPVLTRSSA QTSAGATATTSTSTSTVTVTAPAPAATG SPVKKORPLLPKETAPAVQRVVWNSSSK FQTSSQKWMQDSSSSSSSSSQNQQQQ PQSSQGTRYHTRQAVKAVQKQKITQSPS TSTITLVTSTQSSPLVTSSSGMST
5506	19407	A	5547	2	244	TRLIFVFLVETGFRRVGAGLKLITSGY VGTSASQRMTHLCLPRCWDYRCEQLHP AQRFFKRMLSAVDAALLHTSGGM
5507	19408	A	5548	406	1	FFFFFFSETESCISQARVQWCNLSCLKP

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5508	19409	A	5549	417	43	IRPARKGCSSGLFGAPLAGGGAPPPPPP RQTSPPPPHTKGGGGGPHKPPPKKKRPP PKKGGGKKNPKKKKKNTPPPKSAPP PAAKTDPPLPLTVPPFLPPYIFTKKIPF LKSYYYYFY
5509	19410	A	5550	3	136	QPRFPTLTNINENNPNTLLNPIKRLAAGS LFAGFLITNNISYHSP
5510	19411	A	5551	75	194	NKELSRNKKKKKKKKKKKKKKKKRGGG LKKKNGGGAKT
5511	19412	A	5552	343	493	IIFSFFFFFFLKGsfvFAPQAGGHGNGF GPLKPPPLGLKEFSCLTLSSW
5512	19413	A	5553	148	3	DAVSIFCPGSEHSDDTIHAYSPDLLGS SSLSASTSRVAGITGICHHA
5513	19414	A	5554	407	252	KKKFLKLAGQGGMRLQSLLLRRLRQED HSSSGVQSCSELWGGHLIYSKNR
5514	19415	A	5555	3	231	HEFVFLVETRFHHVGRAGLELLISSYPL ASAFREAKARREDLLSPGVKDKPGQYRD TLTLKKKKKSFFIYLGEWC
5515	19416	A	5556	3	131	SVVVSWEESKDAKELVGYYIEASVAGSG KWEPCNNNPVKGSR
5516	19417	A	5557	3	131	SVVVSWEESKDAKELVGYYIEASVAGSG KWEPCNNNPVKGSR
5517	19418	A	5558	462	255	RSHHSAQAGLELQASSDPPALTSQSAGV TNVSLRAQPIACSSVEVSSRCQVCLHV RRGKCPRAESYR
5518	19419	A	5559	445	29	KSSNILILQKVENGDLNKKILKITDFGL AREWHRTTKMSAAGTYAWMAPEVIRASM FSKGSVDVWSYGVLLWELLTGEVPPFRGID GLAVAYGVAMNKLALPISTCPEPFAKL MEDCWNPDPHSRPSFTNILASCQAWR
5519	19420	A	5560	225	475	GAVESSCTEEHMMWIPEKAVEGSLTPTPE SRSAHAGVQWHNVSSLQPPPPGFRRF CLSLPSSWDYTSAGEGCAASYRSKVLK
5520	19421	A	5561	248	142	NKNIWVQKKCVFYIYLPFCVCVCVCVC VCVCVCV
5521	19422	A	5562	262	456	NFPLKTTYFLKKKKKKKKKKKKKKKKK KKKKKKKKKKKKKKKKKKKKKKKKKKK KKKKKASSPPLIKRGPKN
5522	19423	A	5563	314	444	LKSMFCFVLFCEFEIESRSVAQAGVQWC HLSPLQPPPPGFKRS
5523	19424	A	5564	220	486	LNSSHPEPLPLFGLVLQFFYPSPNPKSF NKKNLIRMLLTVDGRPNHPDLSFFVHS NVDTVFLPQEGPSFLQPLGQGITEAFEH NQAYV
5524	19425	A	5565	176	492	CTKTAVASKARYLQALLYALASVTIAAT ATRLASISGASPIFRSFPYLQPTAPGLV LPSILILVDVGLRKEKGPDTVAHACGPG TLGGRGGRI TRSGVRDRPDRH
5525	19426	A	5567	24	470	PMDXKXPXXETPLNGGAGENQDDMFAK LKEKLFNEINKIPLPPWALIAIAGVAGL LLLTCCFCICKKCKKKKKKKKKKKKKM KNAMNMKDMKGGQLPQDDDDAKTGLTEG EGEGEEKEPENLQKLFSLDYDFQANQ LTVGVQLQAA
5526	19427	A	5568	45	485	GXDGRLLRGHNQYAYDGLDYIALNEDLS CWTAADTVAQITQRKWEAAREAEQLTAY LEGLCWEWLRLTHLENGKETLQRADPPKT HVTHHPVSDHEATLRWALGFYPAEITL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						TWQRDGEDQTHDTELVTETRPAGDRTPQK WAAVEVP
5527	19428	A	5569	221	422	FFFLTGRVRQSLADLEQKIEVHSMPPFE SLALSPTLYCRGAILGATSASQVAGITN ICHHAQPSYLF
5528	19429	A	5570	401	477	IFSRDKDVAMLPRIVLNSWAQVILL
5529	19430	A	5571	102	36	EVENNDDISHHHHHHHHHST
5530	19431	A	5572	106	407	AGRQGVVLEGCRAAWPTLLTPPATSSR GASRPPTATCPTPDPAATTTWQPWPPR PLWAGVQVHDLGSSQPPPPGKQFSCLS CPSSWDYRGRRVACHH
5531	19432	A	5574	253	363	YHSNQCVCGLRKWPGAVVHACNPSTLGGR GGWIMRSGA
5532	19433	A	5575	1	132	MECHYVAQAGLELPGSSDLPASASQSTG ITGVSHCAWPGFFFFF
5533	19434	A	5576	18	378	TPGGGGCIEPRWHCTPAWATRALKSYK KKKKKKK
5534	19435	A	5577	21	232	ILRCTTIETLLKVQDNHNLNPGGGSCSEP RSHHCTPTWARERDSVSKKKKKGAALW DPGGGQPSAGSQTR
5535	19436	A	5578	377	2	LSLIQTITLCLGAITTLFAAVCAVTQND IKKIEAFSTSSQIGLIIVTIGINPHLA FLHICTHAFKAILFMCSGSIIHNLNNE QDIRKIGGLLKTIPLTSTSLTIGSLALA GIPFLTGFYRTRG
5536	19437	A	5579	2	227	IESWLEPVRFLRSMFANNLVYDTSDDDD YHLLKDLEEGIQTLMGRLLEDGSRRTGQI LKQTYSKFDINSHNHVDAA
5537	19438	A	5580	113	3	NPPFFFFLRLQSLAVAQAGVQWCDLGLSLQ PPPPWFKQ
5538	19439	A	5581	184	3	IMPPHSRLSPTARFCLQKKTNNNTPIE MASIQCPGWSQTPGLKPPSCFVLPKCWD YRCE
5539	19440	A	5582	381	3	FFFFLGDRAAPPGEKNPLGGGLKTPGKP PGGWGVSPPPQKKMPPNFFPPGKKKS FGGGGPIFFPGKNFPPTQKKKRGGGF FFFFKKPGGFFFFFPFFFFSSFFLGK SFIKISFKRRRG
5540	19441	A	5583	314	389	FSCLSLSSWDYRCVPLHGLNFLYF
5541	19442	A	5584	131	1	FPLWTSEQGVGRNKQTYVTWQADCKENA GGDYYWTFPPQPTFV
5542	19443	A	5585	484	3	MTEILLKQAMVGIVGSIGSAIGGAVGGG ASASGCTAIQAAAKFHFATGGFTGTGG KYEPAGIVHRGEFVFTKEATSRIGVGNL YRLMRGYATGGYVGTGSMADSRSQASG TFEQNNHVVINNDGTNGQIGPAALKAVY DMARKGARDSNSAGDQIFHH
5543	19444	A	5586	136	48	NTMQPGVVTHTCNPSTLGGQGGRTGSG R
5544	19445	A	5587	306	479	DSFFPGVGSFAFLYQVAAVVTTKYFKKRV ALSTDIARSEMRLTFLAPFTKFLIDVC DW
5545	19446	A	5588	201	2	ILETGFFHHVAQAGLNLASSNLPASTSQ SAGITGVNHAWPSFLIQGTKHSFKNSK PVFHIKLSKN
5546	19447	A	5589	30	477	TPSLARGVYPCWLYTGFLHDFLFSKPIE ERFMDVGVLRATEPSNSLFAIISTPIE LAIKSWHIIGDGLSIELVAVERGNRTTI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						ISRLPEFEKSSLSDSLVTLSGYFAVY RVKLTAKKLEGIHEGAFOITTDYEILTI PVKARNALC
5547	19448	A	5590	208	91	KGHFWVTGKKKVPCPPPRFFFFFLDGI SLCYPGWSAVV
5548	19449	A	5591	325	467	ADLCSPCDILQLDFRHIRKTVDTLLALG EKAPPPTSALRSRDLISCF
5549	19450	A	5592	332	403	LSLCVXHTHTHTHTHTTREIFY
5550	19451	A	5593	292	26	FLDMEGAEEAGAEGLYHCLLCWETPS RLAVLQHLRTPAHRDAQAQRRLQLLQNG PTTEGLAALQSILSFSGQLRTPGEEE GTGE
5551	19452	A	5594	387	51	LKKIFLGRGQGVSLFFSPPLGGPGGRFL GLEIGALFGLPGKTPPPFKIKKNYPGLW GGALFPLPLEGLGGKMAFPRKGGAPFSQ KNPPPPPLGGKTKPPPLKKKKKKKVL
5552	19453	A	5595	88	362	AETSPGQGSYQDGLRRPGFAEGPPAGRN PRRKTQTDRRGSAGSQPQACADGVRL CTRLQCSGAISAHCNLCPLGSSDCPASA SRVAGIT
5553	19454	A	5596	92	366	DQPWPGQLPGRSPEAGIRGGSTSRKKPQ EEENS DRSPGRQGI PASGVGRCAALY QAAVQWCHLGSLLQPLPPGFKRLSCLSLP SSWDYSH
5554	19455	A	5597	3	138	TRPRTRGVGQAGLELLTSSDPPTLASQS AGITGVSHRARPQSSS
5555	19456	A	5598	150	3	SCVIYSWMKFFSFLRWSFTLVQTQGVQW CDLSSLQPPPPRFKLFSCPG
5556	19457	A	5599	148	3	TOHLNLAKKSQITPGMVAHSVHAGROW CDLGS PKPLPPGLNRSCLP
5557	19458	A	5600	195	1	MVYFKKFCGFFLFVRSRIACSVAVGMQ WCNHSSLQPRTPGLKQSSHFSFSPSRWNN RHMQPCPGA
5558	19459	A	5601	228	415	VNVSIPKDVFLIIIIILFFFGPAPQAGG RGCNLSLLPWPPGLKQFSCLTLPRSWN YGLPPP
5559	19460	A	5602	405	2	AATGVDRHAQRTQAGLPLKTPQTPCPNF TSKARGTPSAQHPSCTQRHQASNPQR RRRRPQAEHSIRTDAGHGPLPASGHMAG ERPTRKAQSRDVSVLQRILALLPRLECT SAISAHCSQNLTGSGNPPVSCL
5560	19461	A	5603	3	236	RQENGMNPGGGACSEPRSRHCTPAWATE RNSVSKKGIKIKGHCSSAMHHQVLSPF GWRQVCSCVCPKPWLLVRGH
5561	19462	A	5604	184	2	RPFLRIQKIRMFSGSRFIENFLILETW SHSVPQARVQWCHRSSLQPKPLVFKSSS YLLP
5562	19463	A	5605	261	2	GWFLKGPPPLFLGPKKPGGLGFFQKKLV QKNPPPGIGPPKNLKKTPLFFFFFLRR SLALSPRLECSGTISAHCNLRIPRTSNS PA
5563	19464	A	5606	134	2	GSPFKNLVFFLGQSLTSPRLECSGTIS AHCKLRPLPGPHQSPAS
5564	19465	A	5607	3	269	RQESHNPGGGGCGEPRSRHCTPAWLAT ERDSVSKKKRKRNFNFIGKKKPCLP KPKLTKKKKWGGITALVLKLYKRAIAPK TGGY
5565	19466	A	5608	36	380	PPFXXPPGGETFGGTPRGPPPKKKKSPR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KRGGGGKKKFPFRGAPPPKHLGGKNGGG GTPPPPRKTPPLNPKKRGGGKRGVFFP PKGGIFQKRGGFFSRGGGGGAPPPHPP GGG
5566	19467	A	5609	3	411	SSRSRAAALFYFFFFSRRGQKEKEPEFLG GKTPPVFVFFPGGVGKKNRGFP PPPAG KGPFGSGGGREQTPIWSP PPPRGKWK PPKPVTNPNFNLGRVGF LGKNPSPGGVC PPPKTPIFFFGRRPPPGGFFWGGGG
5567	19468	A	5610	364	483	ISWVLFLLFKWSFVLVAQAGEQWRGLG SLQPLPPGLKGF
5568	19469	A	5611	399	285	GGCSEPKSRPCTPAWGTERDFVSKKKNK NNYLVKKSN
5569	19470	A	5612	408	3	KEVFSFPGLHGGVFVSLPPLPPRVKG FSP PPPPGGGGPRGPPPPGYFLLFPKK GGFPPLPGGFSSPQIWPPRPQKVGVP GAPRPGPNFFFFFRESFPFLARGFPKK KKKTCWNVTLSHSASVQSSVLL
5570	19471	A	5613	1	112	LAQHVFLLNTSIASPADSSELLMEVHG NGKRPSPER
5571	19472	A	5614	2	389	FVREGERKKEKRKKKEKRKBGTKEKGKE EGRKERKKEKVRKKTVD RRRPQVTFQA VNLESEGAPGNCGVTA PPGGHIWLKQVE VQTHLENRCHRLKATVTTTTTRPGAEP PPFIITCGEIMNVFSDM
5572	19473	A	5615	385	3	KPPPGD PGKTPFFLKSQKITGGGGGAPL FPP PQVKAKKRGYP RRQSFKRARLGPC PPSRGGKKKAGFKTNPPTKKKNQTKKPM KAKTSKLLQENRSGPGTVAHACNPSTLG GQGGWIMRSGDRDTK
5573	19474	A	5616	218	402	RSYSFSQLVGTVIKARKPESSCWLCA PNRKNAFWPGAVAHTCNPSTLGGRRGRIMR SGDGD
5574	19475	A	5617	2	235	KSFGCASRLQMHRGTHTGEPYKCKQCG KAFGCPSNLRRHGRTHTGEPYKCNQCG KVERCSSQLQVHGRAHCIDTP
5575	19476	A	5618	347	421	IY LXXXXXXXXXXXXXXXXXQKKKKK
5576	19477	A	5619	92	1	ENLALLPRLECN GTT LAHCNLR L PGSSD SP
5577	19478	A	5620	3	402	APPPSFFFKGLIM AISPTLGAIKLINF LFFFKKGKKKKKPPLEKKKKKKKKGGA PLKKKKFSPPGGGRKIFFKGAPKKISRA RVKKQRRGEKTRGNPKKRGKKKRPFPN TVSR
5578	19479	A	5621	420	3	HPP PQGSANFFPPPRKIGINGPPPPAGI IFVFLECRGF PQVGQGGFKIRPPNKPPP PPPKNLGLQKKSPPPPPIFFFFLWRWG LMTLPRLVSNWLKQSSHLGLLKHWDYM SEAPHLAKNFLKEYEVVLSFHVES
5579	19480	A	5622	246	132	EVAPHL LGCISPTMCVCLCVCVCVCV CVCVCLCSW
5580	19481	A	5623	219	424	ILNVMVLGIGTFGRLLGLEGRALTNGIK ALIRDMGPGAVAHTCNPNILGGREGWI MRSGDGDHPGQH
5581	19482	A	5624	32	454	GLEKVHSM TXDRNSRLSVQLRDWDGGGE LLQFVSLDGEDTAYSLQLTAPVAGQLG ATTVPSPGLSVFPFSTWDQDHDLRDKNC AKSLSGGWVFGTCSHSN L NGQYFRSIPQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						QRQKLKKGI FWKTWRGRVYPLQATTMLIQ
5582	19483	A	5625	166	2	LFGLVKLTALKGLKMLPSQVWVLTPTVPTLWEAKAGGSQGGQEFETSLANTVKP
5583	19484	A	5626	120	406	GGAATQENLAELRPEPELLSPSTVLSREPELPSPSTVLSREPELPSPSTVLSRKPDLLSPSTVLSRKPDLLSPSTVLSRKPDLLSPSTVLSRKPDLLSPSTVLSRKPDLLSPSTVLSRKPDLLSPSTVLSRKPD
5584	19485	A	5627	324	16	LSPPPLFKTAPRPQKKNP PPKKKPAPPKKKNLFFFFFFFFLVFFIWC SWRLAEWNETIGECMDRWGQAVGTGTSREL RP GGSRSQPRRLAGKELGPHCAP
5585	19486	A	5628	378	72	GRGGERPPPPQKSGAKKKPGVNLNFPQRGKRSGPPPGPGFFKIFSQEAPGFFSSFFWGRSLALFPSWGARGGFLVPANLGPPAGAPKGNPPSKKKKEKIED
5586	19487	A	5629	3	204	QESCLNMGGRCSEPRSCHCTPAWATEKDSVSKKKKKWKFGGFYEVIGNFLHLFPKWSYPPSFRIF
5587	19488	A	5630	177	1	SFHEMRFWKLFIIRIYVHFERRSCVPVQSRVQWHDLSLQPLPLGFKRFSCGLLSNW
5588	19489	A	5631	154	3	KWFQMGSRSVTQAGARQCDHSSLRPPTPQLKRSSCLSPGGWDYRHVPPC
5589	19490	A	5632	239	17	EGVRNYLILQPRSLCRLNCSFFPNREKELCHISSFSPLAAAKESQGEKGRLLSQDEGLLLVVEVFVEDVEINS
5590	19491	A	5633	2	110	GCSEPRSHHCIPAWVTEGDSVSKKQPPPQKKKCIAG
5591	19492	A	5634	433	0	FFFFFFFFFLKKIPPPEGGGF
5592	19493	A	5635	306	433	FSISIERSSSGRAQLTFVMPALWEAEA GRSRSQEIKTILAN
5593	19494	A	5636	2	285	QSRTSVIFNSEKAERGEETTEEKFEASRGWLVKFKERSCLHNKIQVSEAISADVEAAADPEDLAKIIDEDGYTKQHIFGQALCLMSNP TTLGG
5594	19495	A	5637	160	1	LYCGKIYVVKFIRLNFFLSQGLTLPKLECTGTITAHCSLKLISPSNP PARAA
5595	19496	A	5638	3	261	KIQLNPGSQGCSGLSLCHCSPA WATETLSQKKKKKNPPFGFKIKGEIEPLREFGTKKKKGGFLKKFPHPPLGFFLEPFTWGGFWN
5596	19497	A	5639	2	121	SELRSCHCTPAWRQSKTTS HKKKKNIKKKNKFFLPFREN
5597	19498	A	5640	370	180	VEMEFCHVDQSGLELLISGDTPTSASHNAGITGVSHRTWQPSFFSFFKERNLKSVTSLNVSP
5598	19499	A	5641	254	1	FYILRKVFVFLFPAVSYGKGTYP AVDASYSADTYSKPDSNGRKHMVVRVLTGVFTKGRAGLVTPPPKNPNHPTDLFDSVTNN
5599	19500	A	5642	292	106	NFVILFYLFKQGSYVAQAGLEPLSSDPLATASQRAGITSVSHRAQTQAETVVPFSLFT
5600	19501	A	5643	3	100	DTFFEVEVEMEKEVCRDLMCTSPKDEEGFLLI
5601	19502	A	5644	1	282	EKVPEAKRLYGKRGDPFYEAQENHNLIQVANVFLECLFCDVKLQYAVPIISQQGEV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						STGQPWRTMVQVFCGLFWFSFYLSYV LEVVDQETKAN
5602	19503	A	5645	142	67	NKNRPGTVAHACYPNTLGGQGGQIT
5603	19504	A	5646	350	213	GLELLTSSDPPASASQAGITSMHRPW PPLASRLDLCCGTYLI
5604	19505	A	5647	3	180	EHNAERAFLAQAHLGPGAPCTPGFSPFI PTQFPFRSSGLPNIPVQTISRAAEKL FG
5605	19506	A	5648	366	1	RSWFTTYKERSLLHIIVQREAASADIE TAASYSEDLAKITHESGYPKQIFNVDE TAFYWKMIPLSTCIAREEKSISGFKASK DRLTLWLGANAGDIKLPKMIYVHFKTP RALKNYASSL
5606	19507	A	5649	1	355	QIQSSQSGKGLLLTSFIDEETKLFPPGN KVWFCIPPGPGGKLCFKKKIFGLYPGG GGFWGPQTPLAPTFFPGFPPPPGPNFS PRGPFPMGPALRGPCKKKPKPEKTKPA KGCTGP
5607	19508	A	5650	348	124	RAPPVFFWVFLGQFPKKKSTNSPRGGGP PRSFQPFSLPFFFRNVFKKKPPPPFFEG GRGPPAPPFKNPFFFFSRL
5608	19509	A	5651	194	43	KKKFFFFFFYEMESHPVTQAQVWHHLGS LQPTPTTFERFSCLTSLIAIP
5609	19510	A	5652	27	244	KKQOSTLFLFYFLSFLFFLVKTGSHY AAQAGLELRASSNPNTSVSLPKSWDYGH EHTVPSPTWFLAAKTP
5610	19511	A	5653	38	429	GLFLSCLFFFLEKGVPLTPPGATGENP APKKKGTGQKLLKNRDFLLKKAMFGKQK QKKFFFAPTITGDQAPRVFKGPGAQKE PFAQKKKERGGGKTRAAPNKKKPGAF FSLKKTPLWAGGGPPPF
5611	19512	A	5654	391	68	NLYPHGGVPGVSPGKGLPKAPNPLGGI PPSGEPPPLPPQGFPPCLKPKKRLGKAP GPPFFFFLAILLGFQISNTDSCVQVFI IQTIWIIFTTIKGCCHLHFTFLF
5612	19513	A	5655	159	34	GARFLFFSPVLSPLIEHCVCVCVCVCVC VCVCVCVCVLCACMCT
5613	19514	A	5656	88	388	SIFCFIYVFPLRQSTTLVAQAGVQRDL GELQSPQKKKGKETFSFLGENRYLQPK NFFTFLTQVCFEKIIPNGLINGKRPKW IPGCEFLKTLVVGPPV
5614	19515	A	5657	176	371	HFYFCFSDINLAAEPKVNRGKAGVKRSA AEMYGSVTEHPSPSPLLRSGTLLFITAL CPSVGIFSF
5615	19516	A	5658	3	113	CSEPRSRHCTPAWATERDSVSKKQQTKN LSYKKIHW
5616	19517	A	5659	409	67	SSSNKPPTRPVFILPFFGHGVPRLPPGK KPPGPPPPPPQVEQMYGRKGGFALNL PPRRQKNMLYSPELGEK
5617	19518	A	5660	2	377	GRISCSRNTPLRHRSMLIVCGLRMLPS GFLPWVGQVFLALIPVNPQPSLGVRTI MDMLRCCRDFIYGQFWGQFMARLWGACS QQYTEFFRFKIIFISLLFNIVLEVLR AIRQEKELNGMLQ
5618	19519	A	5661	256	381	NFNTGQAWLMPVILAIWEAEAGESRGQ EITILANTVKPHL
5619	19520	A	5662	19	313	LYSSLAILGFLPLLIINFIIIIFFFFER DPGQQNQNFVSLKKRETPPPPFSLGVPG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KRSLPPPPGPKHAGPPVLPAGLWGGPE PPTWGRGAKQKREI
5620	19521	A	5663	78	365	ETGRKRKETRWNLKKVCLLKMSLQGEKE ERKREKYRRTEMKRQKNSEKQRGREK GK KSKYQRRRKKEKKGENQTKPKPKVEESS SRQ
5621	19522	A	5664	159	28	DTSTLPTPTGFKRFFCLSLPSKWDYRRP PICLPNFFFFLVVTGY
5622	19523	A	5665	350	151	IRCLCPDKFLAFCDRGVLLCCSGWSRTP GLKRSPCPSLPKSWDHRCLADIYIYIF LKDTSTIMSF
5623	19524	A	5666	394	248	LTPGGGGCGKRLRLRHCTPAWATRANLPL KTKKKRKRFLFLAETSKVY
5624	19525	A	5667	1	194	RLNPGGRCSELSRHCIPAWATRKLH LKKKKKGQDQGRGDHTKNIWLFPRVFLP LHSLNTLK
5625	19526	A	5668	2	312	RGQNSARGTIIAILKKVCVYIYRCGLT LSPKLCRGTIAPCSLELMGSCDPSTS ASQIARTADMHHTRLIASLTFCLLKK KKNVFCGTYNHCPPKGFYL
5626	19527	A	5669	1	245	RLNPGGGGCGEPRSSHCTPVWATRVKLS LKKKKKKRPPFFFFGIRQPPQGGPFQTL TPLNLLKNLTLLGAKKFFFTGGK
5627	19528	A	5670	1	135	ARTPSPSLSESSEDEKPTKKHKKGKALR LKRRFWVVLMSALPCIH
5628	19529	A	5671	97	2	KKFTHVWPGVVAHACSPSTLGGRGGRIT RLN
5629	19530	A	5672	362	173	VFSPPPPFKTPPPPKKIPPKKKKTPP PKKKKLFFFFFFFFFFFFGTRIVIDN ILSGNRV
5630	19531	A	5673	237	13	SPGGGGGFAPYWMFFLDFERQSCSVAQA GVQWHNLSLQSPPPRFYFFSRDGVKNR PVPRYAPPSPKGISLRPYK
5631	19532	A	5674	245	14	ANFLKAHIVSTLGLQIISLQLLNFAI VFYFLRQSFALVAQAGVQWRDIGSLQPL PPRFKRFACQRFSEAEVAVS
5632	19533	A	5675	2	249	SHPTHSHPQHLPLTPTWNWSSTPVDIF RKAPPVFWHQHHRAGPGLIPTDAPQ EASPPPPYPSSPSSTPTIPRETFLRQ
5633	19534	A	5676	115	241	SSTLGGQGSITLAQELRSCHCTPAWATG QDSISKKKKTLG
5634	19535	A	5677	460	2	RLGVTGRWQKLKPQERMRAWRENGKGP ALPASWEGETVNLLWKHEHRAWVSCD SGFCAWCQGLGSEQSLPSLIPSWDGLV LTSPPNPTGPPPLKTRSVLRGDDVLLP CDQPSNLARALWLLNGSMGLSDGQGGYR VGVDGLLVTDQAQ
5635	19536	A	5678	2	346	ENCLNSGGEGCSKRLRLCHCTPAWVTERD SITKEKKKNFKPVLEKFGEIIFLKGWK FFQLNPLKSSKEMEFTNTLPLEPCFNG NKPFWAAKIWTNLNFFQTQKGSIFKWGGR KK
5636	19537	A	5679	181	4	PKEVRTLFGRFFFFFHMEHSVQAGVQ WCNFSSPQPPPGFQKFSCLSLPISWNS RHM
5637	19538	A	5680	549	410	FFVQTDFFCHVAQAGLQLLGSSNPASAS PKYWDYRREPVCWPSSGF
5638	19539	A	5681	111	403	SRQINGFFVVSRTKVAIGQFLVGPSVKI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FENNNEICMIKSIQSYIVLNHKKHLKVYS SNIWQLKNILLRGGAVAHACNP SILGGR GRRITRSRDRDHP
5639	19540	A	5682	189	3	NNNRKASWKKKDRVLLYCPGCNWC DLGS LQPLPPGFKRFSCLKLPKCWDYKHEPLH PAPHV
5640	19541	A	5683	2	227	IHVVCVVRVCVCILREDSAQPARCVCVC VCVCVCVCVCLDPRRELSPTSQLESSCH PLYVPSGGSRINRYPYGGC
5641	19542	A	5684	318	421	DVPCFPVAFCCDCKFPEASPAMLNCE SM KPLSFI
5642	19543	A	5685	213	398	SLCCLLFCCCYFETESRSVVQAGVQWHD HSSPQPGPPRLKSSSHLSLRHDHSSPQ PGPPRL
5643	19544	A	5686	398	1	SPFSTSYSSSVQGGGQGAHSYKSCTAP TAQPHDRPLTASSSLAPQQRVQNLHAYQ SGRLSYDQQQQQQQQQQQQALQSRHH AQETLHYQNLAKYQHYGQGGQGYCQPD A AVRTPEQYYQTFSPSSSHRE
5644	19545	A	5687	2	288	SDRPRSFSFSPSSPAGVGRASSIFPIL SAILLLLGGVCVAASRVYKSKRNIIILGA GILFVAAGERQREGATGAHLGAHVCVC VCVVRARARA
5645	19546	A	5688	314	2	CRPGSQLQELGDGGGGESFVGGHGQQHP GAPQGRGYLQPLLMCGASPHASPRQPLA ILAAGVKFRVLRHEAGRPLRLMLQINPL PYSRVVHTYRLPSCGLTCI
5646	19547	A	5689	122	3	MGGGEFSKKMNINGQGVVAHACNPSTLG GRGRQITRSGV
5647	19548	A	5690	144	1	EAVKKYTCPTWAGAVAHACNPSTLGGRG GWITRSRGRDNNGKHGEIPR
5648	19549	A	5691	377	65	LGVFPFPFFFLRGEGLSPPPGLVKNQF FFPPGQKGPFGTPERFGQGLGPKFFPP LPPQGPKGIFFLKKKKKKKIPICALAVL TYQHFCYRTGQERVDGLREL
5649	19550	A	5692	12	147	YERRFCHIGAGLELLTSGNPPASASRG AEITGVSYHALMRNIS
5650	19551	A	5693	183	395	GHRFGFLHPPPPGFGGFRPPPPKTEGK RAPPPPPRFFFLGGGGFSGGGPRGVLF LEHENPPPGAPKGVG
5651	19552	A	5694	177	283	THFLNRTDGRWLSLASLPSSGYGTNTPS STVSUSA
5652	19553	A	5695	266	460	LSQRKYAFFFFFFFFGKKIFFSSPGGEI RAQFFLTPSPFWVKGFSPPLPKTWDY IGRDPPPLG
5653	19554	A	5696	1	412	MQPLKVNLLQKNLGLFVAPFTWIHCP SYWSIAYNVYSQYSFTWVFCTMFTVN IPSKKKKKKKKKKKKKKKSSSPGSP GYAPKKAPKNKKK
5654	19555	A	5697	379	0	FFFPSSQKKKKKKKKKK
5655	19556	A	5698	1	187	PTRPPTFRFENGVN LGGGCGEPRLCH CTPAWVTERDSVSKKKKKKAVGGPWF FQKKKV
5656	19557	A	5699	374	0	DFLLQKKKKKKKKKKKKKKKKKKRGG
5657	19558	A	5700	219	413	PFCPQGGGGGPNFVFLGPPPPGLKEIPP PPPRGGGKKPPPPPRGGFFFKKGVVS PGGPGGSP
5658	19559	A	5701	381	249	FHRAGQDGLDLLAPGSAPLGLPKCWDYR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						REPPRPAPFFFFFFF
5659	19560	A	5702	382	197	LANFCIFSRDGLPCCPGWSGTPGLKQS AHLCLPKCWDYTHKPPCPAPQVIKPSIN ILIVN
5660	19561	A	5703	1	381	ERGSKHPPRGLKHIRGRTCFVLKGCMTQ LCVVPPGQGGKKKEGGGKKKDKKREEE GREKKKNGNQGERVKKKKSKRKKKKRSS SS
5661	19562	A	5704	291	167	NGPPFFFFFFLVKMGFCHVGQAGLEFLTP GDPPALASRLGL
5662	19563	A	5705	367	23	KNDCPPPPPEFFLAPKKKGPPPRKKTRF VPPPLFLIKGPPFKRGKGGPPGGFPPLF CPLGGKRGGVFLSPRVGKPRGKGGNPLF PKKKKKKKRRRRKKEGKKGRKERQGYIH TV
5663	19564	A	5706	411	116	FLKRWGSHYAAQAGLELLDSSDLPVSAS QSAGTTGVTHCSRLSYSALACQLCQPVW RIPWRGRGVGRETSFRGWRRYGRAWSS SGGGAESLPGLSPG
5664	19565	A	5707	162	2	SYCFPNSDDFIPFQPLPHTWFLWPRFFF IFKTAHGWARWLTPVIPALWEAEAG
5665	19566	A	5708	1	416	LPLLYKIPPPAILFLFIKDSPPPPPPP PFFFFFFPP
5666	19567	A	5709	403	142	LSKEKKWGWPRGFSRPFKPPPPKIFF APPKKKIFPPPPGEEKFFPKGAPPPFFF FFFSFFFFFFDCYNSSTWNSAWHIRCSI SIC
5667	19568	A	5710	339	461	PSTFILFILRRSFALVAQGGVRWRHLGS PQPPPPGFKRVPA
5668	19569	A	5711	408	42	TGARIIFSGPPKKTYPSPRAFIILSEK RAAPQLIYFYLNLFAVKRLVKTITVIMR RRPTFFLLLFKTFLFVEPGFCHVAQAGL QFLGSSTCGSLPQCWDYRCEPQHLAKRS TFIKSESAV
5669	19570	A	5712	277	9	GVCVCVGGVVPPMGLQTPSAPWGLSLA PPLGTLCSVQWLAESIHLICQALVEPL RRQLYQVPVRKLLASSIVSGFGDSIWN GSYLR
5670	19571	A	5713	411	0	FLQILLFLIDIAFFLVFFFFFWKK
5671	19572	A	5714	205	400	HYLIQSSSSMASSESVQLDVVMKIPLTWP GAVAHTCSPSTLGGRGRITRSGDGDHP GQHDEAPSL
5672	19573	A	5715	1	89	FFFFKTESRSVAQAGVQWCTLGSLQPPL P
5673	19574	A	5716	176	392	GVHLVLEWKLSMVCAEDDELFLPLCSWKK FFFFFLRQSRSVTQAGVQGRNFGSLQP LPPGLKRISCLTRPSS
5674	19575	A	5717	1	89	FFFFKTESRSVAQAGVQWCTLGSLQPPL P
5675	19576	A	5718	306	42	GSGLRRCALNSVKCLNTLECILLGIYLR QIKICVYTKTCTCKFIVTLFIIAKKYEY PSVEQLINKMWHIQUIFLVIKRNEGCGG SCL
5676	19577	A	5719	1	263	PTRPGRFFLILGDRGCSELKSCVCTPAW VTEGDSISKQNKQVELRSPAHLGLGGL VPNRPQASTRIGDPCTKKLLELISKFSK AAA
5677	19578	A	5720	3	278	NQEILKNVESSRTVQPHFLEFLLSLGWS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						VDVGRHPGWTGHVSTWSINCCDDGEGS QQEEVISEDIGASIFNGQKKSMHI IQ LKYFLSH
5678	19579	A	5721	127	3	KKKKKKEEEEQGGERRRRKKKKKEKEKK EKEEDGEKKEGE
5679	19580	A	5722	204	96	VTSRSSLFSTPGIKRASCGLPKCWDYR PQPPHLA
5680	19581	A	5723	3	261	QIVRQWKYNDDDDDQLFYTRVYLDPLR VGKAEWAHPALWEWRPQAEWDLGSKG GCKEKNVCLGVVAHACHPRLLGGLGRR I A
5681	19582	A	5724	134	358	PPPPPPXLLFFVSAVPPSPSPSLSFPP HRPCYSPSPPTLSSLPPPLLFPPPPSSP PPPPRPSAPSPPPSPSPFS
5682	19583	A	5726	248	470	LLNVQNGIRNVCSPHYTPFHKVVKYLS VFLTEVDSSQLRRQLCGGSQAAI ERMIH FGREKVQILHLAL IYFLV
5683	19584	A	5727	1	281	NQHNRGFFDSCDGGFTTNNWREEHLERM LGQAGERRADVILGVDVFARWNVGGRF DIDKGGGGFLSKGQRPSASPGTSFPHGP SIPVCTSKE
5684	19585	A	5728	460	3	SQTRTLTLDREITLPSSGTALISLVDGS GNPVSVEVQSVTDGVKVKVSRVPDGVAE YSVWELKLPTLRQLRFRVCSIRENDGT YAITAVQHVPEKEAIVDNGAHFDGEGSG TVNGVTPPAVQHLTAETADSGEYQVLA RWDTPKGGPVTV
5685	19586	A	5729	70	465	SQCSPHHSVLCQKVQDLESGLTQSNWKK ITPFDENVVCVCVCVCVCVSMCVYVCV YVCLCVCVCVTVCMCVCLYIKGLLFLLA KKETAGSFFHSQLTCLGVPCAFTIHPVP FLPQCRSHCVSGGRFWPGVL
5686	19587	A	5730	281	427	SWLTAAPNFQLQMESRSVAQAGA QWHDL GSLQAPPFGPQSAETQKQMI V
5687	19588	A	5731	418	194	TKFHHVGHAGLELVTSGDLLSSASQSAR ITDMHHCSPASVLSMNRPSGSTRCLRN GIFGPLKDFKPNDLTVQL
5688	19589	A	5732	229	2	PGGAPPLVRSGFPGWGAPPFVFPNGE PPKNFFFFDGVSLCRPGWSAVAGS QLT ASSTSRVHAILLPQPGIVA
5689	19590	A	5733	435	138	PERYPPPLWGAPPPLSRGGGSFTPLTPQ GKPRFFLKIKINPGGGPPPYSPFFGGGG PRNFFSPGAKGPLVLISPLFFPPPGDQKK NSFFKKKKKERERE
5690	19591	A	5734	113	409	KDVC GGVL TGLSGVLTSP EYPNNYPNSM ECHWVIRAAGPAHVKL VFVDFQVEGNEE CTYDYVAVLGGSSPTPVHQYCGSISAPY LFFLAKNIMSYSLPN
5691	19592	A	5735	3	122	GGWQVQVFSEPCSL SINGVIFGLTSTD L LFHLGAE EISR
5692	19593	A	5736	14	428	FLALRWGHIRLPASGPRDTATLFTSLDT QLLMTLYVGKDETFYVSKALVHTGVAL VPRGLTLAPADGPTTDEVTLQVSGEREG SPSTAVRYPSGSVALPSQWLLIGHHELP PVLHTTMLRVHPTLGSGTAETRPEN
5693	19594	A	5737	415	1	QHINTLGQFWTTKAF LERMLELQNGHIV CLNSVLALSAIPGAIDYCTSKASAFAM ESLTLGLLDCPGVSATVLPFHTSTEMF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						QGMRVRFNLPPLKPETVARRTVEAVQLTQALLLLPWTMHALVILKSILPQAA
5694	19595	A	5738	335	152	GVEMGFHHVVQAGLEFLSSSDPPASASQ SAGITGVSHQASPFLLPLSGITLPLSIY SSGSD
5695	19596	A	5739	35	462	IDASDFGECSQAAINDNVVIVYELLEEM VDNGFPLATESNILKELIKPPTILRSVV NSITGSSNAGDTLPTGQLSNIPWRRAGV KYTNNEAYFDAEEIDALIDKSRSTVFA EIQGVIDAACLKLSGMPDLSLSFMNPILL DD
5696	19597	A	5740	429	325	NPGGRGCSELRSHPCPTPAWVTEQDAILG GRSGRIT
5697	19598	A	5741	344	423	FWPGAVAHACNPSTLGGRGGRITRSR
5698	19599	A	5742	431	103	RGPFFPRPRQKKGGSPGGPPQNKNGP PLHTGGAKGGSFFKKKKKKKVPKKGPGL FFPGPGQPRKGPVGAPVLIIPNRLGPPR IPPGWEPGRQIFFLAPVFFFPSPKPK
5699	19600	A	5743	31	224	EEMGFYHAEQADFELLSSNDPAALAFQG AGIASMSHCSWPGKNFMFCCIWMKRL AIHWECEIA
5700	19601	A	5744	217	400	HSVMGGSPSFFFFFFFFFGEKGLFFFCP GGPNLGKGNPPPPGKKGFP PPPPKGN NGAPP
5701	19602	A	5745	4	455	DGLEFPGRFRGRQRCSSPFRGRGQVEA LLTSQTGRGRGAPHVSDGRRGRDAPH FLDGLVAGKRRSSLPIDGGRAETLLTF QTGQPGRGAPHVDDGRPGREAPHFDPG VAAGQRLQSRHFGGQRRLLGGGGCIEPR SRHCTPAWAP
5702	19603	A	5746	381	212	PRGGGGGRYSPPPGGGGRGNSFYPGGGG LNKPHFGPCPPPGGPKMKPPPQKKKSL
5703	19604	A	5747	334	432	MFCENYKEIAWPGAVAHSCNPNTLGGRG RHITC
5704	19605	A	5748	190	1	IPPKKGLNFFSPPTPKGVKSKPPQGGK VFFFLRRSFTLVTHQGVQWRDLGSPQPP APGSKHE
5705	19606	A	5749	425	297	ESAFHHVAQAGLELLGSCDLPVSASQSV GVTGMSHHTRLYCS
5706	19607	A	5750	425	0	KKKQKKKKKKKKKKKKKKKKKKRT KSDE
5707	19608	A	5751	136	3	AQSSRPAWLIFLFLVETGFHNVGQAGLE LLASGDLPTSQVPRRP
5708	19609	A	5752	3	237	GCSEPRSRHCTPAWVTEGDSVSKTNKQK TQRLKSLALFPPIHSLLPVVIKLAMPI LAMDI.FPHPIVEFSYHWEQM
5709	19610	A	5753	1	358	GDRGCSELKSCHCIPAWVTEQDLPSKKK KKKKGGKTRNGPQTCGDLPPPLGGG KNFPKGETFWFHSGKKRFFSLGKGEKC FFIPRAPKGPGLTGGPNRGGGAKKKLK RPPGPVY
5710	19611	A	5754	2	191	QGCSELCSYHCTPAWETRARPVSKKKKP KTKNQTKKNRLGKKPPNLIFFPFQKKKK WVQIPGK
5711	19612	A	5755	42	408	KHAAPPASLSLSLLHHGQKRACFPFAF CRDCQFLEGGPAMLPVQPAKLTPrSTPP HPCSLENDSAHFFN
5712	19613	A	5756	179	410	LQAFLRPSPPVLFLLYADLSNQNLWPGM

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						VARACNPTTLGGRGGRT
5713	19614	A	5757	166	2	GRPGPADFRVRPQLLQRFIFYLFTEME SCSVTQAGVQWCNLSGLQLPPLGLPD
5714	19615	A	5758	334	3	EEKVFGLPSPILLSKGQGAASGPFCPI SPRAMGPQKKGWETMVFTKAPPSFGFV LVKQSPGTGPVPRNFFFLRRSLALS AGVQWRDLGSMQAPPPGFTPFSCNLN
5715	19616	A	5759	373	470	SSCWSLRNSSDPGAHACNPNTLGGRGGR RITR
5716	19617	A	5760	210	384	EALDTTITTTTTFETKFCFVPOAGGQGO NLGSLGAPPTGLTPFSCSLTLRKTWDCGP PP
5717	19618	A	5761	257	400	SLGSEYTWVCFCVFETESRSVGVQVQW CNLSLQPPPPGFKRFSCLR
5718	19619	A	5762	400	2	ARAVGSVGEDPGLGTGPSARETWEWAV VCRACRGSQLLWGKLFILRHWDLRKVLA RNGTTECLKQLWSQCGAGMGRGPFQGL KGKPVGCLCSSREVFYLLFLYLFDRVSL CHPGWNAVKQTRLTAASASQ
5719	19620	A	5763	34	440	RVRAPLGWEEGNYFVLRAPRSRSGKRSCL PFLRCGHQEPPLWGIISTASPLRHLVGAS QICGVFLFCFQVSLKPAGSWKVIVIGNNG ERKAORLCPLRATRVEGIFCFRFVFLRW SFTLVAQAGVQWRDLGSLQPPPL
5720	19621	A	5764	297	468	LVGAGVPTGCGQRNGVNVSHKSVQAQWL MPVIPALWEABAGGSRSEIETILANMV T
5721	19622	A	5765	1	205	GFKLTDSFASGAKAILRSQLLGRRLQEN RWNLGGGGCMGLKWHNCPPAWAIEGNLL FKKKKKKGGTF
5722	19623	A	5766	307	1	KERDPPPTPFPGKTFFFFKRNFCEFPF KEGQGGILGPRHPFFSRLSFLGRGVPRG FPFPGPRNFFFWILVKMGVPHVQADFK LLTSGDLNKTASQNAIGK
5723	19624	A	5767	2	319	LLNGEELSRTFFQRSSQAWVFESSAGI FGGKAGATGLEKLTGSFQLTGHPDPR PEELGDPEKSSASEKTRGLQEANGVPEI LKAITYTQAWPKEAKVDPIITP
5724	19625	A	5768	787	1118	EAAWRELEAERAQLQSQLOREQEELLAR RKAKEQLSEBIAALQEHDEGLLAES EKQQVREPWRGLCCSLSCSSSAGPCSA TWQLGALGQATALLGASVSLPAGGED
5725	19626	A	5769	2	452	NGAGTMSVSLEADENPFAQGALKSEDCF ILDHGKDGKIFVWKGQANTEERKAALK TASDFITKMDYPKQTQVSVLPEGGETPL FKQFFKNWRDPDQTDGLGLTYLSSHIAN VERVPFDGGNLDFTAMAAQHGMDDGT GQKQIWRIG
5726	19627	A	5770	2	130	GTQGGKIVDLVKELDRDVFALVNYIFFK GKWERPFVKDWKS
5727	19628	A	5771	422	8	HIARWGAPQGGWALLKAECLNPAPP PIGARTAPLWPGCCFSLRPVFLFFFF SLFIQSFRILYPQPWPLQGRSTTLSRM GTTDTHVIVLASTNRADILDGALMRPGR LDHVFIDNPTLQERRKCMRRLGASRN
5728	19629	A	5772	432	3	YSLNLKKRWFVLTHNSVHYKSSSEKSA KLGTVVINSLCSVVPDEKIFKETEYWN VAVYGRKHCRYRLYTKLLSEASRWSSAIQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						NVTDTKAPIDTPTQQLIQDLKENCMTSH VVEQIYKRKKILRYTHHPCTAAVEDHD ND
5729	19630	A	5773	20	432	SRAAALLEAVTETLFFYYEVAEKIWSNRA NRQCADCSSRPDWAAVNLGVVICKQCA GQHRALGSGISKVQSLKLDTSVWSNEIV QLFIVLGNDRANRFWAGTLPPEGGLHPD ATPGPRGEFISRKYRLGLFRKPHQP
5730	19631	A	5774	433	2	RGAFQTLQKKDLQAFVLSSVQLQVLTG S CFKLRTVHNIIPVPSNKVDDPCPLVGF L HVIVHFAKGFQKQSATLSALEVDSFGYF VSKAKTRVFRDTAEPKWDEFEIELEGS PSLRILWYEEYNNKSKVNNLYSAAVGF S AWQ
5731	19632	A	5775	133	436	MLISLPHPSTHLSLDFCADFGTRQT T AASHVLTLSAHSVSCSPPLMGEATTSR AQDLPADEHTAFAHELEAPALSKGQGLS ILRALTGHLPLGQEVNL
5732	19633	A	5776	397	58	KGTISTIGKLEEKLRGAARQALADAI E F QLLPASLCTEDTPTGMQVKRSLGSRECH RSKQDSVAGERAKVGFGRGTSSENYIRT TYSQLSVSLSGHHPGATLAAVNGCSCSP T
5733	19634	A	5777	1	324	MRRCVSAGGVELEEYYPFLDMVRSMLE G SIDPTQYEDTLREMFTHAYVGFMTDK LVQNIARQVSRAGVGPALRTAEMALPSF H SPLGRGPVVSTANLSCFFLIETK
5734	19635	A	5778	1	398	RLGSRPSLHDQSPLELRSEIQELKGDV K KTVKLFQTEPLCAIQDABGAHEVKAAC REEIQSNAVRSARWLFETRSLDVINQDP SQVRLIRGISLEEGARPDVSAATRWIFDT QSLDAIREILVDEKDFPPSP
5735	19636	A	5779	281	12	VACNLGWRVRTPTPASYPCCVPQLSVRG K NRKELLGGFLRNIVKSADEALITGMSG LKEVDDFFEHRTNLLYHTLYCGRSED HATSR
5736	19637	A	5780	406	23	DSQATGPGISRGRRISSPSSLCTRFSTS I VKCSPLEHVLKYLDPPPPPTRCSRFPAS LRSSPKHCVQQQFPFIACRPGAAAPPPPP AQCNPNGPAAASARHEPKWGSRTGCGPA RARRREGTGRKKRR
5737	19638	A	5781	415	18	TSQAGDDLHGSLLRRGPEMGYLPGYDP D PTLATPPAGQTLAVPSLPRATEPGTGP LTTAVTPNGVVRGAGPSAPELLTTPPGTT APPPPPSPASPGPPLGPEGGEEPPPTII TTTTVNTTITSPMYCGRSEG
5738	19639	A	5782	168	432	GMRRQTGLDQQSRGVGNWRVDDFFPSS L SFFFFFGKESYFVLKFGIHGLKFGYL EPLSPGLKEFSRLSPPKGGHLKCRPPSP LFFF
5739	19640	A	5783	1	423	TDDDLNWLDSRTFREQQVDENETLLLR R KFFFYSDQNVDSRDPVQLNLLYVQARDD ILNGSHPVSEKACEFGGFAQIQFGPH VEHKHKPGFLDLKEFLPKEYIKQGAEK RIFQEHKNCEKISERSAKV
5740	19641	A	5784	273	400	DSVLLMLSPGVCPHVQVWPISCTLGAT F GYVAGLVISPLWI
5741	19642	A	5785	445	28	DTNRAPNHMEIKSGSGTEAKVNGADSID

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KEAAGDETMERTMEAEATGAKPTGVEA TGAKVTETKPTGAEVREMBSTEEANME SKPTGAQATDTETTGVAMGVEATKTKA EEAEMQAYGVGAGQAEPPVTGTVLRPL
5742	19643	A	5786	380	2	QRQESPEASSLHILERQVQLQQLLVE SQEEKESLGREVESLQSRLLLENERGN TSYDVTTLQDEEGELPDLPGAELLSRQ LSPSAQEHLASLQEQVAVLTRQNQELME KVQIMENFEKDECI
5743	19644	A	5787	663	2	FGVERRATRTIRLTTRTVLDLYSFLAGVS ENLRHATQDDASRTRAPGLSSQHPKPD TVSGDTETGQSPGVFNTKESGMKDIKSE LAEVKDTLKNKSDKLEELDGKVKGYEGQ LRQLQEAAGQPTVTMTNELYQAYVDSK IDALREELMEGMDRKLADLKNSCEYKLT GLQQQCDDYGSSYLGVIELIGEKETSLR KEINNLRARLQEPSAQANCCDSVY
5744	19645	A	5788	398	1	TRCYHSALRYGGSFAELGPRIGRLQQAQ LWNFHTGSCQHRAKVLPPLEQVWNLHL EYKRNYGAKRGPPVKRAAEPVVPV PAALSGPSGEEGLSPGGKRRRGCSNQ GLPPGLPLPPPLPPPPPPV
5745	19646	A	5789	116	371	RHPKIWGLRGPPGLTLEKRGKEEPLDP RSWGFKEAETPPRPFTRGKKGTPLRKKK PKERKTRERGGKKEGKKKKNNEGKTNP L
5746	19647	A	5790	406	284	RRGFFHVDQAGLELPTSGDPPTLASQSK PGPLCPALLHTF
5747	19648	A	5791	200	3	GDALIYMEPEKQVMSRSSDECVALCDQ WLVSYSKKIPLVNLLTFDLKKNISICPL PGTWIMEMY
5748	19649	A	5792	372	278	LQIQSPAGQSRCGGFLVREDFVLTAAHC WGR
5749	19650	A	5793	1	167	VAPPKLDPHSGRVRAQAGLELLTLCDDP ASSSQTAATGASHHTRQVLGSYKALS
5750	19651	A	5795	112	3	SSWGKVGAGAGEYGABALERMFLSFPTT KTYFPHCI
5751	19652	A	5797	356	238	FLFCNNGVVSLEHFRCLAENAGDDAFVK DVTVLQNTDGR
5752	19653	A	5798	379	60	VKIRHCHTMVMSLLKNIRLILEEEQVE GNYSFCVLDNQNLQQLWDWDHRSLTIKA GKMYFAFNPRLCVSEIYRMEVVTGKGR QSKGDINTRSNGERASCE
5753	19654	A	5799	377	3	KVAFPGEGRQGESWSAFQGHTRVVSCLK WAVYEPDLMTSSVGTIYIWDIKDTRK LTVALFVVAGASQVKNKKNANCLATSH DGDVRIWDRKRPSTAVEYLAHLSKIHG LDWHPDSEHNLY
5754	19655	A	5800	143	316	CPTSPPLPYTEFFGGVSGLTVEQFRKI NGFPNFWGEGEDDLWNRYLCRSFGV F
5755	19656	A	5801	390	2	LLLLLLLLLRLQSLTLVPAQGVWRDLSS LQPPPPGFKRFSCLCV
5756	19657	A	5802	342	465	VIFFFFLKQGLTSLPRLECSGTIITHCG LDLLGSSESPTFT
5757	19658	A	5803	1	378	VYSSEFENIKEEYRGRGFTTICVFEKGR FLIQYDNYGSTARDIVEWLKNPQPQPQ VPETPWADEGGSVYHLTDEDFDQFVKEH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SSVLVMFHAPWCGHCKMNPDEFKASEA LHGEADSSGVLAAY
5758	19659	A	5804	152	1	KPEIFFFESRSVTQTGVQWCNFGSLQPP PSGFKLFSCLSLPSSWDYTAHV
5759	19660	A	5805	207	31	LYLQLLQQTASSGNLNTLSSLHPMGGKC FTAAEEQQHPGQQTQLTTLVGVWHRFCE NIF
5760	19661	A	5806	199	2	GSECSCLLSRGGMHVSLSSFKVTFSCD AIIHFSFLFFWRQEFPSVQAGVQRDLG SLQPPPPGV
5761	19662	A	5807	385	239	QDQPGQLQKMCVCVCVCVCVCVCVVIC KSCIRLSYMKMPINFGKLN
5762	19663	A	5808	39	184	GRIIIKFFGEMRSHHAAQTGLELLGSSD PPTWASQSAAITGVSLRIRP
5763	19664	A	5809	376	2	WAEPTSFHVCITSYTOFFRGLTAFTRVR WKCLVIDEMQVRVKGMTERRHWEAVFTLQS QQRLLIDSPLHNTFLELWTMVHFLVPG ISRPLYSSPLRAPSEESQDYHYKVVIRL HRVTQPFILRSV
5764	19665	A	5810	271	120	FLCFIGKTSESGSFLYSRDTGLPGCQV SLMIKKSNEMVFKHINKGSINR
5765	19666	A	5811	367	3	DKSFKWHKMLEDANAPTEERDERIAGL YEEIERDLMLLGASAVEDKLQEGVIETV TSLSLANIKIWLVTGDKQETAINIGYAC NMLTDDMNDVFVIAGNNAVEVRELRKA KQNLFGRCI
5766	19667	A	5812	294	37	FRGENPDDGVRGSPPEYRLRQVASSLF RGEHHSRGGTGRLASLFSSLEPQIQPVY VPVPKVSHWAFFPNSSLEPLTYKAIFLP TA
5767	19668	A	5813	184	3	ITISYLNKYLFSPLQRQNFVLLPRLECS GTITAHCNLKLVGSGDPPAPASQVARTT GMRH
5768	19669	A	5814	468	1	DDMEYEGSVSVFTQVPRKSVNKGDLDTL MVAGEFGLGKSTLVNSLFVSDLYRDRKL LGAEERIMQTVEISKHADVIEEKGVRLR LTIVDTPGFGDAVISTECGKRRAMY
5769	19670	A	5815	24	314	QAPFGPKCFNVNLCFSLSLSKGEPEFHY IAGAHGNEVLGRELLLLLVQFVCQEYLA RNARIVHLVEETRIHVLPSLNPDGYEKA YEGVMALAHLTQ
5770	19671	A	5816	474	3	TTLRKGYSRHKGLLHSIRQEVQATPLEG IIVSGQMSTMNLSSTLWPSPKRVRLCI GRTLRLSLRIRPCKRTPLQTRMPQKMRA LYGDPGDSPLRSRAIPASSPGSTGSFR ARPPHPLHPPHPLTREGEPLLPVLQPR RGPPLPLHSQASRPV
5771	19672	A	5817	511	389	GMCTEGREVVPTRFNEIEIERDHCGRV SASIIITHCSNR
5772	19673	A	5818	510	2	PLSCEVENPLFPVPGVRMIQHIEACAQ VRGMQEIVLIGFYQPDPLTQFIEAAQQ EFILPVRYLQEFAPLGTGGGLYHFRDQI LAGSPEAFFVLNADVCSGFPLSAMLEAH RRQRHFFLLLGTTANRTQSLNYGCIVEN PQTHEVLHYVEKPSCTAAAIEDQASSRQ R
5773	19674	A	5819	282	152	FSLFLFLQSERHFIMQVVCEATQCPDT RVSVRLYEKSVLHLS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5774	19675	A	5820	347	1	EPHPVTPPAVGTSRYNPLIMMDNRSAV TPPSHPPQQPSSMQTGMNPSAMQGPSP PPPPSYMHIPRYSTNPITVTVSQNLPSG QTVPRALQILPQIPSNLYGSPGSIYIRQ TKV
5775	19676	A	5821	482	13	IYEKLITGCYNILANHADPNISGLDESIL EECLQYLEKQLESSQARKAMEEFFSDSG ELVQIMMATANENLSAKFCNRVLKFFTK LFQLTEKSPNPSSLHLGLCSLAQLACVEP VRLQAWLTRMTTS
5776	19677	A	5822	608	7	FRFAEKVVEGMFIIVNSITIKIHSKAPH ASFELWLQGYSVNPNWQQSDRLRLTRIT DPCRGEVLTFKEITWQTLRIEADATDNG DQDPVTTPLRLITNQGRILQIALKRRTKD CNVISSKLMFLDLLWVLTDSQLKAMM KYAESLSEAMEKSAHQKSLAPEPVQIT PPAPSAQQSWAQAFGGSQGNSNSSSSPV LRPL
5777	19678	A	5823	328	3	AEVASEDCSLPCFLAVWNRIIEPVAAMR KEADMLRLFPEYLYKGEELFGLTVHAVLR IAESLPGVESCONYLFRYGRHPLMELPL MINPSGCARSEHKILTHYKRPSLY
5778	19679	A	5824	69	308	TSVPSCVRCRYIILRTSSALTNILGTHS NSSFFHASSSALHSCCFPFWSLQTLDI NVKAPALMTKAVVPEMEKRGYRE
5779	19680	A	5825	424	2	LQRAFSESIRKLRGYQADRKQIYHRR SFANHSVRPSADEKCSNFFEQRHGGSH QSSKWTVPVGPAPSTSQSQRSSGLQSGH SSQRTSAGSSSGTNSGQRHDRESYNNS GSSSRKKQHGSEHSKSRSSSPGKPQTV
5780	19681	A	5826	107	2	SSLTAGVRMGVPAQSTQGTNGSSPQMS GTAALTS
5781	19682	A	5827	2	437	FPTEDSRTSKESMSEADRAQKMDGESEE EQESVDTGEEEEGGDESLSSESIKKK FLKRKGMTDSPWIKPARKRRRRSRKKPS GALGSESDKSSAGSAEHIGPCDSTGDM VSSGLPGSRRPENPVFLCIWVAVRAICP GFLWS
5782	19683	A	5828	487	22	MPEPVFPLSHFRQFIAAIKLQFQARLSR CVRDLVRSALAPNHDTRLMLFQHLCRVI EHGEQNRMSVQSVAVFGPTLLRPEVEE TSMPTMVFQNRVVELILQQCADIFFPH
5783	19684	A	5829	2	871	RGICSRWRREGSQSRGFLVITSPSGS LVTASSAQTFPIAPMIVSALPPGSQA LQVVPDLSSKKVASTLTEEGGGGGGGGS VAPKPPRGRKKRMLSEGLPEMNDPYVL SPEDDDDHQKDGKTYRCRMCSTFYYSK EMQIHSKSHETETKPHKCPHCSKTFANSS YLAQHRIHSGAKPYSCNFCESFRQLS HLQQHTRIHSKMHETETKPHKCPHCSKT FANTS YLAQHLRIHSGAKPYNC SYCQKA FRQLSHLQQHTRIHTGDRPYKCAHPGCE KAFTQLSNLQ
5784	19685	A	5830	463	1	LPESRLPSPHKREEGSRARVIMTSYPIE PHERKGLADVVATLKQKKLEEMTRTE QEDSSCMEKLLSKDWKEKMERLNTSELL GEIKGTPESLAEKERQLSTMITQLISLR EQLLAAHDEQKKLAASQIEKQRQMDLA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						RQQQBQIARHQQLY
5785	19686	A	5831	462	2	MTLEFSSSLYFLCGWYLSNLLIGTYGVK PWYFFFTASYWKSQVGLFEKRQYFLSS LFFENENFDNKGSSLQNREGLEGSAPG VTLVSVTKEYEGHKAVVQDLSLTFYRDQ ITALLGTNGAGKTTIISMLTGLHPPTSG TIIINGKNLQTVY
5786	19687	A	5832	396	2	VSTPASKRKGIVPRCDIFITYDRGGALP KDIHVAGILFASAWMNVWPLLSAIEFHS AWAMGMGVNFFVASTHHVSLNMSGSGRY APNGRKVYHYDMKTEMGELLLEVDSDHP LSSLAYPTADNWNAYATLY
5787	19688	A	5833	384	137	EEICLNPGAGGCSEPRLWHCTPAWATKR DSSKKKEKNCLSKNKKEKEKEMFACVCV CVLFESIYAFPSKAQELSNPKHYGNF
5788	19689	A	5834	171	2	FVEGINISGNFYRNKLKYLAFLRKRMT NPSRGPYHFRAPSRIFWRTVRGMLPHMY
5789	19690	A	5835	278	404	SVLIKFEKKTLYKAIWPGAVAHACNPS TLGGRSRGITRSGE
5790	19691	A	5836	417	3	SKKKEGRCEWQYDLPSGTHAVFQFFLKQ QGRVPGLTQAVQVAKMSLIDLAGSERAS STHAKGERLREGANINRSLLALINVLNA LADAKGRKTHVPYRDSKLRLLKDSLGG NCRTVMIAAISPSSMTNEDTYSTHV
5791	19692	A	5837	409	230	AGRAYCYNGMCLTYQEQCQLWGP GKAL LGSTALPSPPLPSQPPLALRVVWNLGPK WHL
5792	19693	A	5838	3	409	LRVPCDKYLTQNHYYITSLSEEEAFAFP LAYVMVIHKDFDTFERLFRAIYMPQNVY CVHVDEKAPAEYKESVRQLLSCFQNAFI ASKTESVVYAGISRLQADLNCLKDLVAS EVPWKYVINTCGQDFPLTTRPV
5793	19694	A	5839	385	174	GLAVEIGSRRIADGLELLASSDPPTSA SQSAGSTGVSHHAWPDTVSSVYWCFLCC TKQVVVGALSIVSL
5794	19695	A	5840	260	2	PLPRYTAACSRLLVQYKAAFRQVQGSEI SSIDEFCRKFRLLDCPLAMERIKEDRPT IKDDKGNLNRCIADVVSFYITVMDKLRQ CI
5795	19696	A	5842	299	3	FSGIKYICIFIPLFVCFLLYLLGIGSPYV AQAGLTLLGSSDPPPSASQSPGIIGVSH YVQPIHTVAQLSPSSIFRTFSSFQTFV PIKHTSHSPSPSLY
5796	19697	A	5843	391	2	APHAPAFRLRARGEPODPLSHPRVPAVSA NCRMWKHLPVHSSPTPLRLPLWKLRARW LLPQLVYLQGWGYSLLRPAALISMVLL AREFLYPAKMSVSEVCSSGLSSPLEQH KTNLIIFYASGDICANV
5797	19698	A	5844	479	59	FVGMEPGVGHASLAMHGLHIRSLGKIKL RRRKCTLFNTQEKSAARRRGLLGENIY LLLFAIALRILNCLLVQTSFVPDEYQWS LEVSHHMFVNYGYLPWENTERLRSYAYP LICASIYKVLHLLGKDSVQMLVSGNKSS
5798	19699	A	5845	406	548	SVQTKPFFETESHPTVQAGVQWHNLCSL QPLPCRSKQFLCLRLPSSW
5799	19700	A	5846	2	394	TLCHRAKDPTVHHESGRIMYLNGLCFLM GPAQLTQRLSVSRQGE
5800	19701	A	5847	472	201	LSILSDTSLCLGRFFTYENGCAFYHEE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						REGLARICRLSIHSRYEDFVVDGFFNVLY NKKPVIYRSAPARPGLGQSLCNQVMWYQ VAILNK
5801	19702	A	5848	127	3	SSNVKAAWGKVGAGAGEYGAELERMFL SFPTTKTYFPRCI
5802	19703	A	5849	238	1	MAETHPNPTGLPLAPALPCLAGSATHPC LFSPEISLDVADRDGVVEKNNPKKVP FQGRHHPEPRASEDTAPDPAGMY
5803	19704	A	5850	423	2	LSPLGNWSSANQKVFDVSVKPSRKDLFA VDTQVGTVPVSLTAGEQGFDDGGKGRAGE QATQAAGDWSSNMWGS D G I L S H S A P L T V PQPLLTGPQGPCLCRPLNPQOTSFPALL PFSTQLCSMCPGPASARPPPLLLKPTMY
5804	19705	A	5851	326	682	PSYSLLSLLQVKNVEKLPQRQKESMK QKMEHTQKKQLLVSPWQLGSAGAGAR PGMVTRPPLCLCPAPQIPRSEYLNLA SSFMAPLSPPPCSLHRLSCLHLEVRNSI SGYPNCI
5805	19706	A	5852	263	30	HEKTDDERGPQGSARS GAITKPPGPPLP IEPHETTPPEHPAPSGTIPPEPLPVELHE TTPQHPVPSGTIPEPPYLLSQ
5806	19707	A	5853	389	2	GLPTQREKFGASMRTRMTIQSIADVTSF VCLVGEENNVQGFRAESRCWRYDPRHNR WFQIQSLQEHADLSVCVVGRIYAVAG RGYHNDLNAVERYDPATNSWAYVAPLKR RCMPTKAKRWGRGRCISP
5807	19708	A	5854	379	2	GRSLRYSGSCSGEENSTNSAGQSRVAVI AAAAARRRGNSHNEYYYEAEHERRVRKR RARLVVAVEEAFTHIKRLQEEQKNPRE VMDPREAAQALFASRAMQKYLRAAQ QNYNTMESILQHC
5808	19709	A	5855	374	2	SDAGAPVNIYEFRRHPQCLEDTKPAFVK ADHADEVRFVFGGAFLKGDIVMFE GATE EEKLLSRKMMKYWATFARAGNPNGNDLS LWPAYNLTEQYLQDLNMSLGRLKEPR VEIWNSTIPPCI
5809	19710	A	5856	516	18	PYECKEKGKAFNCGSSLVQHERIHTGEK PYECKEKGKAFSRGCHRTQHQKIHRGET PIKCKEKGKAFSWGSSLVKHERVHTNEK SYECKDCGKAFSGYQLSVHQRFHTGEK LYQRKEFGKTFTHGSKLVHERTHSNDKP YKNKECGEAFWTTYSNEKCIASAK
5810	19711	A	5857	392	3	CERGMGGSRALGRHWT SFLKRLNCSV PGDSTFYFDVLQALTGPVNLHGRSALFG VFTTQTNSIPGSAVCAFYLDEIERGFEG KFKEQRLDGAWTPVSEDRVPSRPGSC AGVGGAAKFTSSRDLLY
5811	19712	A	5858	391	3	ARRTTGMVPAKAGGKGRRGAVFRSYIRE TEELRSKLVESEAMNESLRRSLRASDR SPYSLGASPAAPAFGGSPASMEDASEV IRRAKQDLERLKKKEVRQRRKSPEKEAF KKRAKLQEQENSEETNGE
5812	19713	A	5859	409	3	SLPGEGDPWWAGQEELLFVQEGKLSLPV AERVLLRIACRYDPRSNWAEIAPMKNC REHFVLGAMEEYLYAVGGRNELRQVLPT VERYCPKKNKWTFFVQSFDRLSCHAGYV ADGLLWISGGVTNTAQYQNRQCI
5813	19714	A	5860	405	135	NLSRLSLCRQPMTLVTWVLLFYDSEEKA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FWLLVALWKRMLPDYYNTRVVGECPRVL PRLGLQVPAGSMRVAALPRPSSRLHVGS LGVRG
5814	19715	A	5861	389	2	YYSELEEQLTDEFNAELNRVPLKRLDLI FVTFQDSRMAKRVRKDYKYVQCGVQFQQ SSVTTIVKSYYWRVTMAPHPKDIWKHL SVRRFFWWARFIAINTFLFLLFFLITTP AIIMNTIDMYNVTRPCI
5815	19716	A	5862	525	0	SHLPESERIHHTVGQKEQVLMDSKTRP NNDVPEPPMPIADQVSNDDRPEGSVEDE EKKESSLPKSFKRKISVVSTKGVPAGNS DTEGGQPGRRRWGASTATTQKKPSIS TTESLKSLLPDIKPLAQGEAVVDLHADD SRISEDETESKDDGTHDKGLTIC
5816	19717	A	5863	399	2	ATRRNRNRVPSGMRTRNVREMTAAVGGP PSPYPLPPPEGTSSIEYSNQGNTCQGH GNFDFPHGNPGGTSMNDFMHGPPQLSHP PMPNNMAALEKPI SHPMQETMPHAGSS DQPHPSMQQDKARNTPOPMY
5817	19718	A	5864	3	714	RRPFIALCLSNVAFMLPWQFAQFILFTQ IASLFPMYVVGYIEPSKFQKIIYMMNIS VTLSFILMFGNSMYLSSYSSSLMTWA IILKRNEIQKLGVSCLNCWLIQGSWWC GTIILKFLTSKILGVSDHICLSDLIAAG ILRYTDFDTLKYTCSPFDFMEKATLLI YTKTLLLPVVMVITCFIFKKTVDISRV LATNVYLRKQLLEHSELAFTLQLLAFT ALAILILRLKLVL
5818	19719	A	5865	423	1	APPVSTAVAQSNSSSEEEAREVGSQAQEF KYQKSLPPRFQRRQQQQQEQLYKMQHW QPVPYPPPSHPQRTFYPHHPQLGFDPRW MMMPSYMDPRITPRTVPVDFYPSALHPS GLMKPMMPQESLNGTGRSEDQNCVPPC I
5819	19720	A	5866	497	2	AVGAGQKGGGGGRELMPFQKIWGGGA FTNNAHVGLKIMPRILRTGMLEEIHLE PGVVQGLFPVDELSDIHTFLSLLER RRQALCPGSTRNFVIRLGLDLLISQFSG HSAEQMCKTYSEFCSRHSAKLYKELY ARDKRFQQFIRKVYCGRCRGSQQGR
5820	19721	A	5867	382	74	LALSPRLKCSGQIIAHCSFDLLGSSDEP PSASRVAGTTGARRHARLPYSLRHYHFV LRLFNPSKHSKLKHFHPIILIRNPGKVGS YSFQMSDLLQSRRAQQS
5821	19722	A	5869	378	3	SFSRSANLISHQRIHTGKPFQCAECGK SFSRSPNLIAHQRSHTGKPYSCPECCK SFGNRSSLNTHQGIRSGEKPYECKECGE SFSYNSNLIRHQRIILTGEKPYKCTDCGQ RFSQSSALITPV
5822	19723	A	5870	375	3	IHVIVFNQATGHVMAKRVFDITYSPHEDE AMVFLNMVAPGRVLICTVKDEGSFHLK DTAKALLRSLGSQAGPALGWRDWAFFVG RKGEAECHWADTELNRRRRFRCSKVEGY GSVCCKDPTV
5823	19724	A	5871	373	1	QPEEVSGALSPPSASAYVKLVLLGLIMC VSLAGNAILSLMVLKERALHKAPYFLL DLCLADGIRSAVCFPFVLA SVRHGSSWT FSALSCKIVAFMAVLCFHAAMFLFCIS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						VTRNMAIAHLLY
5824	19725	A	5872	382	2	KSFSQKSQLI IHLRTHGTGERPFECPECG KAFREKSTVLIHYRTHTGKPYECNECG KAFTQKSNLIVHQKTHTGKTYECAKCG ESFIQKLDLI IHHSTHTGKKPHECNECK KTFSDKSTLI I PHV
5825	19726	A	5873	370	3	MGRVRAQNISGVMSGPGKMLMQSQFPTQ GQQGFCEGKEPYQAMSONMGNTQDMFSP DQSSMTMSNVGATRLSHMPLPPASNPBG TVHSAPNRGLGRRRSDLTISINQMGSPG IGHLNSTTCI
5826	19727	A	5874	362	2	GGKFLVLGNLPSKLEESMVQYYRLVTAA SLVRGQISEYNISLRASDGGSPPLSTET HITLHVIGINDNPPTFPHLSYSACIPEN NPRGASIFSVTAQDPDSNNNARITYALT EDTLQGVY
5827	19728	A	5875	369	1	RIRPRPTARLASARTLHEVSLQESIRYA PGDAVEKWLNDLLCLDCLNIARIIVSVCP LPEACDLSYVNRDTLFWCHKASEVFLQR LMALYVASRFKNSPNDLQMLSDAPAHRL LNKCLLCPPPV
5828	19729	A	5876	119	39	VIQDYTTTPNEELSRDLVNKLKPYMR
5829	19730	A	5877	461	2	RRGWTSSRRPKEDPSGAAPPEMPKSSK IASFIPKGGKLSAKKEFMAPSHSGIPK PGMKSMGKSPSAPAPSKEGERSRSGKL SSGLPQQKPQLDGRHSSSSSLASSEK GPGGTTLNHSISSQTVSGSVGTTQTGTS NANSVQLPQPLCI
5830	19731	A	5878	503	3	PSPQVPGECPSPKKLGARAAFTTDPAP LSPQSRVASSGSEQTEQGSSRNSFQED GSGMKDVPSWLKSLRLHKYALFSQMSY EEMMTLTEQHLESQNVTKGARHKIALSI QKLRERQSVLKSLEKDVLEGGNLRNALQ ELQIIITPIKAYSVLQATVAAATLY
5831	19732	A	5879	421	34	LVHKVLSASNVLDVDAEGTVKITDYSISK RLADICKEDVFEQTRVRFVSVMAMHYRTG NKGDVVRLGLLMLSLSQGQBCAEYPVAI PSGLPGGFQDFLKKCVCLDDKKSMESPA VVETKQNKSPANVLRPL
5832	19733	A	5880	379	3	AQGLLLAWPNLNRQHCPSCSHNLSTFI QNWKSPGLSLKTRAPGQGSVLSSSDLPR AVLTGTFVMSVMVGSVTESLAPQALNG SMINETARDAARVQVASTLSVLVGLFQV WNSQEYVPPTTCI
5833	19734	A	5881	429	1	SLVSYMDTESTAEKLGKELGLQAKELSA VHSSHHEIGVNDNSNLFSLMREPLESSN TKSFHSAVEIKNRSQHLPFCFQHHGIDT PTSLQKRSACCPSSLRLLEETASSSQDG DPQIWDLDLPFSES LNKFLT VLESEIAVT QCI
5834	19735	A	5882	436	3	WSLVSYMDKKSTAEKLGKELGLQAKELS AVHSSHHEIGVNDNSNLFSLMREPLESS NAKSFHSAVEIKNRSQHLPFCFQHHGID TPTSLQKRSACCPSSLRLLEETASSSQD GDPQMWDLDLPFSESLIKFKFTVLESEIAV TQCI
5835	19736	A	5883	195	353	DSYSYVRSTAPAVAYDSKQYYQQPTATA AAVAAAAQPPSVAETYYQTGGFS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5836	19737	A	5884	432	1	LSAKVPVASVSDQAAAMHLSQCPKNLAT SLAELRTASQKAHKLCPMEIDSALNTV QTLKNELODAKMAAVESQLKPLPGETLE KCAQDLGSTSKAVGSSMAQLLTCAAQGN EHYTGVAARETAQALKTLAQARGVAAS TTDP
5837	19738	A	5885	313	1	GKSPHLLILQTSPLSKAPQLILLLLLYW SWVGVSVTAAARETEAGIQVSSEEPGP RNVSPHSRLQDETNRLEAENNLAAAYRQ VREVQGRDRREGRKGLMATLY
5838	19739	A	5886	432	3	GSGFCSPILCLWWVEEAVGIIRLHLWL ELGCWHSFSLPGTYSLEFLSTCTQVL PYSWSGLLFASGNYSLSLYLPSRAETDSRG SQPLPVARHGVGACKCKPRQTRPGLSPQ VCVEKLMPLSSFCSAFQONTYNQPMSP PV
5839	19740	A	5887	417	2	ASLMVAPDYAEISPLAMPAPSSGVVCTP IMSTSSEAMSTPLMLAPDSGELSPILM QDMNPGVMSTQVPVAPSPFAMSPQLITD EDTEAMSKVLMTALASGEISSLLMSGTD SEAISSLIMSASVAGGTSPOPTSTLY
5840	19741	A	5888	420	3	KFDLIKLDLKTMSYDLDIEASDGGGL SGKCSVSVKVLDVNDNFPELSISSLTSP IPENSPETEVALFRIRDRDSGENGKMIC SIQDDVLFKLKPSVENFYRLVTEGALDR ETRAEYNITITITDMGTPLRKTEQSV
5841	19742	A	5889	321	414	FNMRIWPGAGAHACNPSTLGGRRGRITR SAD
5842	19743	A	5890	415	1	PGLPGTSVKGIPASKQSPHESPTLHLK TSPIIQQLGLYLSHTAIRYHPQETLKEF VQLVCPDAGQQAGQVGLNPNNGSSQDKV HNPFLPTPMLPPPPPPPPMARVPVLPVPD TKPPTTSTEGADYPTSTYSTPSLY
5843	19744	A	5891	193	3	KPSSKVWSRRDPFLLSVVEQPIKDAVIT VPVFFNQAERRAVLQAARMAGLKEMQLI NDNTACI
5844	19745	A	5892	412	2	KHQSVDNKSDFYVSLYPDFSSLSRAILD VVQFFKWKTVTVVYDDAGLIRLQELIK APSRYNRLRKIRQLPVDTKDAKPLLKEM KRGKEFHVIFDCSHEMAAGILKQALAMG MMTEYYHYIFTTLDLFDLVEPSV
5845	19746	A	5893	413	3	ELLCSNTSCRCFCVCEVLVGTGTA AEAKLQEPWSCYMCLPQRCBGVLRRRKD WNVRLQAFFTSDTGLEVEAPKLYPAIPA ARRRPPIRVLSLFDGIATGYLVLKELGIK VGKYVASEVCEESIAVGTVKHEWR
5846	19747	A	5894	424	3	CSGRREPSVRGVQCKGQGHHSARMAPS EAPGTRSCTPSHGQNTAAEATPAQKTPA KVYVVFSTEMANKAAKAVLKGQVETMVS PHIQNISSSKTERSTAPLNTQISALRND PKPLPQQPPAPASQDQNSQNTLQPCI
5847	19748	A	5895	400	1	ASVQNPALRLVTRREEFAIMQTPAGELYD KSIIQSAQQDSIKKANMKRENKAYSFKE QIELELKEVSTRRLRKVAELGGLKL VAFPTAHMLFTWNILRPMHSSDAPDQC LVHWHTFPSPLLHSFFHPQLY
5848	19749	A	5896	421	3	VSSIQMGAVNLLGGGLDLSLLGGGDI AGSPAVGQSFISSVQATCAPSPTPAVV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SSGLNDLSLELSTWIGMAHGGYVAPKAVW LPAVKAKGLESSSGTFRROGHIYAMDF TNKALQHM TDSAIQFTKNSFGVIPSCI
5849	19750	A	5897	384	1	PRASRFIHEAGIVPLPMRTHTPKKPFTC EVAGVQFSRNVKVKIHM RKHTGERPYSR QSCSVRFVHSYDLKNHMLHTGDRPYEC HLCHKAFKEDHLQRHLKGQICLEVTR RRRKDDAPPHYPPPCI
5850	19751	A	5898	429	2	QDIAAWQSLTQVLTPESWRKANIMTEPO KSQERYKGIYVKEKLYRRARHDESLNWT SCDHHESECKGEDPGRHPNCGKNLGMK STVEQHHVVHVLPPQFTCNCGVAFADD TDFRAHPSTHLGEKSYKCDQYKGKILS QSLY
5851	19752	A	5899	424	1	GTMLQALAAHDAGSRAHVLLSLSQDGI EQHMDFDSDRYTLLELFAETTSSEEHMA FEGIHLPQIPGKLLFSLVKRYLCVTSLL DQLNSSPELGAGDQSSPCATREKSRGQR ELEFSMAVGNLISELVRSMGWARNLSEH V
5852	19753	A	5900	135	459	YFMLKAEHVISYVCSENSLMVVVNMRF C LIGLIHIQEFYFFEMEPHRAIQAGVQWC DLCSLQPPPPGLKRCSCIPSSSRDYRC APPYP
5853	19754	A	5901	418	10	GRSPKPGDRLWESVHLSFFPGPADSLSGG SAPASSYEPSQRSSFSSNRSQRGSTSTR NSSQKGSSVLSIKQKGKRELYMEKLQEH LIKAKAFTIKKKFSQNLVAQLWYFVKCV YFGLSAYQIPRGYPTRVLGNFLTK
5854	19755	A	5902	402	2	GYRHPELEIKSVDFGQPEKQPVILSLV RSNRKGEVGFVPEDRRINVDVTRARRLV TVICDYRTVSSHAFKPLVEYFTQHGEV RTAFEYLDIVPDNYSHEDSQSSQAAT RPQPGTSTRTKKQREQGMY
5855	19756	A	5903	346	1	GICPLSHTKMTDARQCITYEMKGEKSPK DTGKEPHGSEAKTGPPQVLAVGPAQPEA PQPGPNTAAPVDSGPKAGLAPETTETP AGASETAQATDLSLSPGGESKANCSPE DPMY
5856	19757	A	5904	139	212	EVENNDISHHHHHHHHHHSNSKS
5857	19758	A	5905	2	345	PCGCWGRCALLLISAAAKAKSKCGPTFL PCASGIIHICIIGRFRSKGFEDCPDGSDEE NCTANPMLCSTARYHCKNGLCIDKSFIC DGQNNCQDNSDEESCESSQGVGYVCGFK KA
5858	19759	A	5906	432	17	PQTTPHRTFGGGAADVLLAVGGQFLLC WSPYFSFHLVALSAQPISTGQVESVVT WIGYFCFTSNPFFYGCLNRQIRGELSKQ FVCFKPAPEEELRLPSREGSIEENFLQ FLQGTGCPYKSWVSRPLPCIAAALRV
5859	19760	A	5907	407	1	PYACGECGKSYRQSSSLVSHRRHSGVR PHHCDECGEFFSRKYDLLIHQRVHSGER PYKCECGKSFHSCSLIAHQRIHTGMR PYECSECGISFIHSCSLITQQRVHLGTR PYMCSECGKSFQSCLRIKHSV
5860	19761	A	5908	419	3	VLAKKTIITKSARDCHEFGNLIHLSTNL VASIQRPDKHESFGNNMVDNLDLFSRSS AENKYDNGCAKLFFHTEYEKTNPGMKPY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GYKECGKGLRRKKGLSLHQRIRKNGEKPFECTACRKTFSKKSHLIVHWRTHTGVY
5861	19762	A	5909	441	57	KVMGIFKSSSLFQALVDIQEFYEVTLINSQKSCEQKIEEANQVLQKWEKTSLLAPCHDRLQKSSSELQSLIGQHSSELTDDGPQWLFPRGSEHGRGKTYDHCISIGLQIAVDQRKMLHVLISKIKKIRV
5862	19763	A	5910	3	317	CLLMLWRRWGSRGSRQRRLQATPSWESTKTADGQDRRESGSRHCSSPHQSKSTTTSSVPAAREGAQEAQGGPRKQTSRPQVSTRQCAMP PARHRKLEND A
5863	19764	A	5911	183	1	QNSDSKDSLNRVASRDHAKPNLTCHVSPAIOGTGSI SESSIPSVSDTSTPRRSRROLPPCI
5864	19765	A	5912	395	1	KTIQFNICVKVFHFRFSNSNKKDKIRYAGDKTFKCKEKGKSFHVL SRLTQH KRIHTGE NPYTCEECKGAFNWSSILTKHKRIHAREKFYKCEECKGKFTRSSHLTKHKRIHTGEKPYICEKCGKAFNQSSTPV
5865	19766	A	5913	449	2	FGSHLEKEDEKKQELVDKAIKPSTIATLESIQRLQYKRAESSRPEDIKDMTKAQIANEKVALQKALLYYESIHGRPVTKNERQVMKPLYDRYRLVKQILSRANTIPIIEEEEGSEADSNVKPDMVNKKTD FSARMVKRPLGGSARPD
5866	19767	A	5914	464	23	SAHMTETRSKSFYDGSLSLTGPSAPAPVAPPARVAPPERRKCFVLRQASLSRPPETELEVAPKGRQSESEPQSSSKPSAKSSLQISSAATSHGGPPGGKGGQDRPPLGPTVPYTEALPVFHHHPVAQTHKHEKPYLPLYCGRCG
5867	19768	A	5915	366	1	LVSFINFFTSVLATLVVFAVLGFKANIMNEKCVVENAEKILGYLNTNVLSRDLIPP HVNFSLHTTKDYMEMYNVIMTVKEDQFSALGLDPCLEDELDKSVQGTGLAFIAFNEAMTHSPACI
5868	19769	A	5916	246	366	TSVKEQQMPGAVAHACNPSTLEGQGGRTTRSGVRDQPCQH
5869	19770	A	5917	400	3	NDNAPEFYQSVMKVTVLENAFNGTLVIKLNATDPDDGTNGDIVYSFRRPVWPAVVYAFTINPNNGEIRTGKGLDFEEKLYEISVEAVDKGNIPMAGHCTLLVEVLVDVNDNAPEVTITSLSLPIREDTQPCI
5870	19771	A	5918	410	200	CTPPQPVKCRFLNRDRVSSCCPGWSQIPGIKRSSYLSLPECWDLRPVILLFCFLSHISSKQPYFLPPSYR
5871	19772	A	5919	214	407	MYFYIDRASLLSPRLCTIVVTIAHCSLELLCSRDLPASASQSAGITGIRHHTWLKTHFYSSFKT
5872	19773	A	5920	476	39	VPYGLFVGSTGRLGLPYLRGTSHPLRGLHAAALNGRRLLVQPLTRNKHEGCAEEFSANDDVALGFCGSHSLAALPAWGTQDEGTLEFTLTQSWQAPLAFQAAGWHDPIHVDIFEGLHWSMVEKGQGTVLLLSVPVTD AOPHM
5873	19774	A	5921	430	2	SLRPSSTGPSPSGGLSEPAAKDLNRM PGLVGQEVGSGEGPRTSSPLFNKAVFLRPSSSTMILFETTKSGPALGKAVSEGAE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						AKLGVSGSRPEVAAKPALPTQKPAGTLP RSAPLSQDTKPPVPQEEAGQDHPPSKAS RC
5874	19775	A	5923	411	2	MSLKVDVEALENSAGATYIRKKGKVTG DSQPKEQQGV LKKKKKKKGMVPKNYD PKVTPDPERWLP MRERSYRGRKKGKKK DQIGKGTQGATAGASSELDASKTVSSPP TSPRPGSAATVSASTSNIPPRLY
5875	19776	A	5924	402	2	LQSGAIMNKFYQPHEAHIPYLLQLFIDY NLYGMNLINLA AVKFRKARRKSNITLHAT GSCKNHLSGNSLADTLFRWEQDEIPSSL ILEGVPEQSTCELEVDVAADILNRLDI EAQIGGNPGLQAIWEDEKQRR
5876	19777	A	5925	215	403	AETSTYFFFLERQFFAPQLGGHGRNL NSLNLLPRGLREFSRLSLPGGWYGGAP PSPTFFC
5877	19778	A	5926	320	1	PGRDRWIWGQGECELYLLASMTQWCER EISSIAPGELCCLLLSFLPQECCQNVVR VLIVAGRKFVFCGTNAFSPMCTSRQVGN LSRTTEKINGVARCPYDPRHRV
5878	19779	A	5927	400	1	VVATDGGPLPLASSATVSVLQDVNDNE PQFORTFYNASLPEGTQPGTCFLQVTAT DADSGPFGLLSYSLGAGLGSSGSPFRI DAHSGDVCTTRTLDRDQGPSSFDFVTVA VDGGGLKSMVYVKVFLSDEMY
5879	19780	A	5928	398	62	HNTEVLVGESVTLECSATGHPPPRISWT RGDRTPLPVDRVNITPSGGLYIQNVVQ GDSGEYACSATNNIDSVHATAFIIVQGG YPSSVPEPGLSPILTPPLARAAIPTDAP
5880	19781	A	5929	403	1	LASDGGDPVLSGTSRICKVLDANDNAP VFTQPEYRISIPENTLVGTRILTVTATD ADEGYAQQVVFLEKSPGETSEVFELKS TSGELTI IKDLDYEDATFHEIDIEAQDG PGLLTRAKVIVTVLDVNDNANV
5881	19782	A	5930	408	3	VASDGGDPVLSGTSRICKVLDANDNAP VFTQPEYRISIPENTLVGSRILTVTATD ADEGYAQQVVFLEKSPGETSEVFELKS SSGELTI IKDLDYEDATFHEIDIEAQDG PGLLTRAKVIVTVLDVNDNANV
5882	19783	A	5931	126	391	PVLTCAHFHFSAGAGGSYFMISRLGPE FGGAEGCLYLATTFATAMYILGAIQIL LVSQAEPWSTLAMIKQFLWTPNRRMLVL IPTC
5883	19784	A	5932	436	359	NKEWLP GSKVPEKSINDVKNTSGLL
5884	19785	A	5933	365	3	LIIGMLTAIIGDLASHFGCTIGLKDSVT AVVFVAFGTSVPDTFASKAAALQDVYAD ASIGNVTGSNAVNVFLGIGLAWSVAIY WALQQQEFHVSAGTLAFSVTLFTIFAFV CISVLLYR
5885	19786	A	5934	394	3	FQYFSRTDRVLKHERMCHENHDKKLNRC AIKGGLLTSEEDSVFSTSPKDNSLPKPKK RQITEKRSSGMDKESALGKCDLKKVKND YSPLYSSSTKVKDEYMAEYAVEMPHSS VGGSHLEYASGEIHPPCI
5886	19787	A	5935	393	1	REDLIAGIDEFLDEVIVLPPGEWDPNIR IEPPKKVPSADKRKSVFSLAELGQMNGS VGGGGGAPGGGNGGGGGGGGGGAGSGG AGGTSSGDDGEMPAMHEIGEELIWTGRF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
5887	19788	A	5936	410	126	FGGLCLDIKRLPWFPSCT PICYYKKAGRARWLTVPVIPSSWDYRHQA QLIFVFLVETGFHRVAQAGPELMTSGDP LAYNFLCSYPNEVFRSQASASDLQFVLR NLEPPDAGNV
5888	19789	A	5937	426	1	DATFHEIDIEAQDGPGLLTRAKVIVTVL DVNDNAPEFYMTSATSSVSEDSLPGTII GLENVHDRDSGQNAFTTCSLPEDLPFKL EKSVDNYRLVTTTRALDREQFSFYNITL TAKDGGNPSLSTDAHILLQVADINDNAP CI
5889	19790	A	5938	438	3	ADPTKGLLRNGSVCVRAPGGVSVQNSVN LKNSKQACLPSSGGIPSLNNGTFSPPKQW SKESKAEQAEKRVPLPEGPCPSGAASDL QSKHLPKTAKPASQEHVRCSAIGTGESP KESAQLSGASPKESPSRGPAPPQENKVV SPVV
5890	19791	A	5939	3	191	YSVCLWSQLLRRLRQEDHLSPGGGGCTE PVVNTERLSKNKTKKRERKQCGFHS WYCNLK
5891	19792	A	5940	399	1	QYSDNDMSWKVTRAAKCLDAVVSTRH EMLPEFYKTVSPALIYRFKEREENVKAD VCHAHSLFKQTSVPQSWLCGLDAMDQ GTPLAMLQSQVANIVKAVHKQMKESVK TRQCCFTLLTELNVNVLGAVY
5892	19793	A	5941	411	3	SPCEGPRRFQCKSGKRVDDGKVCVQRD CRDWSDELLKVCWCGACLRPLAGLSLLPS PSWYLGSRPSSAPCPDTFCSGPLFGFMC REMAHGAFRPQASGLHLYKVLACPSQ VLKNYVFSHKLGLSSFLPRSDHV
5893	19794	A	5943	431	26	KAVVGIPGDMGPPGITVRPGYNGLP GVQGGKGEPEGVGLPGLKGLPGLPGIPGS PEEKGSIGVPGVPGEGAIGPPGHQGIR GEPGPPGLPGSVGSPGVPGIGPPGARGP PVGQGGPGLSGPLVIKGEVSRVR
5894	19795	A	5944	396	3	PLPEVELIRVPAFLDLFMQSLFKPGARIS QDLKHXYIHLAYAASVETCKKNKRVS INKDELKSTSKAVETVHNLCCNENKAS ELVAELSTLYQCIRFPVVMGVKWDW TVSEPRYFQLQTDHTPTV
5895	19796	A	5945	465	32	ERVTLADITVVCTLLWLYQVLEPSFRQ AFENTNRWFLTCINQPFRAVLGEVKLC EKMAQFDAKKFAETQPKDTPRKEKGS EEKQKQAEKKEEKKAAAPAEEMDEC EQAMAAEPKAKDPFAHMKSTFVLDDCI AAAL
5896	19797	A	5946	414	2	ATFPVRCIRKEIRNWWYDIQPVQEPKQ ACGNHGGIIIIAETSTGCLFAGSSLGKR GVNADKVAIEAAEMLLANLRHGGTVYBY KQDQLIVFMALANGVSIKGTGPTLHTQ TAILYDEQIVKVNCKENHSVDEQVY
5897	19798	A	5947	411	1	EPCVVRRIADSSVQTDDEDESRYLLSR RRRARRSADCSVQTDDEDSAWEQPVRR RRSRLPRHSDSGSDSKHDATASSSSAAA TVRAMSSVGIQTISDCSVQTEPDQLPRV SPAHIHTAATDPKVEIVRYISAPCI
5898	19799	A	5948	153	409	LPFFFPILLPFISFFRYRVGLLSPKLKCS GVIIAHCSLELLGSSNPPTSASRVIFLY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						LSLCLFVFMESCSVAQAGEQWRDLGSL Q
5899	19800	A	5949	21	447	RAAAMSSSRNFRFLSSHRELYFGVDLPSG NLVVREPADREQLCRAKACVLTYDLVL EDPLELHKIRIHVLDTNDNSPLFPAGDV QLHIPEFLTTPGARFTLPNAQDDDEGSNG ILSYSLSPSQHFRMDGSRVDGSEYPEL VL
5900	19801	A	5950	268	19	QDNWYYCTVPEYCKTKNLILANWLVIN YLSGDFYFFFIFFLDGVSLCHPGWSAVA RSQLTATSSSQVQGRFSLSHCIAAL
5901	19802	A	5951	389	3	QQMDLARQQEQIARQQQLLQQQHKIN LLQQQIQVQGHMPPMLIPIFPHDQRTLA AAAAAQGGFLPPPGITYKPGDNYPVQFI PSTMAAAAASGLSPLQLQQLYAAQLASM QVSPGAKMPSTPQPMY
5902	19803	A	5952	2308	307	RRRPARKKTWVRDGGPHQGL/YPQLPSA VLQPTQPGHGPALGKGRELESWQKRP GK/GQTHRRKTRGTASPAVYFSVEWD\ SGGCPMTGKGAQQQAGLGAAPNPESG EQGTGRGRAQDSQGHGGGKGRGQHPPG ND/PRGVSGMQESVHSPEARPTGGGTG /EMLGRTWRHQQLVGGTGNLLETGSWS GSGSWGGRGVVLRPQEGQVTTGMGLAGR/ YQPARQRAVELSPGAQGLRQRRGGWSGP PQETEQSGVPGG*GSWPLESHQGEQ\PA AGQKQSLQMLPGGFPCWS/SGMGGGPQQ LLESEGAGPSPGGGRHHGKGRVAVTTTP REGD\RGQSPGGHTLQLFPCPLWS*ETQ GQGSRTVQHQEWGEGEGEGAGSDQSR ALGIA*ICPHTLRPTSMEPQSTAPAPGQ PPGPPSWGHRGHQGMGYGGRCPGQ/IQG RGRAQLGSTVG*RDG/QRG*MQGRDQQG PRSNAGVGSCHTSQK*IPPSSLCT*N SSHGPASG\QLWSSSPFIHSPGETNIPH TLTEPHSVPGWCWDTLRRHGAGQGHGPM ARSGTGEQ/QRGRY*ERGRRGRQKQ KKQGLKEPG*RAAPTLLKGATRPLCRCLR KVQKPKQDGDVGS*LLKVFRAPGALGK PQRTCRGPADFFHALSGLSNVHRSYCST NSGFGACM
5903	19804	A	5953	461	117	HPRDIIGPVHQGLPPSPQPPPPCKQAPT TPSS\M*P*TNRHDITLGSFPVQVPGADW KPLNAP*LPELAFGEETPCRPVDPDPYV WLPDSAPEHCVTWATSPGLSDLLSYPRR KQA
5904	19805	A	5954	845	610	FFETGSY/SVAQVGAQWCFNGSLQSQPP RLKRSCHLSPPSSWDYRGAPPRLARFFF FCIFYRNGVSPCCPGWS*TPELQ
5905	19806	A	5955	1	378	KTPVSDR\ATKCCSESLGNRRPCFSALE AYETYVPKEFNAETFTLHADICTLSDKE RQINKHTALAEVLKHKPKARQEQLKAVM DDFADFVEKRCMADDKETCFVEEG*TLV AASQAALGLLHRIK
5906	19807	A	5956	723	343	GCQEGICPSPCPVIPATREAEAGESLEL RRRLH*AEIVPLHS\KAQRLCSDSDFI RILVIFSGMFLVFTLAGALFLHQRRKYR SNKGESPVPEAPPCRYSCPREBEGSTIP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						IQEDYRKPEEACSP
5907	19808	A	5957	55	491	AQHFNPHNWPVT*LLPHFTNEGGQVTEA RCLKWQAR\CLVPMQKVENAMPGT**PS AEVTPPVCNQHHWPQVEGIPSS/APAFQ WPLTMGHPC\WESAPRQDASTSPRPGTA SHCPSAVAFQERGSSPCPPHSDSGLCL LPRILLPAP
5908	19809	A	5958	2	413	KKPDQ\AE\REHLCTSL\WGRNTDKNG EELHGGKRVMBRLKKAUKIANQCMDFSL QMQLYIEILNRYIYFYEKBYDAGTIQVL NQLIQKIREDLNLESSEPEQIT*HFH NTLEHLRLRRESPESSEGIYEGLLIYE
5909	19810	A	5959	871	564	WMCHATFGSHLN*AWRLRPVNSG/LLM/ PSEGAKESTLMVGVTNPD\MKGKIRL LLHSDGKDEYVWNAGHPDILG\HPLTLQ CPIIKIKKKL**PKSGRTADGPDHSRIK V*VTPLGKEPTTDEVLAEGKENME*VTE TC*IDMN*VLQGQTWNLR
5910	19811	A	5960	390	271	GINFFSRN/RSLTT*SRIV*NSWAQVIV LPWPSRVLGFQA
5911	19812	A	5961	333	922	GLSCRVFGRITLSCPPCILRHLSEVETLQ TLQKKEIEDLYSRLGKQPPGIGAPAAM LSSRRRLSKGSFPTSRNLSLQSRSEPPG PGIMRRNSLSGSSTGSGEQRASKGVTF GDVGRM*IQNRSHVSPPHQPPWSLCSQ NLMLSDQQN*ARKIPTLKG*KA\GGHGE CSSIIVKSQTYVNCCLCGVSSAAYHLH L
5912	19813	A	5962	705	387	CVAQTGVQ*HDLGSLQPLPPGFKQSSHL SLPSSWDYRRVTPRLPNF*FFVETDFC HIAQAVLQLL\SSNNLPASASQSAGVTG VSHRARPTLTLDIQAEIPDLKPSG
5913	19814	A	5963	425	182	ASNQ*DSVGVGPSEPGAGYNLLVFLKC \LEKHSSWVGVTQFSRCHLSPLSLTRKG NSLTPCTSRVRQCLALLWLTHGSRTH
5914	19815	A	5964	388	14	PPMYTQLCSIRSTQAFCFVFFSRDE/SL ALLPRLVLNSWVQAILLPWPVKVQG*QA QWLTLLVI PALWEAMAGGLLEPRSSRPAW ATTQDLISTKENKTKSLASDAEELCVH WRLKI
5915	19816	A	5965	1	373	DDQVRKSVINLLLAAYTGDVSALRRFAL SAMDMEQRDYDSRTALHVSAAQGHVEVV KFL\LEACKVNPFPPKDRWNNTPMDETLLH FGHHDVFKILOQYQVQYTP*GDSNGKE HHTVHKNLDGLS
5916	19817	A	5966	3	329	HEETSRVETIYELIHVHPYAVKQSPDLEE YSLSQSTLEQVGHF*GFVSSMVYVYKTF PGSCRGSTALFSSLYFLPPFQVFLSLSK EQELGDFE/EDFDPSVKWLLPQEEP
5917	19818	A	5967	2	47	MEDRRRLVRGIPCPQHNAQCFAVPPGIQ AYGAAPFEDLQVDFTEMSKCRGNKYLLV LGRTYSG*VEAYPTRTEKAREVTRVLLR DLLPRFELPLRIGSDNRPAFVADLVQKA AKILRITWKLHAAYWPQSSGKVERMNQT IKNSLGKVCQETGLKWIQALPMVLFKIR CTTSKRAGYSPYEILYHRPPPIRLGLPG TP*ELGEIELQRLQALGKITQTI/YSP SKWPSVSLFSPVHPLSPGDRVWIKNNVA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SLCPLWKGPTVVLSPPTAVKVE*IPSW IHSHVKP*TA
5918	19819	A	5968	2	150	KSQSI*QSSLLSYFEKLPQPQPSA\TS TSKQDPPLATRLWLAEGSDDH
5919	19820	A	5969	3	371	HEGKSGPMTGVVLVAVGEVAMKILLCL CLILLRVRSCRRKAARALGMEADAVT D*SPDSRLLPD\PPHPVPPQSERPCFLC RLCMVCPLLDSPDPSFPCHPTSPQTLRA KDSAALDTLHV
5920	19821	A	5970	396	58	YWVLSKGPVTCMLLNSVFSFQASSCLSF LINS*AP*PGIFLGMSVFILPFFVFGQ AGLELLTSGDLPSASQ\ARITGVSHCA QPHTALSQYLEQCLAPSRQLISVSLIR
5921	19822	A	5971	442	120	ICMKQGLALSPRLDSSSAFSNTVQMPFP RFKSSYGLSLP/RSWDYRCTPPHMARSG NGV*P\FMVETGSW*AAQGGLELLSSN LPP/SAFQSAGITSKGHCTRPVFLVC
5922	19823	A	5972	459	434	MWPLPWFSISPPSPPT*VSSNNHPCA VPRAYPGADIPGPWQRLPPPHRLSGP PESCLLTTLCSKHPNGCPLTQNPRSLP GPRPCLITYSTPSPPP*AQL/YAAPSP*L YTVVREALIR
5923	19824	A	5973	681	1758	VANKCQIPDIKAKTYCICNTKEKRSYLK T*NLHRGF\IKKQIEEFNIGKRHLANMM GEDPETFTQEDIDRAIAYLFPSGLFEKR ARFVMKHPEQIFPRQRAIQWGEDGRPFH YLFYTGKQSYYSMLHDVYGMMLNLEKHQ SHLOAKSLPEKTVTRDVIGSRWLIKEE LEEMLVKESDLDYMQFIRLLEKLLTSQ CGAAEEEFVQFRFRSVTLESKKQLIEPV QYDEQGMFAFSKSEKRRKTAKAEAIVYKH GSGRIKVNIGIDYQLYFPITQDREQLMFP FHFVDRLGKHDTVCTVSGGGRSAQAGAI RLAMAKALCSFVTEDEVEMMRQAGLLTT DPRVRERKKPGQEGARRKFTWKKR
5924	19825	A	5974	1232	980	SLSLSPRLCSGVTAHCSRLRPASSNSC FSASQVAGTIGACHHIWLVFVFLVETGF HHVGQTGLELLT*VICPPWPPKVLGLQ A
5925	19826	A	5975	1	259	LTSYDYRRALPCLVN\FCVYFLKREELA LLPKLFWNSWA*ATLLP*PPKIFGLQAQ VAMRLKFPACLPACLPAYLPPFLFSFI PP
5926	19827	A	5976	24	223	PYLTIQISTNESSVCSHARAEFLDHQNQL /WLGTVTYTCNPS/TLGG*GGRIT*GQE FKTSLGNTARPCL
5927	19828	A	5977	395	136	GSWDYTHVPPRSANF/LVETGFRHVA*A GLELLGNPPTSASQSAKITAMSHCTWPS SYY*CEYNARFGSLHKRSGMTIYIKSYK RQN
5928	19829	A	5978	1	785	GTRLKSGTNTKKALQAVYSMMSPDDVP PEGWNRTRHVILMTD/GSEGTSLLSQP PHLLRPACGP*VHL*HYTHGWGPECD* LAVHLSCDPS*GILPKPCDQLSLTLPQL AHPAMCIPAFSQIFLISYPHGPVSSAG LHNMGGDPITVIDEIRDLLYIGKDRKNP REDYLGE*PA*DPAPHFLRAWTLILPFY PSDVYVFGVGLPNQVNINALASKKDNE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						QHVFKVKDMENLEDVFYQMIGREIQGNK EPNSPQVPLK
5929	19830	A	5979	2	419	KATAPIDSDSSDGSQGNKLT*KEFITL NAIKSIYDSWEEVKISTLTGVWKKLIP LIEDFEVFK\ADLVEIARERELEVEGEL /LQSQDKT
5930	19831	A	5981	1	154	KKC*MMLTWWCMPVG/PTPRAEAGGSPE TGNLRL*CTMIMSVNSHCTPAWAT
5931	19832	A	5982	12	311	RKSLNFVEGCNIRLNKCRHTNFVPQTIF FFLLFL*LGQC**VVVSFFFFFVFCFV LFFVVFVCFVFFFCFF/GCLFVVELL /YFYELFCIVIIMCYLR*YV*IVYMLF FVCWIFVLYLCFHY*LFLFFVVFVLLF ICGVFVVFYELFCIVIIMCYLR
5932	19833	A	5983	3	203	IGQKRASEDTT*GSAD/PKKSSAGPKRD ARQIYNPPSGKYSSNLGNFNYSRLQ GK YRWPRLGHTKRS
5933	19834	A	5984	368	138	STVGKMLSGQHPCYRE/IL/REQKSQSM *QISLLSYFKKLPPQPFQPSATTALISQQ PSASRQNPPPAKRL*LAEGSYDH
5934	19835	A	5985	2	155	LANF*ITYFC/RDKCLPVLRLVSNWPQ VILPPWPPKVLGLQGMSPCAPRHS
5935	19836	A	5986	325	403	FIYYLFFLSSLYLIITYALFLSSF*R*V VYHVMVLLKVVICHHFLTLFFSFRSLI LYLFFILFM/YLLIFVLEFFIQFSFYLF FYLFYLLFFNDYCFDLIFFLCLIIYYHF QSYFIS*FIYYLFFLSSLYLIITYALF LSSFSI
5936	19837	A	5987	81	651	KLQVAGCRTLSQIDVKFKPSVHSSLAVC LRANYFTSQPNVIMQVTLTRCVAHSKH LGTVSYSWYIKLLFPKSHFIYLFILRR SLAPVAPGVQWLDLGLQPPPPGPKRFS CLS/LPR*LDYRHPPRLANF*FLVEK GFCHVGQAGLELLASSDLPTSASQNAGI TGVTPAPSPQKATLNLILGGQFHI
5937	19838	A	5988	301	341	PCFCPCKNRVS LW*WHAPPCPANF*LF IYLFLVETGFSHVGQASLKLTLDDLPA AASQSAGIPGMSHHDGLFL
5938	19839	A	5989	71	1252	TKEQSRSLRSQQLGVQRQSRHLKFGGGG APSARGVGGSWSLATRLGFPVSTANMSRP VRNRKVVDYSQFQESDDADEDYGRDSGP PTKKIRSSPREAKNKRSGKNSQEDSED SEDKDVTKKDDSHSAEDSEDEKEDHKN VRQQRQAASKAASKQREMLMEDVGSEEE QEEDEAPFQEKDSGDEDFLMEDDDDS DYGSSK/NEKQKD*EVQT*KKRKENAQ TQTKGYSDAKSSERQRESGSP\QASKAS KEKTPSPKEDEEPESPEKKTSTSPPP EKSGDEGSEDEAPSGED*K*WGERFY *KKKEKKRKKREEKKEPT*DRTPFWLWL DSWGFQCFPPFVESNISLSLFFFFF ANHCMCKCLSYLFFVWSLQPSPPFMKA MSN
5939	19840	A	5990	630	316	RWNVNSVA\QAG\IQWCDLGSTGNRPP GF\K*FSCLSLSSWDYPHTATMSSKFL YF*WRRGFTMLARLVSNWLVLS*PSDP PASAAQSAGITGMSHRAQPIYLS
5940	19841	A	5991	2	182	WQEQKAE/CLRDVWTAMCTAALLTIKAG

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						R\NIPCPMMKEWVRKMGPITYTFEYSAV IMQVILKF**HATTGMNPDVISEVCQS QKDK*RILLSCNNAGNS
5941	19842	A	5992	79	278	EAK*RVNGCSKPTWHMYTYVTNLHTYV/ IKPAHCAHVP*KLKYKIITIIK**RWG LTILPRLVSNWAQVILLPWPPKILGLQ A
5942	19843	A	5993	22	274	AGDEHRAWGYQPAM*ARLEMNTGPGDT/ MPAMASQRAGITGVSH*GCPFFSLNKKI WRSH*VAQAGEQRLPRE*TPGLSCYSCS LPSN*DYTSAPLCPPYDT
5943	19844	A	5994	347	195	YMHTKHTHTHTHTHTHTHTHP\EKHLKA PNEV*KSKNNV*IKPKQSQSCFS
5944	19845	A	5995	1	122	RYELEDLHLQMTTQLHALKENNYQLR* SSHVSIPST*GYRHVPSCPANF/SSLTM FPSLVSSCWAQVIHLWPYKVLGL*ALK ENNYQLRTI IIDCTLNNNIF
5945	19846	A	5996	365	229	RPPPCPANF*FLVETGFHHVKGAGLEL LTSSDLPAPALHQVFA
5946	19847	A	5997	357	17	ILVDKINNWNLFQNNLVVC*RGWGYK* DRSFHLLKTVVAE*WVYEGSLY*SLSSY YLF/C*ROGLTMLPRLVLNSWHQAILLP WPFSLLLCILEVFQNRLEKKKNQKPM TGS
5947	19848	A	5998	1	207	PILYNLFQKIEAEGILPNSFYEASVTLL PKPKDITR/ITTY*FILLT*NILNKVL SNQIQLYIKRITY
5948	19849	A	5999	603	269	EDRVLVLLPKAKSAVAWPRLTATSASW\ VQSFHPSLPSRWDHRHVPVPHSANFCCV CL*ROGLSLLPGLVLNSWAQVILPPWP\ PKVLGITSMSHHARPLSFYIGHFKYIQK
5949	19850	A	6000	3	150	DYRHAPLHLATFKK/FFCRD/RGLSVLP GLVSNWPQTVLPP*PPKALGLQA
5950	19851	A	6001	365	62	AITAHCSLNLGSSNPTASATRIAGTIG EAAMSYF*ISSTLTHFSYT/C*LHHVWL IFKFFFVDEVYVAQASLELLSSDPPAL VSQNAF*TVSHCTEPV
5951	19852	A	6002	537	236	DRVSLCCPGWSAVARFQLTATSFR\VQ *SSCLSLPSSCDYRSAPPCPANFLSFCR DEGGGLPGLPRLVSNWAQAIHPQPPTS VWITGVINGTWPKIPLS
5952	19853	A	6003	22	368	NFFLQNKENIKRKIF*ERKHKLMOQTSL LSYFKQLPRPPTTSQQPSTWRQDPPAK R/LRTYKGLDDR
5953	19854	A	6004	327	335	NQSIFTFNYPFP/CKFKFKN/TLHL WADKVAHTCNLSTLEGQGGRIA*GQEFE ATLANMVKP*LLCKVK
5954	19855	A	6005	2	367	WQFLKKLNTKLLYGPVF/PYLGIIYKQEK WKHVHABCTCTQMFITVLFIIIVPK*KQPK CPSMEE*ID*M*FVHMLEYRAIKENKLI HATWMNLRLNTMLSEISQTQIITCMNLLH KMFRKVTETES
5955	19856	A	6006	1	176	PGFKQFFCLSFWTRGIFIEMGFHHVG*A GLGLMSGDPPASASQSAGITG\VSHCA WTY
5956	19857	A	6007	1	289	EVLTKIPR/FFVEIGKLIQDLKDTGPR IA*TMLTKKTEMGRIVHSDLVAYYIVAV IKMVWYYW*RRHINQ/WERLEISEIDS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						QNMFNWVFTKMQLF
5957	19858	A	6008	439	223	FFSPGSH/SIT*ARVQW/PHHSSLQPEP PSLKQSSHLSLPSSSDYRCAPHPADLC RDWVSPCCPGWSQTLGLK
5958	19859	A	6009	1	252	MVSIS*PRDPPALASQASGITGMSHHAQ LFFLN/CIS/ELISSTVTPGLKESACLG LPKCWHYRREPQHPACTVLYLQFQSDFO LK
5959	19860	A	6010	131	514	PWPYSLSSSGLSSSFEN/VEKWVPEI IH \HSLFLGTTIDLRS\EPCTTEKLN\KDK YNPLTPQMADMMVCDLKVVE*LECSAFM WKRLK\VFDEALWAALEED*RSSCRKET STLLQSTPLLVSALPCTP
5960	19861	A	6011	625	141	ETGSRFVTHAGVKVHNHDSLHPQPPRLK *FSYFSLSSWDYRHHVPPRANLVYPL *RGGPPSMLPQASLEF\LDK*IPPCLO PS/AKVLGLQVSHRPSPKVTFHQRAKEG DVS HVSRGKSIPDRGNSQCMHRSIPC VFEEQKGGQCYCSIESKEETSRI
5961	19862	A	6012	302	42	GLAMLPRLPGTTPGLKQSSCLSLPSSWDY KHILS*PAVY/C*FLKNIK
5962	19863	A	6013	363	82	VSVSLSPSLKTKVNYAVASASFTIAKIW KQLKCPMDKQMK*IWHIHTMEYSA/I KQKIMSYSTWMNLEDIMLSEISISQAY KGKHHMIYGI
5963	19864	A	6014	329	99	HIFGNTYFFQVASSFIYLFDRDSVSLCRP GWSAVA*SWFTATSG\FRPSACGLPKC /WDYRREPPRANVLFMSRVTH
5964	19865	A	6015	324	238	LAMLSRLVSNWPQAILLPLPPKVLGLQ A
5965	19866	A	6016	2	308	FWKAIAGIEGDSSDKCRQ/SKLKTIWKK FISLDAMRNHDS*EKVKMSIFWKMIPT PRDDF/EGLKTSVEKRTEDVVKTARQ*E LKVDRT*TDEELLLLQQRK
5966	19867	A	6017	2	457	FFFLRWSL/DSVAQAGVQWRDLGSLQAP PRGFTPFSCLSLPSSWDYRRPLPRPANF FYF**RRGFTMLARMVSIS*PRDLPALA SQSAGITDVSHHRAERVISQORIVSVMW KPLPEIHIPCILNLSLRFNHRSVAGLRN SLIVRMLSILTHG
5967	19868	A	6018	389	142	AHMLFAAQGDSSIPMLVAPLFTVVKMWE QSKLPLADEWSGFW*HIHVTEY/YAIKR REILTHATTSKALCYVI*ALTGRTL
5968	19869	A	6019	384	232	LNLPSSWDYRRAPSHA/NFSYF*RDGG LTML\PGWPQVIQMPRLKAL*LQA
5969	19870	A	6020	333	84	GLIDQEFATDTTKSTSLSLT*T/IPSRC SLCLRGSSDSPASC/SOPPASVAGITDT CHHAHIIFVFLVETRHHVGRANTEKPR LH
5970	19871	A	6021	106	366	DTISFFFLKAPIEPVFIIFIFFFFFFI FFFI*FFFLFLFLFIYFVF/IFFFIL LCLFFFFLVLLFYLLFFF/SLFFLFCFV FCFFF*FCYFYFYLLFFLFFFFYLALF IFFFFGSSFLFIVFLFLFFLFCFVFCFF F
5971	19872	A	6022	384	18	REKKPGPGTGKPPKKKGGPKFGPKGPKK RGEKKKKGGP/NSFFPRGGTTPGGNF*R GFPPENQKKRGRKKFFQGGKRGANPGIP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PLLGPKAEGGFIPGKKKKKKNSNKKSK QTKKALSRTSHS
5972	19873	A	6023	3	191	LVKKGKIRSWREETWVKTW/RFYPGVMAH/TYNPNPLGGQGRWIA*AQEFKTSLGNVV KPHLYKKKI
5973	19874	A	6024	364	142	IINGLIHLHNFKINGHTLSTWYTFHIL CVCVYIYICLC\CIYVSVCVCVYTHI QYTY*INKHIC*RLKAK
5974	19875	A	6026	338	102	WGFTILARLVSN*HLVICHLDLPKFWN YRHEPPCLALFLIFVGT*VYIFMGYRR Y/C*YRHAMCNNHIRVNMVSVGLNF
5975	19876	A	6027	99	77	REICTPTFTEAFSIEAKGWK*PKQPLTN EWINTMWCIIHMRGKF*P/YAKTSMKLED VFHEISKSQDKHYI*FLSPTYVKIQ
5976	19877	A	6028	2	328	TITYRGAKIRITSDSSSETMQAREE*SE IF*VLK/EKKTH*PKILYSGKLSFKSK GEIK/YF*GKQN/LKEFVSSRPVLQGM LKVVQREGKLYRSETQTYKKKEKASEKE
5977	19878	A	6029	8	241	GFAPLPRLCSNTNMAHSHSLNLSGSSDS PASANFSIF\IETRFQHVAVL*FLSS SNPPISPSPSVEITGVSHHARP
5978	19879	A	6030	108	362	CCYLMVTEISAHQNPAAQGLA/HTAFP* KTFFLKVSWTGTVAHV*KPSTLGG*GGR TS*SQKFKTSLGIMRPPSLQIKKKVFKI YP
5979	19880	A	6031	1520	77	ASSSSSSSVILSS*NIPNYNYIVIFM/ CL*IIF*AASSSSIYVPGICYIYH\IL CVCVCICMCIYVCICIYSIC*YIVYVSI YYIHY
5980	19881	A	6032	405	100	EGFFLPFRGGGGKR/PPGPLTPGGPGNP RPKPPQKWKPGPPPGGGPF*WVLLSPS LPPGGQVESPGAVSGPRQVPPSGSRPFS P TAVGTTVTFLSKKKKKQV
5981	19882	A	6033	42	309	CDKFFHKASNHIVSTYIWFQICVCVC VCVCVMCILC*AY/CGCLGIMIWFVLV L*CI/CYCCY*SSLFSVILCFLMCFVSY ERRFILFA
5982	19883	A	6034	397	2	KGPPP*GGPDFF*PRGGPPQKNPFPP GGGPPPPKNGVGGPPQKAPFFGPKRGA PQKGGPPGGPPRGEKKSLCPPPNWENT PRGLKKGPPPPPPPPPPPPPPPPPPVLR STGLRAPFQSVFIVELVEDMS
5983	19884	A	6035	343	2	LWPPQGSFKTAAPFFFFFLFISDFITF HFLYM\YVFFIPLFLL*SFECIK*IFYY VTF*FLQSFSLFFSVVFL\WLL*SILLY SF*LIRIYFRFILT*FQ*DTETLFFYYS IP
5984	19885	A	6036	319	68	SLGEICAPK*FFPPAQKKGPFQKFPSC K FSPSPVFKTRPRAKF*KGPP*GKKFYVA NPGKI\GPPKGSFKRPPPLFFFFFFF F
5985	19886	A	6037	419	191	RIHTIPITALFAVAKR/WQSKYPLVDE/ MDKIWIYIHTMED*AAYGKKEIMSHARTW INLKNIMLSEISQSQDKYFPFI
5986	19887	A	6038	434	401	YGKNFSFSLKV*IFCEGLVLVFFPPKKK /FFFFKNFHRVVVFLYVFF*TGRGVVFF K PPFLEKIFFFLTRVNLGPPRGFF*GAPF FFFFFFFFFFFFFFFFFFFFFFFFFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						*NFYFMN*IFTVI
5987	19888	A	6039	12	346	SFSFVRRSLTQAGVQWCNLSLQPP\LPSPFK*FSCLSLQSNWYRCLPSCLSNFCIF/M*RRGFSMLARLVNS*PQ/CDP PASASQSAGITGVSH/SHLV*NA*SPKTESHF
5988	19889	A	6040	275	45	KDVQHQWKIVQPLWKQYGLKASTESPHDPSILLGLTYPRKMK*IHK\TCIRMF AEALFLISK*KLKCLADK
5989	19890	A	6041	355	1	FCTIKNFFFYIFFFKNYF/FFLYIIFPKKKVLEFF*KKKIFFLFIPNKKIFWVFFF FFFFFFFFFCPRFFFFFFFFFFFFFFFF FFFFFFFFFFFFFFFFFFLVTRHLE EMRKGN
5990	19891	A	6042	635	209	PLNIKKTFFFLRQSFTLVAQAGAQWHDFGSPQPPPPRFK*FSCLSLPRSWDHRRPPR PANLVF\DFLVETCFHRVSQDGLDLLT/S/GDLPALASQSAGITGVSHCARPTLEFLKVKEMIFCSTTVKAVLDHANFLILRFSIT
5991	19892	A	6043	12	348	ESRYSSICLPFSSVYCSRIISLQLYSYVLLVYILFFF/CFLKREFGFCPPLGVQGPGLGSLNPPLG*KQFSGLIFFGIGNTGL APPSPPNFGFFRKKGVSPCGPNRPAISK F
5992	19893	A	6044	192	1	IFHRFCT/HITLP/TTALNNN*PWLGTMYAYNPNTL*G*GRRIV*AQAFKSSLGNMTRPCLYKK
5993	19894	A	6045	338	42	WKTAWW/FLKKLD/MNYC*DPAILLLGIYPKELKAGT*TDIRTSMTAEFAIAKRWQNVDLKNLRQNECRQFIWAKVEGNWLP SWFGEWSIQHRLQAGF
5994	19895	A	6046	300	3	RLDCHYLHSHHTHTHTNPNAGIYTHH/HCWNLHTNPGGILGVALDL*MQFLNLRGWSWGGEQMAWPCPQGHVMWLGDGPKMILKPPLWVCQLQGSSYDG
5995	19896	A	6047	332	3	SLESAGFT*YKMYFYYYKIK\YIYKSTFIILFL*IFFFDLFFIFFFFIFFFFFF FFFFFFFFFFFFFFFFFFFFFFLKSPKRVIYFGFGTQNPQMFSLLTLKYVLC
5996	19897	A	6048	2	152	KNLKISWT*WMPVVSAT/WGGSLLKPGR LRLQ*AVIAPLHSSLGDRARPYL
5997	19898	A	6049	1	288	PIIIYVLLLLFFETDSHVS\RL*CSGAFSTHCNLCPLPGDSSASDS/RVAGVAPACLF*PYRGFSGPATLAFRALDPGLPLHPGFSLQRPSCSRGG
5998	19899	A	6050	358	1	FSIFSILIFDFLGGFLKFFAFFYGWDFLRFFFFYR*PFGPKSSFIFPHVF*R\WIWFLLLSSWFLKWSFDPQFFLKRFFFFFFFFFPKGFFYKRVFFFGFFFSNLLLSSQGGVWLI
5999	19900	A	6051	308	45	ADLSAEAL*TRREWDDIFKVLKEK/NKGQPKILYPSKLSLINE/NEIKSFDPKQKLREFTTRLVL*EMLKGILHMEAQGGYLP*SKHTKV
6000	19901	A	6052	2	124	IFCVLVETGFHWVAQAGL*LLSSGSPPAS/DLPNAGITCVSH*AGITCVSH
6001	19902	A	6053	1	330	LC*PGWSR\FLTS*SACVGLPKCDYRR

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						EPLHLVFFFFFFFFFT*TYLKG FYLNPRK IFKNFFPLLKNPFFGVPPKIQFSPIPNL PSLVVPMNVFFKRVLGKIFRGFFPP
6002	19903	A	6054	34	293	SPILFLLCLRHQSGCHPSWTAVAQSELT AASNWAQAILPHSWDYRHAPPH/LNLF GWSHAALPRDSNF*PQAILLPQPQVLG LQA
6003	19904	A	6055	319	217	YHFTPTGMAISKNRQKTGDNKCC*GCRE IGMLVCC*WQYKMWLL/WKTVWHS LKG IK/L*ELPYDPAIPL*GIQRVSWKPIPH SSEG
6004	19905	A	6056	341	151	VHAGGSPES/REFETNLGNKARLHLYKK *ISQMWWCIPAVPATHAGPSLHFNLYYS PWLFCQDY
6005	19906	A	6057	2	558	FFFLRWSFTLIAQAGVQWCNLSLQPLP PRFKRFSCLSLPSSWDYRHVPP\RLANF FVFLVEMGFLHVGQASLELLASGDPPSG DEDLR*LAFQSLGITGT/HHAGQIFLF /CLETESPSVAQVGQWCNLSLQPLPP \GSE*FSCLGLPSSWD\YRHALTHPANF \SIFSRDGVSPSWPGWSQMPDLS
6006	19907	A	6058	320	21	BICMTTNHPSVSNTIW/SKMTLASVYL LLPISKTSKTSGLPASKEVNRYLGTCAI RYFVFYFIIMLFV*RQGLTMLPRLVSN WAQVILPWPVKVLGLQA
6007	19908	A	6059	294	50	CYFSLSFGL*QFLSLNQSFVTLSSHCDR DTFE*SWSVI/PGIGVYSS*E*TRGLAM MPRQVYNWAQAILMPWLPKMLEVQT
6008	19909	A	6060	616	354	ERVSPCHPGWSAVALSQPTAALT SW/VK QSSHLSLLNSWDYKCMPELLANF/KFFC RNE/SLMLPRLTSNPWAQVICPP*PPK VLGLHA
6009	19910	A	6061	214	11	AATRPSAWQPPLLGSEELCPATTPSG RCTQQ/LH*ERAMMTMAVLWNRKGGKVG KRLRNRLVAMSV
6010	19911	A	6062	349	54	QKSAPPKKRINRISDSSEGYGQSKLKT FWKGFTILDAIKNICNSSEEVKIATLMG V/WDDFEGERTSVKEVAADVC/ETARQL EVEPESVTG*QQSHVQP
6011	19912	A	6063	332	3	SQPASGQISKVTQSTLRCLKMSVQVKS CYKCTATYLCAKFNSHEFRSSGVCENPV SYFYTHSIRSKIL/WPGMVAHTCNPSAL ESQGGCMT*GQHCETSMVNMVTPRVSR
6012	19913	A	6064	174	416	NENELFFCFFFXIFFFXFFFFFFFFFFFF FFFFFFFFGFXFFFFFFFFFFFFFFFFFX FFFFFFFFFFFFFFFFFFFFFFFFFXF
6013	19914	A	6065	826	571	DGSHSLA\RLCSGVI SAHCNHLHPGSS DSVASAS*VAGTTGTCHHARLIF/VVFL VETRFHNLGQAGLELLVIHPPWPKILG LQA
6014	19915	A	6066	1	284	GTSFFF*NRVLFCCPG*RAVPQ\SWLTA ALTSWAQGSS*NHRLKP/HMLSFFNFCK QGLTMLPKGALNSWAQAILQPQPPM*LG LQACTYANSLGP
6015	19916	A	6067	36	384	VSKNKP IHLFLFFFSKTSWSVT\RLC SGVTSAHCYLRLPGSREGAASAL*LSAT TWLCKVALPLGEDLGALCRNPWGAGVKG SSRESPLGEARGGELFWGQVRIRLWGR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GEPAP
6016	19917	A	6068	393	116	PQFIFPRY*QNKDPNL*KTF*HKYMPKC PAK\LIIFIEKGFSRFGQPL*HLSSSN LPALASQSAGISGINPGGRARFPLFFFF FFSLLLLLSF
6017	19918	A	6069	53	280	FFRFCCF/LLESESHSVA*ARVHWRRLG PG/LKRFACLKLPNWNVRHTPTHANF CIFIRDQGMTL*PSWS*T\PDIK
6018	19919	A	6070	3	377	HEEPQGCATVPGEFFKFLWRHGLITYPR LVSNSWAQALPPQ*METHIIFSIGRLH MVK\RQYWSGAVAHAYNPRLLGS*GKKA A*AQEFETSLGYVMRPLHKNLKNSEPGT VAHPCGSSC
6019	19920	A	6071	337	3	RESQAFFSKKKKGFTKMVVFQRCERG KGARQQSHLRKSIYV*ETASAKALRRHM PGVFQKQPGG/WPGVVAHT*NPRTLGG CGWIT*AQELETSLGNPEKPCLYKKYKL V
6020	19921	A	6072	1007	628	FFLLAHSPHSVAQAGVQWGLDLSLQALP PGFMFSCSLSPSSWDHRLPPRLANF\ FIFLVATGFHRVSQMVLS*PCDPPASA SQSAGTT/GARPKVF*IFVYMYFGVRKH SILMSMPQHDLFGYKI
6021	19922	A	6073	27	364	MDLPSVSI FDLRSLWADISRATSTLFWL LFSWNCFLHLLSFNLFLSLGQK*VCCR* HIQSCVT*QWRY\WSGLVTHACNPSTFG SQGGWVASV*EFETSLCNMAKPCLYKKY E
6022	19923	A	6074	2	68	ARACSHGTVALTASCFPLQLDYKCLQYS FVCFFFETKSNFVT\RLKCNPGPISVN* NFNLPGLTRSQA*ASREAGTTGTCYHA* *ILLPSSTRL
6023	19924	A	6075	330	49	KRRFALVVQAGVQWRDLRSLQLPPLPVFS CLSLPSSRDYRCPAS/RPS*FFLELLTS GDLPTSASQSAGIIGMSHCAQPLIYFL FQIKVILFFS
6024	19925	A	6076	2	267	ARGVEVKVGKTKFLNMIRRTLVCWWK CKLIQPLF/WRILPKVKEELPYHLAILP LGIYPKQMKISL\KYICSYI*IVDHFV *AILPLGIYPKQMKISLNIHMFYIDC RSFCIGTFLLL
6025	19926	A	6077	379	236	PPPPQTRTPPPGHVHKDPPPHHPYPP PQEPQPRTPVPNTHPGEEQNHELFNSSL LEPWW\YSSLLPPEQA*EPHIIH
6026	19927	A	6078	2	290	RRSLPSSPLEDGRSLIAPGLTWEPPSH PPQ*RSPPPKKKKKKKSPGPKF/HK FKTGKPEKPPRVL*RGHWPPFKFF*LKP GLPFF*GKPPKV
6027	19928	A	6079	1241	1487	KMYCIEFFVE*KPCLSCAIFIRLLKWS*P TVCNSISGGPPHG*IMPSIIL*FLFLET VFHSV\TRGVQWPDHGSLLQPGPPGLK* SSCLTASQSTQIIGVSHHAWPPSITFEI FKRLAYSMSADGW*KSPPMKLDLGALKK KLSFARPG
6028	19929	A	6080	333	1	LCHHVQLSFKFFVEMEVSLCGPGWPFK* FSHLGLPKCWDYRHDPPHLAFFFSL*\n FFCRDRVSMLPRVLKSWSQAILL*PP KVFFLFVCFLLRRVSFHHAEPYAVSSC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6029	19930	A	6081	2	239	ARGKYIYNRDKISFCCPGWNAII/RSLQ P*TSELKRSSHINRPNSWDYRCMPSHLA NF*IFRRDGLASLPRLGTGWLKS
6030	19931	A	6082	323	185	SACLGLPKC/WDYRREPLCLVSR*VLNS *AQAI CLPWPPKVLGLQA
6031	19932	A	6083	296	2	GERILEECIYARSHRAEITSLHCSLSVS K/HSVAQVVVKWPDFCSMQSMPPRFK*F SCVSVVSSWDYGLPPPCAGLHIWRRNVT LALQGLPTTSLALV
6032	19933	A	6084	443	1	QKPK*KTQTWSSISLQSRKMKKKILSV ITFFKT*GEEEEKEKKR\KEE*EK*K EPSQKKEVEVEVEDEERRGRK*KVDMEV KEEEKDKGEEKSGEEQ*KESAAAVRE* VDS/SELVTFAVLPGDSSEEEQGMMPR A
6033	19934	A	6085	328	1	SNILIFKAQVTKHIYSLETCPDYPGIS QAIKANFSPCTVG*LPSNWAYRHLPPCL DNF*IFCRG\RSILCRLISNSWLQQVKL QEFPPQLGCHARFQAGFLSHCLV
6034	19935	A	6086	299	46	LDDLHLHLSLCLSLFRDRVSLCYLGWSSV A*S*LTVA*TPVILSLRLK*SSHLNLP SSWDYRVVNS*PQGLLPRSPKVHLL
6035	19936	A	6087	266	48	GIEIVRQMRSTGADKVIYIVQSPLKLM QKI/WLGTVAHTCNPSNCGRSGRIT*G QEFKQSSHLSPKCDWYRL
6036	19937	A	6088	2	185	ARVTMLPRLISNS\GFK*SSHLGLRKCW DYRCEPPCPAEISFISSGYLTRSGIAGS YCNSV
6037	19938	A	6089	520	297	LGYRDFLHLSFPIS/WNYRCLPSCFA/N FFILVETN*FHHVQGAGFEHLTSGDLPT SASQ\SAEITGMTYRAQPAAGS
6038	19939	A	6090	388	187	SQHLGKLSREDCL/RLTVPDQS\GQHSK TPSLKK*F*K*AWVW*HMPVVPAlQBAE VGGSLPRKSKLQ
6039	19940	A	6091	188	329	TLGLKRFFCLSLR*FIYFFFRDRVLLYY PGWKAvgIHRDYSMLYSLELLASKDS/ SCLSLRSGWDYCVWLIFFGCM*CKRQDL SIIPWQORSLIGQ
6040	19941	A	6092	124	342	RPAWPTWQNPISAKNTNITWA*AARVAG IT\GTCQRAQVMFVFLAEMGFCHVGQAG LYPKIIILYDKLSHYKCSHLQMRKALET YSGIYSLFTIYLV
6041	19942	A	6093	169	2	SH*PFTSSTIRSITW\GAVAHTCNPSSW GE*GGRMA*DQKIETSLVNMTRPHLYPR A
6042	19943	A	6094	2	324	FFFLRWSL/DSVAQAGVQWRDLGSLQAP PRGFTPFSCSLSPSSWDYRRPLPRPANF FYF**RRGFTMLARMVSIS*PRDLPALA QSAGITGMSHRARPAVYILTSTN
6043	19944	A	6095	76	340	LRKKFCFSVYPFIHRWTFELLPLNDFLM NFYFRIVFRFMKKLQR/WPGAVAHAYNP STLGG*GGRIS*AQEFKTPSGNIVRDFI STKNM
6044	19945	A	6096	349	84	FLLSLF*DTISLCHPGQSAVVRTMTSQL KQSSHRSLSSWDCRCVPPCPVNFSSFC RDE/SLAMLARLVSNLWDQALVAEAGVS VWARQE
6045	19946	A	6097	346	184	LTMLPRLVSN\GLK*SSHFGLPKCDY

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						RHEPPCLAKISLYITKFFHILSLPI
6046	19947	A	6098	378	250	FKQFSCLSLPIISWDYSREPPQMANS*F LVETRFHHVYSYVP
6047	19948	A	6099	3	225	GFKRFSCLSLLSSWDYR/HPAPYLANF\ *FLVEMGFHHIGQAGLELLTSGDPTLA SQSAGITGVSHHAQPLIIF
6048	19949	A	6100	1129	457	YCVSSSKYRRTISFSLIA*LLLTKLGS/V QKVGQWRDLG*LQPPPPG\FKLFSCLS LPSGW\DYGHVPPHPA*FCVF*WEMGVS PCWLRLV\LNS*PSGGSRPPSASQSAGS LQGLI\HRARPEH*F*TS*PLGEGKTLD EIIYIKTKTFYQFCIVCLKLH*RLMEFAL VAQAGMQWHDLSLQPLPPQFKWFSCLS LESS*DYRYWLLYHPALELKEAPSPES PCTH
6049	19950	A	6101	3	296	EIIQALLITIVLGLYRTLLQAS*YL*SA FTISDGIYGSTFLAA\TGLHGLHVIIGS TELTICFIRQLIFHFTSKHHFGFEADA* YWHFVDED*LFLNG
6050	19951	A	6102	1	749	RHEGGFLFKTILLI*TSLTIGSLALAGLL FFTGFYFSKNHIE\TANISYRNA*ALSI TLIATSLTSAYSTRIILLTLTGQPRFPT LTNFKENN\PALLNP\IYVAAGSLFAG FLITNNISPASPFQTTIPLYLKLALAV TFLGLLTALDLNLTNKLKIKSPLCTFY FSNIGFYPSITHRTIPY\LGLLTSQNL PLLLLGLT*LEKLLP\NTISQHQISTS ITSTKK\GILKFYFLSFFFPLILTLLLI T
6051	19952	A	6103	377	1	SKAFGPPGF*APYGLKAHCFFPGFRRGV WAPSGFWARPPIGYPFAGALIGAPVWPS GGPPKPGPP\GPFQVPLKGGKRLGIGGP FPGSPGFLTPGSKKKSTKKGKPKKI TPLDTSCSRITVM
6052	19953	A	6104	1001	531	FFLRRSFTLVAQAGMQWCDLSLQPPPP GFKQFSCFGLSSWDYRHVPPTLANFSV FLVEM\GFSMLARLVTS*PQ/CDPPAP ASQSAGITGMSHCAQLPKPIFNYL* AIDSVTTSISLARDWPNSSENRLGVMGKPS KFKRQEQKMECYRDAPS
6053	19954	A	6105	376	117	CSDWSAVSRSQLTAAPNS*\VKQSSCHL SLSSCWN/YRCQPRHLANFVLCYVLF* RWALAMPLILVLNCWPQAVFLPWPPEM GLQA
6054	19955	A	6106	689	433	LCHPGWSAVVQSWLIATSPSLV\KPSSH LSLLSSWDYRCTSPCPANFFVFFY*R*G STM*PRLWNSWAQAILPPRPPKVLGLQ A
6055	19956	A	6107	2	176	AREYPANFFVCLFFLILCRDG/DFTMLL RLISNSWLKRSRSLPKW*DDRREPPH QAY
6056	19957	A	6108	328	69	LYIFSG*ERVLFCHPGWSAVAQSQLTA ASTFRTQVLSLIGRWDRHVPPLADL/ SFYRDGVSPCCSG*SQTAILLPWPVKV LGFQE
6057	19958	A	6109	777	329	FLEMGSHSVAGVQWRDLGSLQPPPPG FKRFSCLSFPSSWDYRRPRPA/NFFV FLVETGF\TILARLVSNS*PRDPPASAS

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						QSAGITGVITYPRPALTONFSNLTFGEEN RKPNPEDSCVRYLLLSIRQRSPTALLHV ILFQQMIQLVL
6058	19959	A	6110	345	309	ASLIFV*LVEMRFLHSGISLFSNGKNGP TAFSQDPPG\SSVSKKAI I I IINKINK* IQHVTVIQIEVQWHNHVSIQPLNPELNR FSRLSLLSSWDHRHMPPHSANF*NFKN
6059	19960	A	6111	332	3	RKVLVCPPLGSAVAGFQVPARSAFQVHP LFLAEAVAVSPGCAPAFKPGPGQPF*KK KEEERKKKGRRKEEE/EEEEEEEEEEEE EEEEEGEEGEEEEEFYFLRAGKVKSRA
6060	19961	A	6112	498	191	STDVLLCQKARVQWCDPGSLKPPPPPG K*FLCLSLPKSWNYSHAPCLANF*FL VETGFCHVGKAGLELLASSDPPALASQS VEITGVSHHAWPMQEFYFI
6061	19962	A	6113	1381	172	RNIDSKAILSKKNKAGGITLPSFKLYYK ATVTKTA*YWHK/NH/DVD*WNRIENLE MRPHTYNF\LIFDEPDKNKQWAMDSLFN KSCWDNWPAINKRLKMDAFLMPYTKINS RWIK/DLNVKPKTVKILEDNPGSTIQDI GTGKDFMTKTPKTIATEAKIKHWDLIKL KSCTAKETIKRVNRQLTEWEKIVANYAS EKGLKSSIIYT*FKQI*KK\NHPICKWAK DMNRHFSKEDICGQOSY/VKK/CPASLI IREMQIETTTTRYHLTPVQMAI I KMSENN RCW*GCGEKNMLIHCWWKCK/LKL VQPL WKT VW/RIKTEIPFNPAISLLGIYPKE* KS/C/CYKDTCTRMFVAA\CPSVTDWIK KMWYIHTREYYTAIKRNKTDWAWWMLPV ILALCEAEVGGSLVLRSSRPAPWPTW
6062	19963	A	6114	3	155	HEKKISQVWVWCMPPVP/TILWWLR*EDS LSPRKRLRQ*SYDCTTVLPWATE
6063	19964	A	6115	47	368	STPTPSAFLCLAF/YRQRVVLCPWDWGA V\IQHTYSLPT*LSILKQD*PLNLLGT/ WSSRRVAACPENQIYRRNGVS/MLPRLV LNSWTQVILLPWPPKV/LGLQA
6064	19965	A	6116	1	592	RQRIFLLECGAISAHCNHLHPGSSNSP ASVS*VAGTTGVRHHAQLIFVILVETEF HHVGQDGLDLL/NLMIHPPRPPKVL*LQ G
6065	19966	A	6117	1	306	LWKTWLQFVLKLNILLPYNPAIVPLGIY PNKMKIYVHTKTCTQICIGALFIIAKT* KQPTCSSIGEW/IKKLWYIQTMEYYSTP ERNEPSSHENTWKNLKCII
6066	19967	A	6118	2	284	QTGVHWHQV\NLL*PETPG\SRDSPGSA SQVAGTTGMHQHARLNFFSFSFFLSFFF FFSLGKTLGLGLEFFPRWLQMSGPKKIL RLYLQNPKNKG
6067	19968	A	6119	2	315	SRVAGITGVGHARLIFVF/CFFFFFFLE RDFLFVPRVVGQGNLG*LKFPLPGLPL FSGTLTPKTGD*GAPLQPRVNFWIF*KK G\ V*YCGPGWFEILDLRGSPPF
6068	19969	A	6120	42	392	LQWRNLCSLQPLPPVFKQFSCRLRLSS* DYR/HAPPRLG*FCIFSRIRIVFLHGWR AGSRNS*PQDGSAPPQASQLAGITG\VS HHHTWAPHFLFFKNSGCSTQNR*QVHKV GDKETS
6069	19970	A	6121	2	202	VHLSDONQPKCE*MIEWIKMWHIDTME

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						YAAAIKKDKFMSF\ETITLGEETQEWKT KHRLLSLIRGS
6070	19971	A	6122	355	161	FIXYLFFFFFFFLLLLLFLFLFFF XXXXXXXXXXLXVFTGMIS*LVWCLYVYM NVYM*IYMF
6071	19972	A	6123	1	133	LC*PGWSR\FLTS*SACVGLPKCWDYRR EPLHLVFFFFFFFTL
6072	19973	A	6124	3	212	HPGLPSSWDYRCT*PCLANF/SCCCC*R LGLTMLPRLASNSWTQVILLWLPLKLAQ NTSLINNFYIDQMLK
6073	19974	A	6125	156	2	ALLTHAKNKAL\WLGAVAHDCNLTLEG *GGWIT*G*EFNISLGNIVKHHLY
6074	19975	A	6126	345	34	HPSTIHRVFCSL*S*SSPQARNNGSCLS SEHFGITGVNHTWLLFFKKNY/CILIK IETGS*YVAQAGLELLSSSNPPISGSES AGFTGMSHGIRPVSPSLKWS
6075	19976	A	6127	2	328	ARAYLPLCFIIFFI*VSVIYFIWLL*G LI*LNKRYLAHPK\Y*LNVSYSVSFCKT HFFPRHKEKAIQLGVVAHACNPSTLGG QGGWIT*GPEFETILTSMEKPRLYY
6076	19977	A	6128	1	341	GTRKFSYDRGKPPHPAKNRNLLFSIFFY FETLSCSVLLCEVTSSQL/CNSFHFPDL PSSNDPPSASRAAETTGACHHAQMIF* FFVETGPDWS*TPG/LLAVLPPRSPRML ELQA
6077	19978	A	6129	264	2	TAISENKVASRSEHRRHRML*LQVI/LI ALQHRSQRDNLSH*KN*KKKMLGEVAHA CNPSTMGQGGWIS*GQQFQTSLSNMVK PPRA
6078	19979	A	6130	1392	1157	LSLPKCWNRYREPPCPALCCPGWS*TPR LK*SSPLGLPKCWDYR/R*TTAPGLFFI SKSSLRSPAYSCVTVCTLQLSHH
6079	19980	A	6131	383	108	MRLCSQPHHVDVFSLETESCCVTQGV QWHDLSLSQSPPPRFKRFSSLK*LGAIL LLPSSWDYRCTPPHPAN/LCRF*HGPVC LYMFGEKVTP
6080	19981	A	6132	307	1	LKTLPALCELESHSVSQWRNLSLQPPP LRFKRLSYLSLPSS*DHSH*AHQANF\ CIFSRDRETGFHHVQENLIMLIVQSS GLGFSIFATLLAVMQLV
6081	19982	A	6133	351	66	RWSFTMLHRLLLKS*LQ/CDPPASASQS AGMTGMSHHTRLHNL*F*TANNLTQSHTK FYSFISLTPHFAINVTNYIFLYTSINI VCIFLSFKFYARI
6082	19983	A	6134	2118	1392	FFCKGK*IFIQCPDWGG/DLCV*QEKIQ KKTHTGDKYV*LF*KVKPITKI*RQI HTSGNTDAQLSYKENHDQGH*QAKNFKF FLFFVVFYLRRL/NSVTQAGVQWRDLG SLQPPPPGFKQF/SCLSLPSSWDYRRPP PRPANFC/IFE*RWGFTMLARMVSIS*P RNPPTSASQSAGITGVSHCTRQEFKVK GYHFLHLLPSGCLFLFYVFYLYACLLYVS VYYPLRQQESRKISKIEMFLTTWH
6083	19984	A	6135	383	47	HLFLNFYYLSHYNYLYYFLLHLLPSSP KIFFFFT*KIIFFLIKFNKVF*NLSF*K KIF/IFSYTE*FWPP*NFF*KPPFFFF FFFFFFFFF*QTLFLGGCGYNTKLR
6084	19985	A	6136	2	196	TRPSILVTALYYLYIFTTTQWG*\LTHH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion
						JNNIAPSFTRRENTLMFIHLSPILLLSLN PDIITGVCS
6085	19986	A	6137	700	433	FLRWSSASVTRLE*SGAISAHCILCLLG SSYSPALAS*VAGTTGTCHHAQLIFVFL VETGFLHVGQDGLDLL/NLMICPPRP VLVLQA
6086	19987	A	6138	377	298	QMKWKLLLLFRYRVLLC/HPWSAVA*LQ LTAASN\FGLK*SSCLSL/MLTMLVLNS WPQVILLPWPPKVQEL*ATAAYTIKMWV
6087	19988	A	6139	1	199	LYTTYFVTKTLLTSLFL*IRTG/YPRF RYEQLIHLL*KNFLPLTLALLI*HVSIP ITISSIPPQT
6088	19989	A	6140	381	28	STPNRLIERQEDPPES*NTNPPGLPRKT PSFTKNPKINLARWGGENPPNPEEKPR KVPESPKRKKP*TKIRPLPSSPGDPTKP P\LKKKKKKKSVVPATQBAEMGGPLKA RSLRL
6089	19990	A	6141	1	209	LKLLASSDLSTLGSQSAGNIVGMSHCTQ PKINMGILLKLVYRFNINPVKTPAGLF/ TKKKT*KTEIDKRILKFIWKCTEHRIAK QSLKRTKLEDFLLNFKTYEATEIKTS* YRFNINPVKTPAGLFKKKKHEKQKLTSG S
6090	19991	A	6142	3	282	QGIFLTKRVKNF*RGKFKTLVKKNQGD KKGKNPPGPKIGKNNFGKTPFWAKKI*K FNLI\PKKTPPFFFQKLKKTGVKFFWAP KGPKGFLSKK
6091	19992	A	6143	382	158	FFF*DSLAVSAPGVQ\WHDLCSL\RPLP PRFRFWCLSLSGWD\YRHVP\QYPAK ICIFSRDRVLPILAKASRVSF
6092	19993	A	6144	185	316	PCLANF*IFFCK/NGGFSMLPTLGLNSW AQQILLPKPLKVLGLSA
6093	19994	A	6145	489	231	SVA*AGVQWHDHS*LQPQ/PLGLKQSSC LSLSNSWDYRHMAPHTNFKKFFVETG VLSCCPGWSSTPGLKGSFCLNLPKF
6094	19995	A	6146	179	1011	GTILNPQSLFFKPPFFSTLIFLKTLLC CPGWVSNSGSSCRSLPKCWDY*HEPPH SAL*TFPWPF*LVKDTSIHSTQLLKA EIFSASLDAAPSPTPYIRTHPSSGLQRWL LDAARSPTPYIRMHASRLQRWCSTCTL LPSPSYHTPA*AMTTASSLISPFPLPP PAHFSQCRMTFCLFVL/CLFEMESRSVA QGWECSGAILGSL/QPPPPGFK/RGFSC LSLLSRW\DY\GHAPPCPG\NFCIFSRD G\VSLCWPGWSRTPDLVHPPRPKALG LQA
6095	19996	A	6147	348	3	GYHKTINWHCCMSVFANLTCGFNAIPK /IPAKYFVDPDKLVLFKTFWKGKRPRIAG TILKEKKVRLILPNFKTHYKATVIKIG W*W*NNRHNHWNQIGSPEIAPHKYSQLI FDKEA
6096	19997	A	6148	22	228	THRVALFVRT*NWKQPKCPSTGEWNLTL CYIHTIEY*YSAIKRNKLSIHVKT\WI DLKGIVLNENNQI
6097	19998	A	6149	406	279	RSIQGSSSHASA/S*VAGITGARHHTQ VIIVFLVETGVMALTY
6098	19999	A	6150	406	10	MRYHFTPDERLKSGLKLEYW*GSGETR SLIHCWLEYKMSHPLWK*/TVWLFPIKL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						NKNVPYGPATSLLDIL*EK*KHMSTKNTYK*MLQALFIITKNWLLSIKRRMTKQIMVYSNRNYYSTIKNELPIQTRI
6099	20000	A	6152	367	1	PTPWAEAGGSFKPRR/LQ/CPN*PPMCSTPAWAPGSPVSKKKMQFHRRMGHVSSAWWPCGADVRLRAGYVRHRERFPGLPWAAGGRDEVIRCLTVCTACGEDHPGSHLAGPRGGGFP
6100	20001	A	6153	441	38	ILNPGEAITSEKYVQ*FNEMYQKAKRL/QVNRKGPVLLSYNA*POVAQPVSQKLNKLGHEVLSHRPYSLSLSPDYHFFKCINIFLKEKRFYNQDAENAFQEFTES*SA/D FCTTRINTFISHWEKYVDYNSRYFD
6101	20002	A	6154	308	121	GESFPAEKTFPKENDYRWPSFFQWSSVL/CKIHGLMLPRLV*NSWPQAILLPWPPKVLGLQA
6102	20003	A	6155	1	420	QNLQPHWKTLRQF/LYKVKHMMLSIPAIPLLDIT*GRCKPCPYK/ESIC/RMFIEALFIIAKKLKLSKGSAGE*INKV*DIYTT EYSAIKSNKQLTHTTTWIKLSITPSE*SQT*ETACFTMLLIWHSRKGNIIVTENRSMF
6103	20004	A	6156	77	415	TLGLKPTSSSHLSLSKCDYRQEPFPCPTSEANFFFFFGGEFFFWSPS*LKQFFVFMG\FTMLPRLVLNSWPQAHILIP/ASASQSVGITGKSHRAPQKLTFFFFLGGNFPGPQAGCPGAESNYPEP*TPGLKAFGLNLSKCLKYGDSPTAPGKLEIFFFKWGGVSPSCASRVLPQPR
6104	20005	A	6157	436	206	LWYIHTMEYYSALKKNAILIHTI\STWMSLENMLNEIKQENHKRANI*FHLYEIPRKESRMEVNQQLGRRGIWEFTVY
6105	20006	A	6158	416	50	RFFTHPPAGEFFSPPPPKNIFPPPP*KFWGGGGKASPPQKKFPLPPQNGVLCFPPHKKK*FFPPPEKTVEPGPLHVGQRPPQS\PFLCYPPLSFFLYFCYFIFFPFVFFHFLPFFFFFIR
6106	20007	A	6159	443	145	FFFFSIRFLFVVVVLVYQG*EYLCFFMT*IGVLLFLFEICEFFFLLVGILFGMFL/YFFATASPLFFFCFFFIFFFFFFFFFFF FFFFFFFFCEKS
6107	20008	A	6160	322	2	TQDKNKRHRARHIYKRARKSARD*RSIVHR*K*KVQKRNEY*PEGTLHTCIALSQGNNI*DA/HSQE*WITPVI*TLWEAEAGASRGQEFKTSANIVKPDANANAW
6108	20009	A	6161	421	57	FCEMKFTPGNNAVNIV*PTTKDLEY/WINI/DKTVAGCEKTDSDNYERSSTMGKML\SNSIAWYTEIFRGRKSQMLMWQISLFSFKKL*QPLQYSATIALIRQPTTSRQDPSPAKRLRLPEGSGDH
6109	20010	A	6162	333	41	GAWACHLHVGAALNAPTGPLSRFHEEPWSCRTAGGGSRLLELSVFFVQMGSCHVQGVGFFCIFCR/DRGLAMFSRLVSNS*TQGICPPWPPKVLGLQA
6110	20011	A	6163	2	423	KINNTKSQCFFENILKIEKTLNLTKE\REDTNY*YWE*NMDITVESTDIKRIIRNTT\ETLHKFDNL
6111	20012	A	6164	434	5	ICHIFFSISKLLNLRPVSKLFFSINF

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						EGPELYYL*IHFN**GKCLSFLFLQNI CIGFFFNSEFMQI*SYFLRISLFIPVSP LLG\FVQIFIVSINILYLSI*LRLFFSF FLSLFLFFYYTSLFRVHVHIVQVSYI RIHF
6112	20013	A	6165	1238	1017	ETGSHSVTQAGVQLHNSSSLQPAPPRLK *SSYLSLLSSWDYRRTPPQPAN\FCIFG RDKVSPCCPGWSRTPEFR
6113	20014	A	6166	504	210	FFFKTRSHDQGSLOP*PLGLKGSSCLSR TLPHSWD/YRV/PPHPAKKYKNIFIFF VETEFHHVAQAGLKVLDSNSPVSASQS VGITSISHCAQPILCQF
6114	20015	A	6167	258	65	YKTKNTTSIFSLPSSF*TQILTF*NTYY YYY/CRDE/SLAMLPRLVNSWPQVILL PWPPKVVELQV
6115	20016	A	6168	1	156	LARMVSTIS*PHDPPAPASQSAGITGVSH CAQLFFFFFFWRQPRFFLRAGGQGRDLGK VKPLLSGVRPFLS*TLPTGRKSGPPTH FG*VLRE*FGGSH\PVSSLW*QSAGITG VSHCAQLFFFFFFWRQPRFFLRAGGQGR
6116	20017	A	6169	3	285	HASAHASGNILSYVGSFISLTAAT\LI IMI*EAFASKRNVLIVEEPSINLE*LYG CPPPYHTFEPPVYIKSRRIIRSLIDQDA ARKETQGAAD
6117	20018	A	6170	645	15	LPFTYCSPCRNFNLSLWQERDSNNPLG/ ISLPHSDKITFNP\YYT\IKDALGLTSL HSLKDLHSFPHETS*GPQAYYSL/QPT PLNNPSPHARPEWIFPYCAYHNFSGSGP LTNLGGVL\ALLL\SLHLPKQ*FPHPPS YPNKQRH*YFGPLRPITFIDFLGRRPSF ISNRESGGQPVSYPTLIGQVASVLYFT TILILIPTISLIENKILKWA
6118	20019	A	6171	409	25	YTPPGGKIFFKSNPGSKLFPFPPF/PPF FSPFSP*KFFFSKPLNFFGGFFPFPFP PKRFFSKNPPLVFFSPPFKEKVFPFP PLNFAPPRVFLKAPPFFFFFFFPPKGG EVKWLSEALDCKSKDRG
6119	20020	A	6172	73	52	VQLKCRIF*DKVLLCHPGWSTVARS *LTATSRSSCLSPSSWDYRRVPPCLAS F/SF*YIALNN*A*AIILPQPSKVLGL* AVAHAYSPSTLEG
6120	20021	A	6173	325	470	IFTFFFLAFI*FFCRNR/SLALLPRLV LNSWLQAVLPPWPPKVLGLQT
6121	20022	A	6174	2	228	TLEDNSTIPCKTIQSSCTPWYVTQKAA CITLLSM*PKKLWYVYTKSCTQMFIVAI FIIAKNWKQPRCLSVSE*INKLWYI*TM E*YPVLKRNELSSHEKTW/MEM*IQLLI ERSQS*KAVVCLHKKLHTDVYSSYIHNC QKLEATKMSFSKRMNK
6122	20023	A	6175	3	408	RYLTLAIRDQMIIITPVSYHFVPSGDYGO KDNNKCW*RG*KMGSLMHC*W*CKMVQP LWKAQWQFLK/DVKRRAILFLGIYPREM KTYVHAKTCMHIFTLALFLYVHLNALIS VMDWMLGHPIDEEISRDSYSCVCLL
6123	20024	A	6176	2	237	WVWWLIPVFLAAWEAEAKGLLELGSSRL *\WTMPLHYSGLGNRRLCLKKKKKKFK VFPPQKKKKKKKKKKKKGGAL
6124	20025	A	6177	387	154	AVVQWRDLSSLQAPPPGFE*FSCLSL\W

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						DYRHKLLTSGDLPASASQSAGITGVSHCAQPLSLFVFFLTNQRFAALS
6125	20026	A	6178	1	239	FFFFEMECLTVSQAGVQWYNLHSLQPLPGFKQFSC\LSLPSSWD*RVPTSRPAKF/CVIF*DGVSHCQPGWSAVVQPLH
6126	20027	A	6179	325	50	RKFPPLTWRRVSFFSLRLSSTDWMPTPHRHIGGIICVTQSTDSNIGLIQKHPHRHTQKNV*PNV\WHPMAKSS*HPKLTITVYPLSTWHTYTSL
6127	20028	A	6180	157	338	SQHFGPRPQEACSSSEVRDQPGQOREFFHLYKN*KEITQVWWHMPPEAQDY/LEPGRSRLQ
6128	20029	A	6181	3	273	HEGQSKLETFWKGFITI*DVIKNIDDL/WRGVKIPILTGWVEKLIPTLINNFVFKTSLEEITEYVVEIGRELELEVEPKDVTTELQSHEKT
6129	20030	A	6182	2	359	YYPAILLLGIHPK*KNSIYQMHTCTHWF TAVLFTIAKIWNQL*CSSMGEWIKM/WMHTHTHTHIHTMEYYVPIK/NEIISFAATWMELGVIILTEIIQAQKKTGIFSHLYVGAKIFDYM
6130	20031	A	6183	3	211	NPGKLSVSNQDCFPWTPCFPMGRCP TLLF\SFYGGQAIPLITPSVGTQIFRLKM/PEVTHHFHSFP*EPLTAAALNQPSLPLSLLVDF/RDRGLFCHLGWSAVD*SHLTALNS\LVTQLSCPSFLSSWDYRRMLPCLGNP*IFRLKMLKSLTIFILFHESH
6131	20032	A	6184	707	384	LQIFFYNRVKCVKNKSTQNQFYIFSR IYMHANRHGKYEI/WIIKKMPMREG*AVQLRMKVVKIKKNTHIKLGVVVHGYNLSTLGGGGRIT*AQEFKTSLGNIALRLHLYT
6132	20033	A	6185	720	363	FFFWGRSL*TILF*/QTGSHSVAQSGVQWHHHSLLQP*TSGLKQSSHLSFQSSWDHRCAPPRVANFFLDFCRDRCVAQAGLEL LASSNPPTVASQSAGITGGSHRTWPFWDILGIMYWGC
6133	20034	A	6186	439	66	KPKTLGSKKVNNSNRPVPPGK/PWGVG PLGPGP*MGGSKP/S*NPSPPPLFKTRFGFFPPG*RQGHYSGFLQPPPPGKTFPPSPPKKWGHKKKIPFQKKKKERKKRNII GSWTTSETVGNPAPW
6134	20035	A	6187	83	287	NKMFKIFRFRF/CGFLGQSHSVTQGGVQ WHDHSSLQP*TPGLKRSSLPTCWDNRHK PPHLVLCFYRL
6135	20036	A	6188	290	609	RRMDDPPFFKYFFERRVLVCHQGC*S*\K*SSHFSFPCSWDHRCV/PMHPAN\FNFFHTDKSLTMLPRLVSNWSAQVILWPLP P*VLGFAGMSPCPQPPSQFCIEAV
6136	20037	A	6189	2	371	RYIFEKVFAKSELTNDSLILSGKSGI LWKKRLSLFS*Q*SYKWFSLGAIYCGMH*KRFLGTSIL/FTE*VETGFHHVDQGGLELLTSCETLASAY*SAGITGISHCAESQSTLKKYIPGSTI
6137	20038	A	6190	531	205	RWRFALVAQAGVQW/HDLGSLQPLPP*F K*FICLRLQRSWDYRCAPLRPA\NFFVF LVETGFHHFGQT\NLQLTSGDPPASASQSAGITGVSH*ARPVVFIIFTALYK
6138	20039	A	6191	52	375	NRCETSFLFFFFEKKFWFCPPGGGEWRN

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						LK*MEP\LPPGLKEFSCSLTLRRGNG*GP FPPLQENFGVFRKKGVPHCNPG*FQTPD PRELARLTSPRGGDGGGRPPPRVK
6139	20040	A	6192	3	158	FFFLLLNCGLKKETG/WLGVVAHACNPS TLGGRGGWLTTR*ELKTSANMAEPY
6140	20041	A	6193	2	54	FFFETESHVAQAGVQWCDLGSLLQPPPL GLKEFSCSLSSWDYRHTPPHPANLFF F/SFLVETGFRHVQAGLELLTSGGPPA SASQSAGITGVNHRAPVEVFKK*RVSF REGWSAVV
6141	20042	A	6194	1	323	FILPSSWDCMCAPP/RPDWVLYFLVETG FHRVGRAGLQLLTASDLPASAS*GAGIA DGVSLTQCSMLPMLECRGVILARYNLHL PAACGLPKCRDCSLCPAATPSRK
6142	20043	A	6195	619	243	SPETGSCSGAQAGVQWHDLSLQ*LG LK*SSYLSLLSNWDYRCA/PPRIANFLFF VQAGSCHLAQAGLELWSSCHLPALVSQN AGITGVSHHARLAVAWKRTPLYGLPSRI SNLCVLLKFLFFLY
6143	20044	A	6196	385	19	GGHFGAQEISPPGVQLFFRLHFLSNWGF KRPPWPPG*FF/VFL*KGFPFPGRVVP PSLFP/SDLPPPAPPKGWVSGLRPCPRT FFFFFFFDKEC/RLSCPANFCIFSRDGV SPCWPPWSRTPDLQ
6144	20045	A	6197	498	437	ENI.QSSINLVDKAMAWFERIDSNFDRSF TTVKMPSNLTSIIINACCGEIFHERKS*S IWQTSLLSYF*KLLQLAPPLLATTILIS KEP*TSR/QDRLLLAEG*D
6145	20046	A	6198	79	394	SVKLLALFFFFFGENFCFAPQVELKGN LG*LNPPPPGLKNFSGLT/LPKKWELGG HPPPPSKFFFLFF*KKGMAPFSQGWFKT LGLNQFACLTLPKGGNLRREGP
6146	20047	A	6199	2	313	SASHSAGIIGESHCAWPIMPVYSLVLNF FFFLEKKPPFVTQLEGQGNLG/SMEPS PSGLKGI FCLGPPKKWELRAPPCPGYF WFF*KKGLPIRPGRFWKSVP
6147	20048	A	6200	62	732	AFQOARKGTQ\GRLSSPAAGALP\PVLA PSGPPPLPA*\GSSS\PASVAPYPPQAT G/SPPTPPGELRRGWSKGLDHPNRTF YCWESSEP/PPN*GQS*APGGVNSEGRG Q/LPPSSIARCVP*TPSHVPPHPLAFPP SLPHGPASRAPPTGSSDLSASAVSAP GREGHP*GTRMVPQAGRQKPGHRGAS* GSSCSKRTLSPLSRQSGFQSRCCFHPP RQNH SRC
6148	20049	A	6201	424	7	KNMKRSPISCVTDRDPQIKITMR*HYTGI KMANV/RLTGNTKC**GYGAKGPLIQC* WECKIV*PLRKTAWQFSQS/LKIV*/PY DPAIALPGIQLC*KCTS\KKNCM*IFIT ALFIMAKKKQKPRYPSIGEWKYLLHL
6149	20050	A	6202	371	144	RWALPRRTNF*FFVETRSLHVAQGGVK LLGSVSPPISPSPSAVITGVSYCAQPYG HPFELSFLIEYEYIYLDFF
6150	20051	A	6203	409	110	LRRSS*LCHLGWSAMVQSWPT*FKP*LL GLSDPLTSASRVDRGMPPCPRNFIIFD M*FI*CVVCV/RTWGLIVLPRLVSNFWP EVLLHPGPSKVLELQV
6151	20052	A	6204	15	221	KASRKMQIETTLRYLSPMRLAKMQMLI

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						NTSCW/RKSQETRTLLC*W*EGKMVQPL SKGIWPYLIQAEYP
6152	20053	A	6205	23	371	KVACTCMFTTVLFTIVRL*NQSRCPSTD DWIKKM/WLCVCIYSSVCVCLYVCIDR* IERHDIYVYIMEYYLALK*/DEIMFSAA TRVKLDAILI*S*ITQNVKCCIVSTHSGN LIMVST
6153	20054	A	6206	113	417	SAVTLLVIYLNLDKTYVHTKTCTQMFTA ALFIIAKI*KQLRCPS\LIWIN*C*KEM SYQAMKRSYARNLWSSKKLWRNLKCLLL RERSQSEKSAYCVIPTI
6154	20055	A	6207	510	167	GLGQAISPSLPKSGIGAYGFGFFFFFK R*DLVCCPG\SLNLVASSQSSCLSLPKH WDHECEPPCLAFFFFLL*RQGLAMLERI LPLLKALASGGGMAKKKCIYFSMKIHL QAA
6155	20056	A	6208	418	40	SYTHTHTHTHTHTHTHIP**LTGS/RLQ GICRKGSRKHPRGLSQLLP
6156	20057	A	6209	1	258	SGFLLS*VPSVRDPTGNRTV*LTWQPLP APLEF\CPRLS
6157	20058	A	6210	229	310	DFSEAQSKRQCGGGISNVNHPGVVLKPV IQHF*DGVLCCPGWSAVV*SQLP*LPR LK*SSQLSLPR/SWDYRHLVQ\HPANCF VFFVEMSLAMLPRLVSNWALAILLPQP PKVLDDWLEHHTWMIYITYATTLP
6158	20059	A	6211	496	1	CCQESFEILGSINSFPGPLKKGGVKNMR PGAGPTLNKRPFSDNPLQPGRRGGCFPF VSQRGSQKDRVPPKWWFFFFSF*DRVSL WPPGPSARKPSWLPVASTSR\V*QSSCP PLWFPGPPTMVSYYYYF\KRQDLMLPR LV*NFWPQVILLSQLPQPKVLRLLQARA
6159	20060	A	6212	3	340	VTAGITIIIFMI*EAFASNRKVLIV*EPS I*SLQV/*WRGLLLGSPPPYHTLEEPG YVTSKRKRKESNPPKLASSQPHGLHDFP KKKKRGGPFKRILEGAPFGGGWGHREFF P
6160	20061	A	6213	60	493	KSQONFFCFETESRSVTQAGIQWHHFSS LQPPPPGFKVISYL/SLKSNFSGYP*DF FCNGPPCS*GPIRFTYYICVIPSSWDYR RLPPHPANFCVF\IKTVSPGWSQTPDLR
6161	20062	A	6214	414	1	LCNGRPGLLVSPPLGEELIPCLPR*KL GPVRVL*\KGGPFL*SSFAPFF*EMESH SVT\RLCSTRAILVHCNLCPLPGSPDPPP SAS*VAGR IARAQKVEAAVSHDHAALQ PEQHSETPSQQTINKNNQTKLTQKYPF
6162	20063	A	6215	2	403	SLLLPLVQLPLRLCFFFLKRGFNFGAP DKREWGEEG*\LKPWLP*NNFSGQTLR RSGD*RKTPHGGVNLVF*EKTGFSNLGR GGLKPPPSGNTPAWPPKGVITGTTPP PPVFCFLGFCENTNLRAKKFI
6163	20064	A	6216	2	388	KMEQTLWKTDWEFLTKLNILYPYSPAFALGIYPNELKT/C/CYTNTCI*KSIAPL FIVARTWKQPGCPLRDGWLNLGCIQAL EYYS*KRNEL*NHNMAYKKLILFLLR QEDRFSLGVOEQPKHNGEM
6164	20065	A	6217	363	302	NKEFKTTLANMGEPPL*KRGS\MLAR VVLNSLFHDSPPPASQKAGIPGVSPPPR PLFFFFFLETVSHYVAQAGQLISNYDL

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						KLPSCLSLLDTWDRH*PPYPVFKLLNSTYKAC
6165	20066	A	6218	576	6	RAVLRGLLVLLLTCKHTFFLEPPRQSLAL LPRVGVQW\HDL\GSL\QPL\PPG\FKQ FS\CLSI PSSWDYRYP PPRPANF*FSV ETGFHHVAQAVLELLTSSDL PALASQSA GITDLGQSETIHGGSGLDKPPDHKVDKG PTEERACLLSYSAGRKYKEYHILPEQGS EPPHHGDILSISFQAASHIAQTPPAHT
6166	20067	A	6219	44	496	GFRVDPVRVPRVRLNS*PRDPPTSGSAG ITGV/SSHARP*NIFT*KLGISFLVFW GFLFLFFVFCFFFFWKGGFLLVAQVEGK /WPKFGLIEPSPSGVKEFFFNPPPEGWD \YGLAPPPGVIFWVLIKNGVSFFCRAWV QTSGLSWINRLNLP
6167	20068	A	6220	1	421	QRGRLTAISRETSFTLLVAQAGVQWHDLG SLQHLPPGFQGFPCSLSLST\TGNC SVT QAGVQWCHLGSL*PLPPGLKPSSHLSPS SSWDYRL*KPHQGS*VCVT\GAASPEP NTMTAWNKPDIRMKETLLLPSSSEKML
6168	20069	A	6221	3	36	AYCIVKPSP*PLTGALSALLMTSGLAM* FDFHSITLLILGLLANTLTIIY*WRDVT RESTYQGHHTPPVQKGLRYGIMLFITSE AFFLAGFF*AFYHSRLGPTPOLGGDWPP TGITPLNPL*VPLLN\TNE*LA*GVSIT *AHDP
6169	20070	A	6222	895	13	ANSWANN*FELATQIAFSGRIPLTDSHL GLLKAHVEAPI\AGLIVLAAVLLKTGG MLYTASHSFSNPLTK\HIAYPPVLSLIE EA*FITSSHLPSDKQDLKS\LMAYSS\I SPHSPS*LTPI LIQTP\W\SFNGAGQFS IIAHGTYHAYITYSA*ANFKITERTSQC ACINPAAQGLSNS*LQILGLFE*LPRQA \SLTMGLTPPLINPTGENCSVASNORFS /WTQISLLL PYRDSTILGSQALYSYIF TTTQWGS LTHINNIPKSF TRENTLMFI HLSPI LLLSLNPDITTG FSS
6170	20071	A	6223	68	405	HSYALVYNPVGIRVKVHLSKCILYTWHI SNSSQEVCEMPNLNLKRVP TTLAPRF*N IS*GISQLGAVAHTCNPSTLGG*GRW/I QQLKTS LANMAKPHLLKKKKNFNFPK RG
6171	20072	A	6224	591	283	GTSTQAGVQWCNCGSLQPPPPGFKRFSC LNLPCSWDYRRVPPHLANF*FLVEMGF HHVN/QAGLELLTSSDPPALASQSAGIT GMSHCARPRVAF*GEKNHRS
6172	20073	A	6225	302	173	GFFSFFLK*DR/SLTM LRLVLNSWAQ VILPLWPPKVLGLQA
6173	20074	A	6226	417	81	TQTRGPPPPFLGGPPSGPERTVPPPRG GVPQTGSRFFLFRQNP GPALFPKN/EGG F*KKFGPPLPPF*KTPFFFTNRGNPCPF FVGENPQAPPVFGGFNPFPRKKKRNDF LS
6174	20075	A	6227	41	474	TDATETFHFTSKH\HFGF*AAA*YWHFV DVV*LFLYVSIY**GSCVPHPA
6175	20076	A	6228	503	28	AAHAPFRVRKVIGH*AFFTQRCNTSRH* I IKFPKDKDKARILKGAREK/RTTYNGA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PIWLAVNFVETLQ/A/RREWHDMFQMP KEKTFYLRILYPMKISFKHEREIKTFPD KQKPRDFISSRPVLQEMLKSWPGARVHT GNPTLLGG
6176	20077	A	6229	418	175	VSPLSPLKILFFPKGLKFWREGGPKCPP PKKRVLPKK/PPAMF*IPPPKRKSKLP PPRKIWPPQGIFKSPPPQFYFFFFFFF
6177	20078	A	6230	45	308	ACVRLKH*TDN*QPNIYNQP/HKSLLP* KKKKKKKKKKKKKKKKKKKKKKGGGG FKKKPGGGPISWGGEKIIFFFFGGKKN TLGIF
6178	20079	A	6231	440	209	IQHFRGSPRRGLLGPPEARASPGQHRESR SFLKMQP\NKKFS*VWCTPAIPASPKV EARESLEPGRRRLHLTALQPG
6179	20080	A	6232	419	2	SSPPPPGGKFF*KKPGKKKFSPPKKRV FSPP\PPKKFFFSPPKA*NFWGGGQKFP PPKKGVFSKKPKGVFKTPPKKKKFFFP PGENWGPPRVF*KGPPFFFFFFFFFP FLSFNVNILEKPVQAPCLT
6180	20081	A	6233	448	112	QSARITGVSHRTRPMLRTSTPLSATDRN AGQKISKDIADLNNEQDHRDIYRNSTQ *QQNTHSFQAIRNKIDPILGHKKMLTH /CKQSDQTWNKLEISNKYAKPQIKHTI K
6181	20082	A	6234	2	351	MDQGII/SDFESYYLRNTFCQAIWARDG DSSDGSQGRKLKTFWKGFSLLDAIKHTE DSW/EEIKISTGVWKLIPILVDDFEGFK TSVEE/VADVMDLSRELEL*VEPEDGTE LLQSHSQT
6182	20083	A	6235	3	252	FHTYNSLLVCHSNLCYQNSLLFFIIH* / CI/HFHS*AKVSIWKHTYTHTHTHTH MHTHFFQATDRKICNVVMFSVAYIHKG LQ
6183	20084	A	6236	3	294	IITF*LPQLSGYIEKSTPYECGFDPISP ARVPFSIKFFLVAITFLLDLEIA\LLL PLP*ALQTTNPLIVMASLL*IITLALS LAYEGLQKGLD*AE
6184	20085	A	6237	381	121	PVPASF*FFFFYRDR\VSLCYPGWSQTP GLKQSSCLGLLSHWYKYDPPHPAFISF LLSSSLLWVL*RPVLLCATVPAPLDIR EQ
6185	20086	A	6238	395	62	FFFFPIPKFFPWGPNFFF/PLGPPPFGLF FPGSFAPPSSHFSPPD*NFRPPKNFPPG GDLFPQKKGDWFFPKKRGVFFFLGGFSK FSGGPPPSLGPQKKRPFKIKGPKKPCF
6186	20087	A	6239	1066	761	SFFLRWSFLLVTQAGVQWCDLSSLQLPP PGFK*FSCLSLPSSWDHRRPPRLANFC IF/M*RWGFSMLARPVSNS*P/CSDPPT PASQSAGITGLSHRAWRLVFL
6187	20088	A	6240	390	27	GELPTPIYLAPPASPKGVSGGSPPSRV KFFPLEVPPPPPGC*PGFFFYIWPQGG ARVP*QIRFFSLRW\PPRPTRPKNPHL QVGPLRLCLSPETGGGVIKVFRGSLK KKRAAASRN
6188	20089	A	6241	366	1	KIKNFDRPI/TSKGA*SVV/RNLPTKKS PEPNGFPVFCPTFKKKLTVPV/SKLFP KF*KEGILPNSFF*SSLALIPNPFYPSK KKKKTKKNYRAISLMNIDEKIHKY*QT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						EFIRSTLKVLYTITK
6189	20090	A	6242	23	439	IASGRPFFFFFFFFFCLPPPPGPNPSFS FLKKKKKGGGGGGENPPNPPGKAPNPQGV GVPPFPFPPPVFQKNPPPPFF*KNPPPS PKGPPGGPPFFFPGGGGGPPPT/PYFL KKKGGWGGPPFF*KTNPPPKGEITPLVG
6190	20091	A	6243	20	261	WAQETLKKFSCLSLSSWNRYRCAPPHVA N\FVFFVETGSYHVAQSGLELLDSRDPM TGESHHQAQPHFC*ILYTGESQRIL
6191	20092	A	6244	376	76	LLPRLECSGVKIPFSLSLPSSRDYRCV /PTMPNF*KFFVELKFNSL*R*GLTMLP RLVSNNSWCQVILPWPPKVLOGCATTG LTDFTITTFKGYRHGDTY
6192	20093	A	6245	222	233	KSFYFALIFEKNFCYVKKSQVGLVFFSK VKVLVRPFFPMVIKKNP/FNPL/RFFF FFFQDRVLLCHPGWSAVV*SKTLS
6193	20094	A	6246	2	358	EIILTFQSY*ENTFNEAITAIDSDSSD GSGQSKWKSFWKRFTILGAIKNICDL*D *V/KISTLSGVWKKVIPSLMDDFEGF\K TSVEEVIADVVEIAR*LELEVEPEDVIE LLQSHDKT
6194	20095	A	6247	3	322	PDHSLQLTPTPGFRRSSHGFSSSWDYR LEPPHSVCVCVCV\FCVIYFFFFLEKT GFGFVPQAGNLGVKRIKFA*PPGGVEI PGLTHTPGPWGGPIKKGKANPAP
6195	20096	A	6248	1425	1280	SLDFQGLALPGWSAVV*SCLEASTSR\ VKRTSHPSLNTWVYRHALPRLANSVYF L*RWGLTMLPRLGSNS*TQAILQPWPPK VLAL*ADEEMKAKGHISTKWGGQTLNPQ PDCGATSVYSLPIRKFO
6196	20097	A	6249	189	336	HAFPPVSVISLSCQKRRR\WLMVAHTS NPSTLGG*WGWA*GEEFETSQ
6197	20098	A	6250	2	300	FLPSFMGFVPVLGHGRASTVTPSEPLSL PFLPAEPFLFFFFSLFRKRESIFGA/P GLEGQGFNFLEPSPPGIKEIFWPNPPR GWELKIWPPPIINFCDF*EKTGFTMVAR AGLKL*TGLEGQGFNFLEPSPPGIKEI FWPNPPRGWELKIWPPPIINFCDF
6198	20099	A	6251	1	198	LTGRL/SKCEVVSWRFDVQLKDLKRWQN HLLLSQQLACIVLTSAGIMDHKEMR*KH TGKSLGFFF
6199	20100	A	6252	11	214	SLRLKSSSHLSLPSSWDLRCELPHLAN* KKKKKL/CKN/RSLTGLPKLVSNWV*T ILPPRPPRALGLRA
6200	20101	A	6253	402	3	KKGFVLSQVEDKDAISGSFNPGGPGEK IPPPQPPEEVGPPGPPQTRGNLGI/LG N*GGGGGF*PPGAGKSPAPGPQKG\PF GKDKREKPYGPPPKLFFFLRQSLCFAQA GVQWCDLGLQPPPPPRFKQFCL
6201	20102	A	6254	362	78	VGVN/MTFFPQHFLGLSGIPRRYSYDPD AYTT*NTVSSIGSFISLTAVLIMIFI* EAFASKREVSVSYASTNLE*LHGCPPP YHTFEPTYVKVK
6202	20103	A	6255	357	2	DLSCHSHGEATQKHSEKCKASCTHMFIT ALFLIAKHWNQPTC/PHTMEYNSVIK/N EQTIDTTTTWMDLKCIMRHEQORS*KNS VLVCFHAADKDI PETGQFTKERGLMDLQ FHVAGEASH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6203	20104	A	6256	2	305	QWCNHSLLHSPGERETVSSLLKLPKAWN PRHMLLCPTTSFILRWGFIYVAQAGFDT RGHASL/LA*ASPSVGITSKSQVRPVH DIACFHRESTMFAENFN
6204	20105	A	6257	335	3	GPFPSPPPGVTPISCFPPKKGNGRGP PRRGKFWIFKKNNGSPG*KRRVLFDPDG VPPPRPLKKGGLKGGAWAKIFFFFFLRQ SHSFTQAGMQWCNLSLQPPPPGFK*F
6205	20106	A	6258	219	2	PTLSSQKDTKAQRLYSFPLTTTKDERLV TLVS/WPGVVAYTFIPSTLGGQGRWVT* AQKFETSLNTVKPPSC
6206	20107	A	6259	306	117	SFELLGSSDPLISALSSWDYRCAPSRLA NF*FFVVCVEMGSSYIVQ/SWPQ*ILLSW PEKVLRLQT
6207	20108	A	6260	572	269	ETDILSVAQARVGGHLHLSLPAPPPGFT PFSCLSCSS*DYRRLPPRA/NFFVFSV EMGF\TVLARIVSIS*PRDPPPSGLP*G ALGLPGVSLRPLCLLLK
6208	20109	A	6261	357	116	FAQAGLELMGSSSPLASASQSVGITGMS HCA\RLLLFFCGGRW*GG/LK*FSCLSL LSSWNYRHEPPHPANLCIFSFNTISY
6209	20110	A	6262	3	337	HERHERHERHEQSAEITGVSHHAGGGIG LLNFFLFLFFEAGSCTVT*T/GV*WHDH GPQ*PQIPRFK*SSHLHSSWDYRHVP P*LGLQACATMPG*FFIFCRDPISINK
6210	20111	A	6263	515	150	FLRWSFTLVAQAGIQWCVSSSLQPLPPG FKOFFCLSLPSSWDYRCPPCPTNF*L LVEMGFHHVGGAGLELLTSGDLPASASQ SAGITGISHRARPGTLFF*AANGGKQV FLLLRVLNGL
6211	20112	A	6264	1	296	GTSFLPSFLP/LLSFLKFLNFFQIVSHC RPGWSAVA*SQLTAPSI\FGLKPSSQLS RLSSWDYRCPIFFF\SLPMLPRLVSNS* PQAILPTQPPKFLGLQA
6212	20113	A	6266	298	182	LHFFEVSKEIKLIRAEAKWCL*VLFTIA KIWKHL**ICKYLSIDWIKMWWIHTV EYYSAINKEI/PVIVTIWIYMENIMLS EIN**QKDKCMIAL*GIYIQ
6213	20114	A	6267	402	234	PPPLFKNPPPPPPFNPPPKKKKIIFP/ SPPVNLAPPKEF*KGPPPPPPPPPPPP FF
6214	20115	A	6268	125	17	KGOAQLTPVIPALREA/EEAGG*LEPR SSRPAAWI
6215	20116	A	6269	1109	454	GDSAGAEGTMENFTALFGAQADPPPPPT ALGFGPGKPPPPPPPPAGGGPGTAPPPT AATAPPGADKSGAGCGPFYLMRELPGST ELTGSTNLITHYNLEQAYNKFCGKKVKE KLSNFLPDLPGMIDLPGSHDNSSLRSLI EKPPILSSSFNPITGTML/VRLPPPHWP VAGAVSSDAYSASQEEE*AQAQTEPYPG SCPPRNTI*FRSQEEKEKRRGS
6216	20117	A	6270	111	86	VVGITGVSHCAWSRNGTLTHCWEECKV /QPLRKTV*QFLMLKI\PYQMI*PLLGI YLRKNKAYIHMKTLL*MSLFLFEIAK/ TWKQPKYPSASEWIN*LDSFSLYLWGS RTPDLK
6217	20118	A	6271	2	222	RSCESNSQTSACYKSFYLYPLKS/GGFK ILERM*PIYFLIPYVVTIFNQRYFYIW

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						NLKKTRGTYTVLYKMYKSF
6218	20119	A	6272	787	470	LPFFFSFFETGSHCWWRERESLGAQVG VQ*CDLRSLQPPPPRLKQSSHLSPSSW DYRCAPP*LDKFFFCIFCRDGFHHVAQA GLKLLSSG\NLPASVSPSAGTTL
6219	20120	A	6273	2	322	FCMAIAIDSSSSHGSRSLKTLWKRF SILDAIKNTCDSEEV/KVST*TEVWKK LIPTLTDDFQRFKTSVEEVTA\ELLVVE ITREIELEVELDDVTELLQPHDQT
6220	20121	A	6274	175	406	KNSLGGPNLTGEGKKITFSL*NTFFSLE ALIFVGRLLSSFVPPPKIRFFSKNSRNL /CPVGEFFKTRPPVNTFFSLP*RKSYFF SFPG*IWPP*GIFLKAPPPPPPPFLRE RREVSMLPRLMSNSWVQVTPPPWPPKVR VLLGIVDVQ
6221	20122	A	6275	2	181	PRVRGRVGHRRGKKS FVHCWQWKL*P LWKTIVRVLKTLK\IELPYYP/ATKLL* SYPLE
6222	20123	A	6276	397	47	PPFSKNFFFPQKDFLGGLPKKSPPPK K\FFFKKTPKKNPPPSFFKKPPPPAFI KTPLKKKKKFFPPQKFGPPPKFFKPP PLFFFFFFFITTAP*KITKSIPYFYFF TKIFYL
6223	20124	A	6277	2	264	ETESHTVAQSGCSGAI IAHRSNLQGST NPPTTAS*VAGTTDACDHAWLMF*FL\V EMGSHYVAQAELELLSSDDPP\QSPKI LGLQA
6224	20125	A	6278	3	204	IRCYRKIFYERKHQWLQQISLLSYFKKL POP\PPL*ATITLISQQSLISRQDPPPV KR**LTEG*DDC
6225	20126	A	6279	57	306	INKANRDKL/GTIDFLEFLTIVKRMQN TKTESKKRN*ESILHVE*EDTGHVRAAA VCRDMTYLGEKLTDEEVDK\IIREAKYW
6226	20127	A	6280	419	18	SSSSPKACMFVYEWVCTQKCVWVBYMC VFVYV*LVLMMCMNVACM\C*SACV*M CVICECVCM*GLSVICEGVCM
6227	20128	A	6281	459	235	FLRNGVSCCHPGWSAVVQS*LTAASNS* AQVILPSSWDYRPVTSHPAKTHNFYMQ/ CGNKKMVCVTHSIVIFSLQ
6228	20129	A	6282	505	470	GVP*GQEFEPSSLHMRPCFFLKCKINP AWWQKLF*PRRQKFRLTQI/LALAPQPG QQKVNFFS/NKKKKKNPNNC*IALR
6229	20130	A	6283	206	374	GGGGGKKKNWGGEKKRGGEKKIFFF*SP PRFFFSPPYKKKKFFPPPPPPPPNFF FYPPPPPPPPPPPPPPPPPPPPPPPP PPPPPPPPPPPPPPPPPPPPPPPPPP PPPPPPPPPPPPPPPPPPPPPPPPPP LFGHSDILMHVHNV
6230	20131	A	6284	431	269	YIKGGPPPEIETFLIFFYIYLIIFIFF FFFFFFFFFFFFFFF*FVCLKYLIFNHI QRF*TYISIPHFMLLM\YTLHLFTFCIC SLFTIIVFYIFV*L*YCCTVKALCNSL LVSELDKYIKNNYNCKQ
6231	20132	A	6285	298	44	YLFFFFFF*VELVFFLCMFFFFFFFFF FFFFFFFFFFFFFFFFFFFFFKNKVSFNS CFSLSLFKLYFLKYNFIQLQGNLHFNNI I
6232	20133	A	6286	386	1	ANLHIKVNFFVNFTLLNFSFLPVWFGFH FLVV*RVYLSHRGFYVFFQNFRLRFFFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SE*VG\FFFFFLLFFFFFFFFFFF FFFFFFFFFLCIAIVFY*IWYISYFTKY IEEPRTGRTRGRTRG
6233	20134	A	6287	190	134	LEFGRNRFQFSRMILRGSLQWRNYADM VKIAKT*YLRNTFHKVIAIIGDSCDGS GQNKIKTFWKGFSLDAINGIHNSQEEI KMATLTGVWKK*IPVLKDDFEGFRTSVE E/V/TADMVKIAKT\LELEVPE\EDVT* LLERILF
6234	20135	A	6288	394	2	RRQASLSCGGLHPVRSSRLCLPKQAWA MAGAPPPASLPSCSLISDCCASNQ*DSV GVGPSKPGVGYHLLVHRFLSPLEKRSIR VGVARFSRCRLSPLSLTRKGN*LP\TPC ASRVRQCLTLQLAHGALHP
6235	20136	A	6289	233	58	DRVSLCRPRWHVVSRTRLTVASTSR/LQ AILPPQPPE*LGPQASANRSPRSPKLTG LRG
6236	20137	A	6290	385	48	TLQYLCTPTSTV*KKKKPENIKYW*QCG ANRTLFQ*WQVCKVAQTLWKPVWHYTVL NLNTRIVYDPMPLLTNNAYMCCIC\ YQKTFTRMFIAALFEITPK*KMHKYLTV VG
6237	20138	A	6291	273	36	RNGRWTPCGGR*IHPS*GTDPVYLPVPG TLSSSQASNSHPLLKAPGSRP\PWPTDL GYKDPGPPSPNPACRRRPSLFHSD
6238	20139	A	6292	394	5	AKIYFSINPLVFSKQ*FLKNVFPNLIHL QFFSNINSLMLIKV*ALLQDFPLVHN VY NKICDTSKDTTTLFMYLMFVFKMKTFFS LKAYI/WSGTVTHTYNPSTLGGGRMWIT *GQEFKISLANMVIASLY
6239	20140	A	6293	536	190	RRSFALAVQAGVQWRDLGSLQPPPPRFK RFSCLSLPSSWNYRHAPPRANFVFLVE TGFLHVGQAGLELLTSGDPPVLASQK\A GMTGVSHRVQPD*GHGGSRLSSQPFWEA KTGGSPEVRSSRPA
6240	20141	A	6294	2	238	HEADLGTQVLTHPSTAMYFVHYCOPP *ILYGTINT*PPVVKHNPPIHKTP/SPC LQASTAINPQLSHINC\NPKDTPH
6241	20142	A	6295	2	447	FFFLMGVSLFCPGL/WSAMGAILGSLAT SCLLGQVILLCLSLPSSGKLQVCAYPH LG*FLYF*AEDGGFSPCWPG*VSNS*PQ VIHLPWAPKALGITSMSHCCPACFHCTF FRHFRQNPHLNLFLEGLGLSPPPPSQ PLEGGKGPNG
6242	20143	A	6296	2	133	AEERERERERERERE\REERERERERE R*VERERGGVPLRTYR
6243	20144	A	6297	3	244	HDYSSFLAPPALGYMRMLHPAYFILFY FIS/FYLFFSQDEVLLC*LGWSQTPELN QASCLGLQKWWDYRCEPQCLAECD
6244	20145	A	6298	1	361	GTRRSAMLARLVLSGPGQ/CYLPALASQ RAGITGVSH*GCPFFSLKKRWRSHCVA QAGVQWFFRG*TPGLSCFSCSLPSN*DY KCAPLCPP*DTVF*VRAVSSEVPLTITY RGEGAGVWA
6245	20146	A	6299	3	348	HERHELEELIKNLFFFFFFGKKIFFFFP GGKNGGPF*FIGAFSFRPQGIFLPYPP* KW\DWGPWPPCRGDWFF*KKTPFSILA RVVLNSPPWGILSPYPPKGVRFPGGTPR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PGPV
6246	20147	A	6300	1	436	VDGEFSCSLSPSGWDCRRASPCPANF/S VFLVGIGFRVVGQAGLELLTSGDLLASA SQSPGITGMSHCTRPKRHH* IANSSSVL GDFRIDYFQISRKAQWITLGYNPWAESH LLMGAGLRVLPAPRLMISQVDLLPATHP SSGRRG
6247	20148	A	6301	370	70	PKG*STLPASASRSAGITAVIL*SHCTS PPM*LRFKHPTHSTSTPF/ CFFFFGKK ILIFVPQPGGKGNLS*LKPLLSWLRKL PCLTL*RGGDYPGFPPPP\SYFCFFIKK GV*PCGPGGNS*PASASRSAGITAVIL
6248	20149	A	6302	1	285	KHFFLFITYLFRDRVSVCPYPSWSTVVE/S L*SWLIAASN/CLGSK*FSLSLCHHA LLVDFNFL*RRRLIRQPLVNSNSWAQAI LSSQPPKALELKT
6249	20150	A	6303	194	351	GTFCICKPVQ/WLDTVAYTCTPSTLGG RDGRVT*AQEFETSLGNIVRPHVYKK
6250	20151	A	6304	354	211	YRHMP/S*LADFFIFCRDSLFMPLPWLVL NL*AQAILLPQPPKVLGLQE
6251	20152	A	6305	1	346	GTSSLQLISLHSSPTASYPKHLHTRLT ELLSVSLMAHVLVSVPATSS/PILQPHP TYPCTWIMFTHSSGSGKPCQTHHTYT HTHTRMCAHSGGHATLPP*HPLHPRHSA YLLW
6252	20153	A	6306	395	177	WLNTLWYIHTVDYFLAMKRSDLLIHSPW MNLQGIMLSEKQ\SQR*HVV*FYLYNN VEMKKSQKWRTVLWLPE
6253	20154	A	6307	2	718	GVLPHYWPGWSTPDVL/HPPTSASQIAG ITGKSHRALP\KFAFLTSSQVMTLLAH GTTAVVFSKLS*F*EPPMTCAVFSVVTG SCHINSFRIQTCL*YYSVFTSCFYCSMI EKLTGTIS*QKEHELPFSQSSDIFKLAY LIFFW/CVVMESHVSQAGVQVHNLSS LQPLPPRFK*FSCSLSPSGGDYRCPPH MANFCIFSRDGVLP*PGW\S*TPDLRM DEPGLRPFQSAGDLTGMEA
6254	20155	A	6308	377	67	PEPPKIFFFSQTLFFFWGGCPQIAPPPK KFFF*KNPQGFFPPPKKKKIFFPPPPK FLPPQKFF*KPP/LSFFFFFFFFFFF FFFFFFFFPTI*IFYSMSFLP
6255	20156	A	6309	1	362	QTYAKMHVTIIFFGVK\LTFLPQRFGL SGMPRRYSDYPVAYTT*NILSCVGSFIS LTALILIFMIREAFASIRQELIVEEPS INLE*LLGCPPPYHTF*EPGYLKPKRKR KESSPPKLV
6256	20157	A	6310	2	411	VLPTLWEAGARGSLERSSRLQ*AMIT\ HCTPPWAT
6257	20158	A	6311	59	334	THACGNLSYAGSFISLTAVLLITFMI* EA\FASKRKVLIVKEPSINLE*LYGCPP PYHTFEEPVIKSRQKRKESNPPKLVS QPHGLHDL
6258	20159	A	6312	3	22	KPSP*PLTGALLDLLMTSGLSM*FNHFS ITLLILCLLTNTLSIQ*WRDVTRESTY QGHHTPPVQKGLRYGILFITSEV\F AGYF\WPFTHSSLTPTPQI*GHWPTGI TPLNPL*VPLLNTFVLLALGVSI*AHDP

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6259	20160	A	6313	11	182	INKMW*I*VRG*YSVIKK\DEILSFMAT WMEVEDILLSKIREAQKVTHPVFVSFISG S
6260	20161	A	6314	3	421	IQASTMAGAPPQASLLPCSLILDCCASN S/RGSVGVGPSEPCTGYNLLVCLLLRPS EKCSIRVGVT*FSRCRPS/TRKGHSPT PCTSRMR
6261	20162	A	6315	1	111	DKGMNVFMPANTASVLWPMDDQGVILNFK SFYLRN\TFISKYISAIDSDSSVSGSQSK FKTF*KGFTNLDAIHDSWEEIKIST*TG VGKKLI\PTFRDDFKGFSTSVAEVSADV VEIGREL*LEVKPGDRTELL*SVLWPMDD QGVILNFKSFYLRNNIF
6262	20163	A	6316	440	312	TSSFSLSFF/CQDG/SLTMLFRLVSN* PQAILPSWPPKVLGLQL
6263	20164	A	6317	5	404	PRYMIVKLLKI/ERNKILEAAREK*HFT SKGKAIWIIIVDLSSSETMEVRKNLHNPQV LKEK/NKTWEVRILYSKISFQKKGKIK IFSDEGKLR*SFTSRPTLRE**RKFSK* K*NDRRRNLTFRKKEYPKELKP
6264	20165	A	6318	394	182	MFIVA/VFSKAKEWRQPKCLSTDEWV/Q YM*YIHTMKYSAIKSNELVIHVA*IL FENTVLSERSHIWHGSHI
6265	20166	A	6319	1	378	APSDFFLFQSLNKPLNCTHFSSVHNVKK TSLT*LNSQNPQFLRDEPNGWYHCL/QK YLELDGAYVKK
6266	20167	A	6320	286	314	NRCCFSLPTQVKCFNLVLGICCVCDWGY YRWLNF*NPIF*FILRQFHSVAQAGVQW RDLGSLQPLTPRPANFYILVEMGF/TPL LARLVLS*PSLLKYKN
6267	20168	A	6321	23	397	OKTLNMEKEMNIYTHKM*ITPNRSNIKR SSLRHITVKFSKVKDKQRI/MKLAIEKQ PITYKETTRLSEDFSAETL/NARR*WD DIVRYWLKKKKKKKKKKRGGGLLN SLGGPILTGGGKEIF
6268	20169	A	6322	411	2	TEPPPPGGNF/L*TKPGKNFLPPKNLG FFSPFSPKFFFSKP\P*ILGGGGAFFC PPQKKGFPPKIPRGVFFSPP/YKKKNLI FPPPVILGPPKVFFKGPPPPFFFFFEG QSGQVKLSPKCK
6269	20170	A	6323	395	280	MLARLVSN*P\CDPPGLASQSAGITGM SIHVPQVNH
6270	20171	A	6324	3	359	QHYLVFRETOIKAARVCHYIPTGMAKII KTGSTKC*Q*CGAAGTLHCWEECR\LK QPLWKTAW*FLI*MLCD*TVPFLLQIYPT EMKMCVCRMT\RVFLSVLFIIASSWKQ PKYHKLNV
6271	20172	A	6325	3	174	FFFETGPNFVNQAGGQHDLG*LQPPPP \GSRIFPA*TSRVAGITGLNHHHPHPLGS IF
6272	20173	A	6326	265	13	TASPIRIIITSQDVLHS*AVPSLGLKTD AIPVRLN\QTTFSDTRPGV*YGQCSEIC GANHSFMPIVLELIPKIFEIGPVFTL
6273	20174	A	6327	32	259	CYYEHLCTSLCVNWFHFF*VYT*EWQW PKYLSADEWINKM*YIWTVEYYLTIKIS EVL/SATTWLGLENIMLSKRS
6274	20175	A	6328	1	228	PGLNHCSHLSWDHRHALQCPANFG\YFV ETRFTVLPGLVSNDDPALASQSAETGV

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						SHCAQP*VCFHYCLTFFSLQ
6275	20176	A	6329	346	1	LPKKKKKKISRGLPFPQLPKKKKDNEKS LTFSSSETMPGRRQWSKIFKVLRGKKQPQ QPRIISLAKLFLKSEDFL/ETQKLEFV ASRPALQAMLKEVL*REGK*YRSLFKKG RALK
6276	20177	A	6330	349	77	HTTPKKNKHN/RKKIKLDVLRYNKVDN SKMSGLH*QCPSDECDAGVFMASHKQ/F DRHYCGKYCLTYCFNKPEDKAQHCGSLE PRSLRPAAWAT
6277	20178	A	6331	319	46	RPRRPETK*ALNK*KDI/PMCSWKQRHN TVKMLIILSKLINRFNATIKISTE\FHR NKLILAIWKCKGPRIAKTT*KGIKLEE LLYLISRPP
6278	20179	A	6332	496	309	DRATAF*RQSFTLSL/RAGMQWHDLSL QPPPPPGFK*FSCPSLQSSWDYRCPSPT G*F\CIF\VEMGFHHGGQAGLELLTSGD LPASASQSAGITGVSHCTWPNILNWK
6279	20180	A	6333	3	173	HHHSRL/IFFCSVLGTSSHYVA*AGLEL LGSSNPPDLASQNPGITYGSHYAWPDIP VF
6280	20181	A	6334	339	153	FSPPPPPFKGFFFFPPPPPPF/SF*PLRG GGPPPPFGPGVRPPSPFVSWCSPPPV VLASFFFS
6281	20182	A	6335	32	331	QLLNHSVIVFLLSFDHSYFLRNLSLFLA FKLIGVKN*YIILSFYLLHP*HLLNF FFF/CKRQGLPVLTRLVSNWSAQGICQP WPPKVRGLRAWSPGLSL
6282	20183	A	6336	226	177	DGVSLLLPRL\GGAISAHCHDLPGSGD SPVSAS*VTQLQYYFCICLGLFTFTTRL SAYLGTGKLTALPNTPLGLDS
6283	20184	A	6337	302	59	KMLLNTIMCNREIL/RKRKSPRVHQTSS VSYFKKLPPPPQHSAASTLISQQPSSSK QDPPAAK*L*FVEGRLAFPSNNVF
6284	20185	A	6338	197	28	AEKVRFSASVTWHLGSHSL*SKKNL/W LGMVDHNCNPSTLGGRGRIA*AQAFET G
6285	20186	A	6339	46	317	EVPSSISSQISLFSGDFSSVPLEELSNL FFMFCPEHIIVTCERVTSNYS/YKWKP EFSYP*IF/CFKMSLTMLPGLSLNSWAQ VIIPPQPPK
6286	20187	A	6340	4	276	QTTLRGTTVQITKNLSSETMNASRCEKK NL*SAWGWMWENNYQPILYSAKISFEKN GVEIKFTN/KQKIKN/FITSITLV*EIL KEVLQAEG
6287	20188	A	6341	485	2	GVWEFLETESRSVAQAGVQWCDLGLSLQA PP\PGFTPFSSRLSLLSSWDCGSPPHPA NFFFVFFVETGFRHVSQDGLDLMVSIS* PREPPASASQSAGITGVSHRARPXSKI LIAGRRSIQMFVPVFFQKLAVVENFQN TKDFLNPYSEILLHTSQIHSSC
6288	20189	A	6342	2	339	EDLRVKLKKEGYSNISIYIVNVHQPMLN SNGSVTVVALLQAS*YLCILQAS*ASSQ SWTS/VTAAVSFQRIISNQEHPVYQQE ENQTDVWTLNLSKDDFLIYDRCGCLVY HL
6289	20190	A	6343	181	12	RWGLPSGWDYRSMPLHPVNF*II/CMRQ DFTVLPRLILNSQPPVILLRWPPKVLGL

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						QA
6290	20191	A	6344	3	295	YWLHSCF*FLAITNKAAMNIRLLWTCAS IFPR*RSRKEMAGS*GS/SLFNVRNCL TIFSHDCTTL/HS/HQQWGGV/PVLPFP HQHLL*SIFLVFDILIGI
6291	20192	A	6345	334	8	KPSNPGGEGPP*KKGPKVFPWPWGKKENF SPKKKKKI*CPQKPKGPPWGAFAFKKKK NF*NPRGSPQL*KKRGIIGPPTLIPSS QRPPPKKKKKK/GPPKGALLAFGGIKFF FFFLEKNFLFFPKGKTLAPFFKGGLPL PG
6292	20193	A	6346	68	256	WVA\PVTHTCNPNTLGRRGRIT*AQEF KTSLGNIVGPHLYKNLKKKKKKKGEKKP GGGFSPL
6293	20194	A	6347	385	60	KKKKKNRTPYDAAI/PSLGTSSKEFKSG SSRDICTPMFIA/AITKRWK*LKCPSMV NI/VKKMWFHMMQY*SAKKKEILS*MH LKDVMLSERMLSQSQKKNFCMILLIWI
6294	20195	A	6348	234	61	CHRIEHIKMVNL/WLDVVVHTCNPSLTG GQDTWIA*AQEFKMSLSNTAKPCLYKKY KN
6295	20196	A	6349	2	358	FLSLGIHFNYCLVTTESKLSKLRLTYFF FFFLETEFPFCSPA*RPW/PNLG*LKFP PPGSRETPALTLPRTWNNRRAPPHANF GFLRKNGV*FFGPGGFKTLDLGGPTRLW FQKGGNN
6296	20197	A	6350	346	27	KMV*SLWKAVWQFLIKLNIH*PYDSAVP LIG/IYPT*MTT*IYTKP*TMQLAAVSF IMAKNTRNESNIFNWPIDKLWYIHIMEY **AFKRN*LLINTKT*MNLKC*LF
6297	20198	A	6351	36	158	KNSVPSQE*LYYL/RQENRLNSGGIGCR EPIWCHYTPAWAT
6298	20199	A	6352	2	146	RSSHLSLPSSWDYRRAPP/H/LANCCIF CRDR/SFTMLPSLVLS*IQTILL
6299	20200	A	6353	74	303	EPSICGQIYLSFSIYKIQK*/WPGAVAQ ACKTSTLEG*GGWIT*AQFKTSLGNMMK PCVFSKKKKKKKPHPGGGGRKK
6300	20201	A	6354	3	210	NNKKIWTNLKFFRDRVLLCFPDWSTA VHSRLTAAS\TLGLKQTSCLSLVSS*DH RCMPCLALKRKK
6301	20202	A	6355	2	627	GRVGGFLVPMRDLAEASRGQQGQVKLGE MKPSVSCVCGGV*CISKFKLKN*L/WPG TVAHTCSPSTLGGQGWIA*AQEFETSL DNMVK\PCLY
6302	20203	A	6356	584	166	RQGHNVAGVQWRDLGSLQPPPPGFK* FFHLSLPSSWDYTRVPPHLANF*\FLVE TGFHHVGQAGLELPTLSDLPAWASQSAG ITGVT/HQARLQLL*KELINPSTLGPTW ELLEAWGRCPSVVMGDDLALNCFHHFSV S
6303	20204	A	6357	448	202	FTTLVSECI*DIHDSWKDV*ISTLTGAW KTWLIPTLVNGFEG\FKT*VEEVTADV EIARESELEVEPEDVTLLKSHDKS
6304	20205	A	6358	3	237	DRSSL*P*PPGLK*SYLSLPSGWDHKK A*PHPANFCLFTF/V*QRGLDLA*HDP PASASQGN*ITGMSHRAGPPLTF
6305	20206	A	6359	49	242	SSYLSL*P*PPGLR*SSYLSLPSSWDHK HA*PHPANFCLFTF/V*QRGLDLLASHD

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						PPASASQSTSTTGMSHRVWPLTF
6306	20207	A	6360	508	223	FVTQAGAR*LDLSSLQLPPPGFKQFSCLSLPSGWYYRHVP/STPIVF/CIFSRDGFHHVQGAGLELLT*STCLGLRSAGITGLSHRAQQERGFEP
6307	20208	A	6361	2	595	ATVVG*GTHFLIPWVQKPIIFDHRSQPHNVPVITGSKDLQNVNIIPCILFGPVTSQLPRIFTRIGEDYDERVLPSITTEILKSVVARFDAGELITQRELVSQVSDDLMERAATFGLILDDVSLTHLTFRKEFTEAVEAKQVAQODAERA/RNSLATAGDGLMELCKLEAAEDITYQLSRSWNITNLPAQGSVLLQLPQ
6308	20209	A	6362	1	259	LESFYFLLYYK*SS*PLRLKRLILFIFETECCPVA\QLECSGTISAHCHLCLQGS GNSPAPAYRVVGITDSFRITHCILTICIPSE
6309	20210	A	6363	60	221	NTTKLGMVAHTCNPSILGARGGRIT*V*EFKTSLDNIVK\PTPPKSLKIKLN
6310	20211	A	6364	1	393	RPRRPQTGVQWQNLGSLQPPHPGFKRPSCLDLPSGGDYRHPTPPCANFSGFS/HHVGLKLFDSDDLPPWPKFVGIAHESHKCT*RSRRGRRIDPLER
6311	20212	A	6365	19	85	CINSKIMQSSRITTLCKMVQPL*RALWQCLIKLNIHPYDSAIPLLHFYQCK*RHMNPHN\TFTSMFITALFITAKN*KQSKCLSIGQWMKK*CIHTVQ*NSGI**HE*IN SKIMQSSRITTLCKMVQPL
6312	20213	A	6366	2	298	PPRLAKVQKFLFFYLVP*DRVTLCHPGWTAVV*SQLTVTLAHRNLRPSGWYRHPQRLADFVFL/CR/DRGFSMLVGLVSN SRPQEV*ATSPSQSLLS
6313	20214	A	6367	67	636	QDNKKGIRYLFVYFRQSFALVAQAGVQWHDLGSLQPLSP*FKQFSCLSLPS*DYRHAPPRPANFL/QFLVETEFHHVQGAGLELLTSGD*PASTSQGAGITGVSHCTGPRI RFLKTFSHLEAPGGFPEKROPLRSERLQFRAFPQTAPCAHAYLLGCVSHLEMGCRN IDIPELSFFLCPLQCLIYRGKSP
6314	20215	A	6368	3	251	RSRHCTPAWAPLSTQDHFVVFYFLHFLIGSLFIFACFVSSYFIEFSYCL\YFFVDSFGFYRYTMK*NLNSNYFKLSAEILPQ
6315	20216	A	6369	333	193	FKKLVLMAKAKYCKANFFQGVVPVASKN/TGDLWEEPGWSQTPDLR*SALLGLPKS WDYRHEPPPRLANFCI/FLVETGFQHIGQAGLALLT/S/GDPPASASGALE*LGGG SCL
6316	20217	A	6370	36	369	RPTRPEMRFHPVGQAG/PRSPGLK*SACLSLSKCDYRHEPP/*PG*FSFTYIYIYFFFLFFSFSFLEEMGFHHVVKAGLELLC*NDPPASASYSDRIIIGVSHQARPFFFFF
6317	20218	A	6371	2	375	DIQMIDRNKIKN/CSTSQSIRKLQTKRIM*YHLTSVRMAITKKTTHKC*RCGKK\IHC*WQCKLVQPL*KTIQRFVQKTENNINI*PSNSKN/WKSAC*RDICTAMCITT*FI RAEHGGG\PCNPSTLG
6318	20219	A	6372	75	372	NGNSQKKKKKKKKGGPPLKKPSGGPNL

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						PPGGAKKSFPLKGGQKKPPGGFLEKNPP LGGAPL\GPPPPPKRPRGKTKP*GG*R GKNPAKPWLGGKILKP
6319	20220	A	6373	605	350	ISTGICLGMFIAAFTIAKL/WKAT*PS FNR*KKKMCYIYASYSAIKK\DAILSFA ITWMNLENIMLSEISQTHKDKCCMISLI CAI
6320	20221	A	6374	167	378	KKSQGGTNIKPPAITKYLSQMGG*KKLL TGFLKKKSLGGGAGVTILLT\NRTFST KINDPDGGGDHILSQ
6321	20222	A	6375	994	747	VSLALSPRLCNGVISAHCNLRFPGSNN SPASAS*VAGAHHTQLTFFVLVETGFH HVGQAGLELL/NLVIRPPWPPKVLGLQA
6322	20223	A	6376	1956	1592	HEFEMESYVTOAGVQ*HDLGLLQPLPP RFKQLSCLSLP/RWYDYCLAPPCLANF\ *YLVKMGFRHVQAGLKLASSDAPASA FQSAGITGMSHRARPKSAFKIQAIIGEG GVSELHRKINI
6323	20224	A	6377	94	402	KTQELQNKISHCLIRRVDRKM/WLCTVA HTYYPNSLGGQDGRIA*GLEFETSLSNI TRPRLYRKKKKKNVFAQWPLWSNFLRR LRREIRAESKF
6324	20225	A	6378	463	146	GKLGPPKGSLLKPPPPFFFL*R/P/HPP PRGETPFFFKPKKSPRGGGASPPFPPL GRVRPENFPFPRGQGS*PKRGPTPALP PGGQKETLFPKKKKRKKKKYMRLL
6325	20226	A	6379	3	207	LEYQVAQTMCISSRIQLVAEKASVPFV DKTVLS\TMGQL*EAKAEDGFFVPG*YG LAVSPLKFQSTRP
6326	20227	A	6380	328	70	RPRRRLGLPRSWDYRHEPLHPDQLLVEI MSHYVAQAGLKL\ITGVSHHARH/YR F*LGHC*SLVRRPWTISYSFLCLGPPMW EVSD
6327	20228	A	6381	13	77	VIFLLQPPK*SSCFSLPNRQDYRRVPPY PANF*FS/CRHSLTMLPRLLF*TGLQAC ATIPS
6328	20229	A	6382	342	77	KGQGFYPHLFFFFFF*KDSPSLPRVEC CGEISAPCNL*LFGSNDFF/ASHAIVGG KLPKQRKGAFSS*GGGFFFF*M*KHSV LNSSRN
6329	20230	A	6383	1	208	RGRVDKIFYLFFETDSQSVT*AGV*WLN PGSLQPLPPGFK*FS*PQVI\TCLDLPK CWYYRREPLCPVY
6330	20231	A	6384	277	50	LVLKLGRCCKTSSFI*NFKGPQIAKTILK KNKAGSLT\LPNFKTNYKATVIKTV*YW HKH*YRHGFISGLSILFH
6331	20232	A	6385	2	354	AAASTNFRDR/IL/LCHPGWSAVAQS*L TAVSTLN*AQGIG\SSHLSSLNLDYRY APLLAVLLCCPGWPQNSWPQVILLSQP PKALGYRCEPPCPAPLLLNFFFFFFKNRL WFCCPGWSA
6332	20233	A	6386	2	188	FFKYICY/CINMYMCFYIFINIYSLIYL *IHIYKYIFAYIFINTYL*IYICLYIYK YIFIYYR**IYICLYIYKYIFIYYR
6333	20234	A	6387	2	241	WATKCR*G*RRGTLTGG*WDCKASGQL *KTFQQLISITY/PYGPAILLEIDPS ELKTYVHTKTRT*LFIAASFIITKN
6334	20235	A	6388	142	429	YCVCIYIYIFLYLFIFFCTFFTYSSLHL

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						LIFSFFFLERGVCFSPRGGGGGKYLGL WRFPPPE*IKKNVYIYAQQYYSIAKQN EILSFAATWMELEAIMLSEIRQAQNDKH YMISLICGIKR
6335	20236	A	6389	468	250	VHRRTPPCPIIFFFF/CKQ*VLPMLPKL VSNWPQATLLPWPSLTVEFQALTPGWK NFKKMFLMVMSWSIKKR
6336	20237	A	6390	616	1084	LCLCQYAGISVQCPCDVFQFFHNVDSTY EDYLRKLKTSLSFFWRRSFALVAQAGVQ WCDLGSLSQALPPGFK*FSCGLLSSWDY RHPPWHPANFVLLVEMGFTHVQGAGLEL LTSGDPPASASQSAWITGMSHRTQQE\Y FLNLKFSTSPGELLCLK
6337	20238	A	6391	415	200	SPPPRFFFFCPCPKNFFFPFRSKNFFF *RGPPFFFFFKKTPFF/YFFFKPPFPPR /RFKNPPKIFFFFNRGPKNPGGGGKKK PPGPGGFSPLWGPFPFKKPPPPPKKNP PLFGKKKKKKKKKRAAPR*NPRARGVF FFPPPPPLGFWAPG
6338	20239	A	6392	3	117	KLKPSSH\DY*VGETYGRDITSRGKDKP IACVCKTFSPLS
6339	20240	A	6393	3	204	DRVSLCRPGWSAVA*S*LTATSNS*\VK QSYHLSIP*GSWDYSCVP\PLLG*LVIL LRQPPKVLGLQA
6340	20241	A	6394	501	187	AGVKWYEHGLWQPPPPGLKRSSHLSLPS S*DRHEYPANF*KIFF\VETRSHYV AQTSLEFLDSSNPPTSASQNAI*GMS HCAQPMQTFSLVKIGTNFLIF
6341	20242	A	6395	3	393	HACGAIMNSKPHAVTQYHTPLLM*SVLI TT\VLFFFVTILNDGITILLTDNRNT TLFYPSGGGDPILYQHLF*FSGHAGG*I L/LLPGFGTISHIVTYSGKKEPFGYIG MV*AMISIGLLGIIV*AHHI
6342	20243	A	6396	101	135	FDSPTPGIVPGTWQTIIRSLNVYLTRLTT SFSLMPS*FLIFFCRDG/SLTILPRLV SNSWPQAILSPQPHKMLGLQA
6343	20244	A	6397	395	187	SSYLSLLGIWSYRHVPPHPANFLFFCRD GVVYFIFFC\KMGAMLRLVLNSWAQVI LLL*PSKVLGLQA
6344	20245	A	6398	35	334	QNETLSKTKKIKNKKKKKKKRGGLKK PLKGPKLTRACKKKPFSLKG/WRKKNL GIFEKKPYFGGKKWNKPPTKIKSFKEK KKF*REKGEKQPQNP
6345	20246	A	6399	464	146	HIQIREFQRTPTRMSPKSTLSHFKIKK QLVMNKRSEIKQWIS*QKPCQMARRD*H NIFTVQGTNCQIR\ILCPAKLSFKNER EIKPFLGKYKLREFTTA*FIFKG
6346	20247	A	6400	723	632	FFN*DKILLCHPGWSAVERSQTAASTF RVQ\QSACGLPSSWDRHIPSCLATF* *KRGFAPLRLLSNFWAQAILPPWPPDV \LGLQA
6347	20248	A	6401	522	46	FFPPFLSFFFFSKIPKQSLGLVYF*NK VWVFCPWRAIR*FPFPA/APPLGSKNS /SCLNLPSTWGYRISGMVPPKAH*IPPE IFFFFFF/CRQSLALSPRL/VVQWQVQA ILLQPPE*LRLQVGRVV
6348	20249	A	6402	103	261	NIPFTCLIKKKKKKKKKKKKKKKKKKK KKK/IK*KKKKNVWGGVVKKKLGGD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6349	20250	A	6403	146	384	GFLPSLSGHEKLSLFFLFETESHFVAQA \DLGSLKPLPPGFK*FSC\SLPRSWDYR RVPPCSVNFCVSPY*PG*SQTPDLR
6350	20251	A	6404	3	395	ETESHVAQAGVQWRNPGPLQPPPPKPK RFPYLSLPSSWDHRMPPCPANSAFVE TGL/LHAGQAGLQLLTGDPPT*TSQSA RTTGASHRARP SLKYFLISFVISSLHGL LFRSVLGSMYLRISQVFFCC
6351	20252	A	6405	30	205	CRLTRPAEFRTKTHTRKPYECKQCG KFFSCSNLIVHEKTHKVTMGIQ*VMW LFL
6352	20253	A	6406	3	444	ARKITGY*ISKTIIVFLYT/DELAKEIK KAIPFTIVPNK*DN*ELNLTKQVKDPHK EDYKILMKETEODTK/WKDIPSSWIRII NIVKVAVLSKAIYRFSACIKIRVTFKT ECHWKKKIWIGKVAHACNPTTLENQGR SLEARSRLS
6353	20254	A	6407	480	307	QHDSPSAKKPPQKPKDKS/HPSSRS/HPF PPPPPC*TPPPEF*YPPPKGEWGARP PPQ
6354	20255	A	6408	923	833	KAMKHFLIKTRAFFRHVTAHLIDQSIVK TELLYVTSFIAIFALLWYGKEPML/WP GAAHTCNPSTLGD*GGRTA*AQEFKTS LGS*NKTKP*CLSAV
6355	20256	A	6409	382	152	ECSGTLLAHNCNLCLLCSDFP/SLFHN VSLSSNSSS*VAEIIIGLCHVWLIFVSAK LFLGRRVRNLFSPTPKMFESK
6356	20257	A	6410	553	173	CLLI I KNTLPKAKKKKKKKKKKKKKKK AR/WPP*K*RAP*NPVKTGGSF
6357	20258	A	6411	38	562	FLRQGL/DSAAQAGVQWCNHSSQRAPP FGLGRSSH\PASLAGWSAVA*SRLAATST FRVQVILLSQPPE*LGLQSCSITQGVQ QWRDLGSLQPPPLPGFKRLSCLSLPSN*D YRRLPPRPDSSITFSRKFQSPQARNLP PTPELKPQPVPA PPSSELHLSWSSGNK CHFLWFLCP
6358	20259	A	6412	414	144	FFFETESHSAKLEC\ISAHCNHLHFP GSKSPASAS*VAGTTSVCYHAQLIFVFLA DTGFYHVGQDGPDLMFPPRPVKVLGLP RLPLICF
6359	20260	A	6413	3	455	AEAGGLEPRSSRLQ/CSQP*SHPCTPA WAT
6360	20261	A	6414	462	162	TQGPRLFPHPFGAPGGPVPLGWVRRPP APP GKPPFPKPQ\NSPPWGGQPSI PPP LEG*ARKSP*PPKGLVPVTPKGPPPH PQENPTPFPKKKKKKVN
6361	20262	A	6415	499	0	HFTSKHHFGFEAA\A*YWHFVDVV*LFL YVSIY**GSH
6362	20263	A	6416	187	236	MCHINGIMQFFFFFFFENEVFFC PPARI GN*R/WPNLG*LKPFPGLTLF SCLTPP RSWNKRPPPARVIFLFFNKK GVFPLLP GRV*IPHTPEPLATTNLLSV TIDLILN VSYKWDHAVFFFFFFF
6363	20264	A	6417	158	412	SSDPSRRSCLFSF/CFFFLEREFFAP RVEWRGPNFCLLTPPPGKKHFFAPSLRG GGDYGHLP HGPVIFGTLRKAGFSPCG PGGS*PPPPGKKHFFAPSLRGGDYGH LPH GPVIFGTLRKAGFSPCGPGGS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6364	20265	A	6418	457	11	HTGQSPYRCSECQK/AFTQKSAITNHQK PQQKGRKSMQ*LRI*ESFFD*SHQLRHN RSSMNTMIVMGPFGLVGEKPYRCNEYF KPSFLKISLVYRRDLTRRIIGQAHNPMMP VISALWEAEAGRSLEVSSSRPAWPT
6365	20266	A	6419	103	376	SALSLILGITFFFF*IFLETGSHFIAQAG VQW/PIHTCDHSILQPQTPLKPSCLS LLSSWDYRHHVPPVPRTSACFECTILRS SVHTVLWKAKAGGSLEVRSLKLACATQ GAPCLTKKKCDPQD
6366	20267	A	6420	463	6	FPPNPHKKQNOQTP\PPKAPQQQKYTA DP/QDPPGNDPKAQAYKKSPAATYPAA SSPSSPSS/RPPSTAHHVLRVPL*GSPP GLVGNRPDPGGAQHQPDPDTWQKRPA HHGLQSLASPPGIS*EPQLAPRNSPHW TRDL
6367	20268	A	6421	1	479	RGFAVLFSAVEFPSSSKSHLDLETSPKA YKHGAPCSAPGSLQASLPKGRNQRPFS NFFVL*DKISLCCQGSVAIQS*LTVA STSPGSDDPPTTPPPHAPDTWDHRHVP PHPAKFYIFYRDR/SFTMLPRLVNSWA QTVCLSSLFMLLPSSLWSLSP
6368	20269	A	6422	11	242	FEIIFSAVEFGWSDHGSLSLQTQPPG\SSD PPTLDS*VAGTTGLHHHAQLMF*LFVEI GSPGLKWSSVSASESEPLYPA
6369	20270	A	6423	488	335	SCQLRPWNESIGQSRGIRWLTPVIPALR EA/EEAGG*LEPRSSRPAAWI
6370	20271	A	6424	454	229	RDPPASASQSAGITGVSHHARL/VSLFL IVM*AEGCYLSGIWRTLKMNPPQ*RKE RQIQVKSTRSDIFFFYFLFL
6371	20272	A	6425	1575	1309	FESESHSVT\RTECSGTIS\AHCSRHRL GSSDSPASASRVAGITGVHHHAQLIFLF LVELEFHHVQDGLLELLT*VIHPPWPP KVLGLQA
6372	20273	A	6426	276	437	CFHPPPEWDQQWGPPLGNF*IFWKRG PPFVPOIILNPWPQKNFFAWPPKTLG
6373	20274	A	6427	445	240	RPRRADHL/RSGV*DQPGQHGETLRLRK IQKISWVWHAGTLWPFWERDGSRLSA RTQMLGSWACSPGF
6374	20275	A	6428	114	450	LLLLLLFESESCSVAQA/PSAVL/WILL GSL*PLLPGFQKFLSLLSIWEYRGLP PYPANFFKFLVEMGFHHVCQAGLELLTS GDLLASASQHSGITDVSHRAQPVTIFLK GLS
6375	20276	A	6429	380	224	LRHCLFTQAGIQRQEHGSL*P*SPGLKQ SSHLSLPSSWNY\GVKLPCPNKFQH
6376	20277	A	6430	509	228	PHNKGVRSPPPQNFSPPSRNLGGGWL PKIPPPKRVFSKKPPRGKKK/PPP*KK KNFSPPPFFGPPPKI IKKPPPPFFFFF FFFFFFFFFFFF
6377	20278	A	6431	3	117	HSWEST*KRACFNIFIAAQFTIADIWN *FMCLSGDE*IKKLGLIYT/MDCYWG VKKETMPLATTWIELKVNILSEIGQA*KD KYHVF*MNR
6378	20279	A	6432	417	271	LSKKTFRNSPQPPLPCSF\NDRK\WP RVVVHTCNPSTLGGGRWIT
6379	20280	A	6433	385	145	TPGIQSSCLHLPKCWDSCPEPHLANL NF/CKR*YIPIVPNSKV*TFSEQVFSYT

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						WPHSSSFTGKEVILFPKBCPGMFK
6380	20281	A	6434	65	383	LFPNLLKKKKKKKKKKKKKKGGPIKK KP*GDKIKTRQKKKNFPKRGKKNQPG KFKKKNNFWGGKKMEKPP\KKKKTCKEK KKI*KKKGKKPKQIAPEKKKGS
6381	20282	A	6435	3	454	EIQRTVPVRYTK*TLPRHIVTRLKSTL K/EKKKKKKFLRAPTEKGQIPPKIP/I KLTVNF*KKS*RREKKG\PIFNILKKKK F*PKIFYPAKLTFIREGKKKFFPKQGL GKFVTTTRAPLKKILTGVNLNKKGYLF PQNTLKYLAHNHP
6382	20283	A	6436	424	410	NFFFPQGGGGGGFF*DKPPPGNPSSL FFFLGGGKKRGPPPPKG/QTPPPGGL F*KWLGKKETPKKFSPPPPFFGGGKI FF*KPPPPPGFFF*KSPPGGGPPSVKK KKEKKKKKKKKKKKK*R
6383	20284	A	6437	3	214	EIDCAA VWKQPKCPSADE*RKKMWLY TMEYCSATNKNEIQSF/VNNWKEVEIIM LS\KKSQAEKEKHGIF
6384	20285	A	6438	83	420	QSFP*ISCRKYS/WLGAAAHACDANTLG GRGGRAAWGQKFKTSLGNLEPGPKTADP RTSHGCELRSSYTYALTHGFSSTPETA RPAPLLPPPPPTQREDYKEEDLYDDL NK
6385	20286	A	6439	163	289	KMYCYYYY/C*DRVLLMLPRLVSNLWAO EILPPWPPKVLRLQA
6386	20287	A	6440	459	431	DKRIRTRITPLAIRKQIKTTV/RKQLQ SHYMVVVKETTNNK/CGIFIHSWBECKM VQLLWKTVSQVFKRLDLPYNLATLLIFI CQLQIKTLSSPKYLHMKVHSIIKIRKK YIKKNLKPSTDEWIIKI*C*SIHTMEN ERA*K
6387	20288	A	6441	478	36	VFGCRVILVEKFLCEPLRVTFRLGKQ LEKSL/WNFHDLNLNLSLHNQPNRCVH QWRIG*RKRS*CSE**R/TMQFINSNLT LIN*IPSCHTAMDIIIIAQH/ITHVEY YSAIKKNEIMCFPATWVELEAILGEIT QKQSQTWRSP
6388	20289	A	6442	464	206	LVQRSGIHLPPYSSTVPL*GL/HQKNEAD VYRNTRMFTAALFLIVQNWK*HNYLQTG EKINKLPYIHTMEYFSVSKSNQHSIT
6389	20290	A	6443	414	216	CYIYTCLPTQSSRSWVAT*ASSKEWIN KLWHIHTMD*Y/SSNKKNLQINTTWIN LKSIMLTETSLT
6390	20291	A	6444	7	411	SFYCLHSFAFSRVSVCWNITQYIAFLDWL LSRSNSLHVFSW\WD/CKMV*PL/YETV WQFLTCLNILLHDSALTLLGIY*K/DM KSYVHTKMCTQIFIAALFIIAKTWKNL* CSSVGEWRNKLWYLTMEYSSSVLKK/N ELSSHEKTWRELLRERSQSKKAIYCIFQ QYDTLEKAKLWRQ
6391	20292	A	6445	257	419	KSLPFFF/CW*ETGSHSVTQVRVQCNH IALQPQTPLKQPSCLSLQGSWDYKFHF TQACPY*RP
6392	20293	A	6446	20	417	HQYCFASFFFFNNFFKTESHSVAEAGAQ WHDLGLKPLPLRFK*FSCLSLSSWDY RCMPPHLDNF*FLVETGFHHVGQAGLE LLTSDDPPALAS*SAGITGVSHRAPVE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LFLLRQGLRLQLQNIIGIRQ
6393	20294	A	6447	371	3	VIGCQFL/RKTKRYLPYDLPIVLLCIYPR/EKKNLCRH*TCTSMFWTALFIITQH*KYPKCHSIGEWLNILWHIHTMEYYAEMKRNKLLIHEKTYMDLKDILFSGGQRVYLKSSILSIKCIIRQE
6394	20295	A	6448	46	332	LGEHLRQGPITILKVCQVILTHQQYFESQWSIMALSNRKYNANCRYNLKPNSYIKKEML/WPGAAAHACNLSTLGGQGRHIA*AAQEFKTIAPCLY
6395	20296	A	6449	2	381	LCSLVFTHICSIFFLFFFFFKDRALLP/H/PCWRAGP*SYLTAASNSG/VKQSSNL SRGKPLCRANFGSF\CFWFWKGGPTMW PRLV*N\ILLPQPPKVRGL*AAAHAGGQ GHDHTSLRPQTPGLKQSSNLSRGKPLCR ANFGSFWFLVLEKRGSHHVAQASLKQSS CLSLPKLGDYRHEPSHRANMFNFRSLPG LRKADCLYPY
6396	20297	A	6450	2	136	KSVGCRGCG*IGAL/LHCWCECEMVQL LQNAVWQFLKNCKIVPHY*A/IPHLGIH PNALKTATQRNICAPMFIAALCATAKRC CK/PKCPSIDKT*YTHMKYDSA*KKCW LLARVWINWSPVHCWCECEMVQLLQNAV WQFLKNCKIVPHY
6397	20298	A	6451	314	72	MLPLTNGSCRTKVSKDIEGLSNSINPLP LIGIYRTPFPKTAGTPFFFFFLV/PNGT FTKIDHILGHKTRNLNLKMI*ILKYIP
6398	20299	A	6452	54	350	LRSFCSALFCFETVLLCHLGWSAVA*PR LPAGSSNPPTS/CLPIPSWDHRLVPPH QVFLEAFFFFFFFF/CRKGVFFFLPGGV* NSGVKGTPRPNPPKALN
6399	20300	A	6453	368	172	WLTSVI\QRFGRPRREGHLRPGA*DQPG LR*STHLRLPKYWDYRRESQCPARPVIL KEANMFHLG
6400	20301	A	6454	1	365	NILKLNNKLNNL\VKEEVAKEIKK*LV LNKENTYKDLWNEAKTVLHL*H*VKF IALSA*RIVSNQCSK*ASTLRNHKKKSN LNPRLI*QOKSITLKREKSMKPKAGSLI RSIKLIIRLT
6401	20302	A	6455	364	1	PETRSCSVWPRLGQVQRQDHGSLPPLSP RLKQFSLSLPSS*NHRGMPPCPANLLF KFYLFYIL/FCLFVEMGSHHVSQAGLKF LSSRDPSALVSQSVATTGMSRRWQDII LQQKAATAA
6402	20303	A	6456	91	300	GHAHFGRPRWGDCLGPEVRDQPGQHGE TLTLOK\KNKN*PAWWHTPAVPATQEGAG ITGVSHRARPCPPN
6403	20304	A	6457	2	195	RFSCLSLPSSWDYRHEPPRLAIFFFF/C FWNFKKRGFPLWARVWSNS*PRGIGLL WPPKGWGLRA
6404	20305	A	6458	522	202	THNWRPSLQIFTAALFLAKKWKQPKCP STDEMIHKMWYVHKMKY*SVIKRNEVLI HSA\KWMNFENMLNEEACWERPHIV*FH LYEMSRVGKTGETKSRLVVV
6405	20306	A	6459	377	161	EMNIKCPSTDK*VKRY/LYIHTMEHCS ALKGNELVLIHAMTWMNLANIMLSEKSO QNTTYSMITVVKCLE
6406	20307	A	6460	92	484	LLQACFLRTVLIDYKMWAEKGMVGMCVL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						MRNMTVIIIFRDRVLL*HPGWHAVVRSQ LTSA/VKRSSCLKPPKC*DYRCEILCQV ETAFTHRSFLNSFLKRSRMRVILLNYWKD PSLGFCSDSTGMALLRNFS
6407	20308	A	6461	483	192	MGLMLILRANFQSTKKKMICLLKSLTF LNCIVLSNWPCTFNMYIFVCVFAVYKLH VWAE\PVAHACNPSTVGQGQGERTA*AQE FETSLGNIIRPCLY
6408	20309	A	6462	451	98	KQVWQLL*KQVWQLLESINMKLLYDLAV LNLGAYPREEKTHVHTKCTQMFTAAPF I\IKK*KKNFSDMKYEERDKMWTIHVT QHYLIK*SID\YAPTWMNLENIMLSED SQTQKTHCIISFI
6409	20310	A	6463	395	67	FLRFWCTHHWS/DILYPCVSLLSLRNS HSFPRVHKSPLYHSYALCPHSLAPTYE* AHKMF/RLVNFLELVETGFRHAAQASPE LPSASNPPFSASQSAGTTDASHRAQTK
6410	20311	A	6464	485	220	FFFETWSHVSQTQARVQWNLGSL/KPLP P\GSSDPPTSAS*VAGIAGMSHAPTHEI PSIQARQQHLQGEKKIELLSLPTSASQV LRLLA
6411	20312	A	6465	1	371	ISIPPKYLRLNLTIVYQGLYEQNYKTD KRNQGRSSKWRDGPSCRIGKLNIRMSVL SNLIYSFNVILVIVPASVFSIT/RLIL KFT*KCSRPRIVPLFHLLPLLVFFVCS FILCRPGASLVK
6412	20313	A	6466	489	175	YKTIETSRICK/GLL*LWRTHLFSHPH WRRGMAYEKNADFRLGTVAHAFNPSTLG G*GR/WNQGFKTSANVVKPCLY
6413	20314	A	6467	2	367	FGTETLGQAGIKGDPGEKSHWGEGLHQL REALKILAERVLILETMITGLYGS*LTEL PAAAGSAGAPGQTGHPPGSHHLA\EPEL GSGAGPAGTGTPSLLRGKRGGHATNYRI VAPRSRDERG
6414	20315	A	6468	472	260	TTLGAGNSGYRHIQPHVANVLFICRDR /SLILLPRILINS*L*AILLSRPPKVLV LQT
6415	20316	A	6469	88	435	RGVLLHMLSCLPLCKTCFCSSFTFHHH* TSFSFSFFFLLGNKVSFYCQAEQGQPN LG*LKPLPPGLKQFSCFT/LPEKWE*QT EPPGPVKRHFGLSYFPLTRG
6416	20317	A	6470	34	106	EFAIPFLTITYPELNTHVHTKICI*MST AALSTR*KSPCTCPM\INKMWTIFMEY YSAISKGRNHANVHQWIHKM*YIHTVEY YSAIKSNEALTYATTW/MNLENIMLSER SQS*KICI
6417	20318	A	6471	390	92	DFLIDAINHNLKVFYYS*FISMC/HPYN *SLSFSNIQKSLIKTMINVSLSFKY*YL IYFS*KKTF*N*RQGLTMLPRLLNSWA QAILLPWPPKVLELQV
6418	20319	A	6472	414	167	HIHIKTC*AIFSAA*FIIAKK*KPKCPT ADEWINKMWVHTIEYSAIKK\NKLLI PWNLENIMLSTGNQTKATYCMIPFI
6419	20320	A	6473	3	244	TTILLGTTYDALFPPELYTTYFVTKTLLL TSLFL*\IRTAYPRLRYDQLIHLL*KNF LPLTLALLI*HVSIPITISSIPPQT
6420	20321	A	6474	12	224	IASGRPFPCYDVCV/VKRLCRHSIVITM *KKKKKKKKKKKKKKKKKKKKKKKKRGR

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						GGALKKKKPGGEPLFPFH
6421	20322	A	6475	417	155	FQSFTENKMLSSSITCSSEIFGERKSQLM*RPSSL/SY*EKLPLLASTTVISQRPSAL*VQPL/PTAKNL*LTAGSKGHYYFLN SKVFSN
6422	20323	A	6476	1	131	RTRPPTRTTRTRGRWLTPVIPALREA/EEAGG*LEPRSSRPAAWAI
6423	20324	A	6477	830	513	WNSVKESLPADTWFLPFLGPLIDIFLLLIFALCLVNLVVKFVSSRLQ*FHVKMMLAQGFQPIPSDDPEDKDILELSLLEQVS\GILPLQC*AGSMPITSAGSSYRR
6424	20325	A	6478	399	196	SKQSSHLSLLSR*KYRCAPPWWAFF/SFFLINIFCRDE/SLTMLPRLLNS*PQVILLPWPPKVFGLQA
6425	20326	A	6479	1	411	NTGIMPANTVSILLIDQEVLVTVKTCYL RNTFCGFGSDGSGHSV\QTFWIGSTILD AIKSL/R/DSREDGKISTLIGIRKK*IPILMEDLVGFKTSQEEGTVDGLNLA*ELQVEGPRDETELL*PQDQTCMDEKFLMDE
6426	20327	A	6480	381	162	AGFTHHNFLLF*DMVLLCHPGYSAVVQSWLTVASNSW\VK*SSHLSFPKH*DYLOAVHFRMASNSPGLYLLYQ
6427	20328	A	6481	379	85	SILFFLFHPIINFFFFFF*AWIFIIPPPH\RAFKVVRVVGFFLADSVWFIKRLPQYY FFFFFFFPGFFFFFFFFFFFFFFFFFFFF FFFFFFFFLLLLSVCGG
6428	20329	A	6482	355	117	PKVKIFPPPLPRKWDPRGPP*SPGTNFSIFFLVEKDFPHVAQAGLKLLDSSSTPSVAS\QSV*ITGMSPHAWLQVLLSL
6429	20330	A	6483	402	97	TAFHLLDIYHKS*KIMFTNQPLYKCPLE IAKN*K*LKCPRRADKQIVA/WCIHTI EYYSARKRNVLLKYTRLWMNLKSI MLCKRSQSQDVYYVIFPICH
6430	20331	A	6484	714	365	NGFALVAQAGV/QWCDLGLSLQRLPPIFKQVSCVTLNS*DYRSMPPHPANFCIFSRDGV*SYWSEWSLTPDLGLPKCCDYMRP PCPANAKSFTEETHVTYQAYETMLLSDHDESG
6431	20332	A	6485	408	146	LKTETQTETCCPMFIAAFTLV/RRWNQPQCLSTDEWISQI*YICIMNINSDIKRNEALKHAVICMNLKNMVPFISPTKGGKKKEKKK
6432	20333	A	6486	243	11	GMSQYQEYSKSNFFLSNRVLLCHPGWSA VAH/SRLTEALNRFK*SSCLGLPKLWDYRRVPLLLAQNATR*NSL*SCPA
6433	20334	A	6487	403	161	DMVSPRPVWWSQNS\SLK*SAYLSLPRCWDYRREPSCQASRNTSISGRGNRKNQWNT CMYLLFLILPLKKYMCNRRVMEYFKT
6434	20335	A	6488	292	24	DWRGRMAIPLKKGSKC*QGCRTGLLRY*W/MECEVAQPLQEMV*WFLQRLNIKLSYDPDF/PLLGIIYPKE*KAGT*TDICMPMLVATLFSG
6435	20336	A	6489	3	203	SSWDCRCIPPCLANFLICCRDR/SLTMLLRLVLNS*TQAVLLPWPPKGMPLLFVFYGGIVLSYVNIS
6436	20337	A	6490	413	30	RGP/YQPGFLGFSPPNGLGFG*KVFLPL PPPPRKGP GKKGSPRARGFPQGAPPKKE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						NQRGGGFWSRGRRLAKKGFWFG*GPAKG KKFFFFFLGAGVWGLKVLIPIKKKKGFP PPLFFFFFFLQTIHPIRG
6437	20338	A	6491	101	335	SSSFLGFPHYDYRREPL/WPS/LWQFF RLNIHLLYNPSIPILAVYPREMKTCDLI KSCMRMFTVAVF*ITQTWKQPNVF
6438	20339	A	6492	532	127	STVFRARQLPCLHEPGRQSSP\PVPTSI LYT\PLPFPSSRYQQNGPCLSSPKLSPS PELGTQSFVHKSFSPCLPSPKPLTVFP ALPSTGPSQSL*QKHSLSLHSHSTP PAPSCNPESWGLDATAAISTCFYG
6439	20340	A	6493	399	1	LCPAPRGVYRGR/ESSLSWDGLHSVQA SWPLCLPTPASAMVDAPPPA\SLPSRSS ILDCCISSEQGSVGMGPAEPGAG*NLIV CCLLRPLEKCSIWAGVSRFSWYLSQLP LARKGKSPNPLSFPNEKMRPVVS
6440	20341	A	6494	319	75	KKIWGPKKKFGLQTRRPKKWFFKRPPP FFFFFFFFFFFF/HVAIFLLFCRDRG/LA MLPRLILNSWP*RILQFWLPKVPGLQA
6441	20342	A	6495	333	190	LLLLLLLLLLLLLLLLLLLLLLLLLLLLL YSFRDGVLLCHPGWSAAMPS
6442	20343	A	6496	1	299	LPRLEYSGTITASNSWAPAILPPQLIK/ YNFFCCC*GRVLTVLRLVLSNRQIVL PPPPPKSAEITGVNHHVWPKKIISNEKT THCSCSALLAKQQISS
6443	20344	A	6497	51	266	PVNVILPSSWNLRHSPPCPARFFVLFCL LFFGKN/RGLAMLLRLVSNNSWP*VILPP QPPE*LGLQVQATMLSS
6444	20345	A	6498	366	78	LLAHCHSSNNKSLILDNFNHYHGPSN TVTS*F*MSSLMILLSSP/C*GTSWSY LPYALKKIFCKD/RGLAVLPSLV*NSWP QVLLSWPPKELGLQV
6445	20346	A	6499	37	396	FPRPTRPKSSSPAKATQONTISFKKKKK SKQKKGNTVIIIRVKNQRKRQKN*KLK Q*N*EQ*KINKISKPLAKLI/KKKRVKT *IANIRNERSSITT*STDIKRLIWKYY* QL
6446	20347	A	6500	706	394	VPLLLPRLAVQWHNLGSLQPLPPGFKRF SCLSLSS*DRHTPPCPA/NSFVFLVE TRLHHAGQVCLKLLTSG/DTSSASQSA GIKGMSHRTQPIEILFYSVFF
6447	20348	A	6501	403	216	ILNVLSFK/NMLY*HYTTVLRTVRPLSP R*ATVTCTYTSGWPEAAEDPQKMTFPHC DLFLPHPN
6448	20349	A	6502	377	116	LLPY*EN*FLMYLPPICCLPFDGNSGF CHQKNFFFFFFFFKTKSLVA\RLCEGGA PAHCKLCLLGSSDSMNFLNEAEPNLA FNGL
6449	20350	A	6503	3	401	CVQHLRASWSSRWAWNRAPHSEQPAGE AAPGNEGLSIRASGCGGCTGYSSASPP ALCSIS\PRP*LPSRRAGLATCSPCL LPPPPWAPVRPEPPRRVPPAPWRPVPS TTQGLRSASARHRTGRQLHLQ
6450	20351	A	6504	406	55	WPKGFTPPRFPKRGSP\PPFPKVFIL TRQPGPQTKPPFFPPIFKLTRPGGRPP* FPPPPQVRAGKPP*PQSFRVPGAIFFFF PPPLKGHPRPFGFQKKKKKERKKRTRK RGGT

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6451	20352	A	6505	3	281	FFFCDRVLLCHPGWSAMVRVRSRLTATS /SFLGSSDSHACLSSSWDYRHLPLLAN FCIFLKRQGFMTLPRVSNP*AQAMRLP QPPKVLGLQA
6452	20353	A	6506	1	247	LGSLQPPPPG\SRHSPASASQGAGIADM SHRTRQSIIVFLRTNNKPY*IENMMITIS CTTAYKYEILRHSFNKICARSLYEKL
6453	20354	A	6507	34	47	FDPNLTTPRHIRIILWAVNKERMILTASRK KKQII*RSSNLSGDRLLNEEASWEP*CK KSMQETIQATEGWNDIFKVLKEKNL\H SKILCPAKLSFKYEGEVKAFPHKPKWRE FTVTKPILOKC*RENQRTFDLTQI
6454	20355	A	6508	403	106	HYVPPSPSPS/YFFFSPPGKRGFFPNPF ILVSPGFFPSPLF*KPPPEFFFFADLKK IFFSPPRELKFFFFKGPPPPPPPP
6455	20356	A	6509	389	230	LSFFLFFRDKVSCLNPGWSAV/VTFLK RSSCPGLPK/SQSHCTKPPQPGF*KYIYF SFFIK\KR*SLTTLRLVSSSWDQVIHS ALWHPKVLGL*AVAHAYNPSTLGCQSAE WIT
6456	20357	A	6510	101	419	ISFFFFFFFFFFLKKFFFFPPGWRGGGEF* LPQTTPFWVKIIFPPPPKVGFKNSPP PFFFFFKEKGFSVPCGFFKTNPKK/ SPPPPPPRGVGLGGWPPPPGWD
6457	20358	A	6511	41	376	EWWCETRGGAGQGRAHGAAGGATGRVLA IQARKRRPKREKHPKVKSCSVAQAGVQW RDLVLLQLPPLPGLRVSLCHPS/WECGGV VSAH*NFCLPV/IKDGVLPCCAGWS*TP GL
6458	20359	A	6512	2	332	WEKVKIATLTGFWK*LI/SGSSRTLMGD FERFKTSVEKVIADVETARELELEVPEP ENVTELLQSHYKTPGTLAFSRLSPDVSL YSQLPETERSHEWQAASKIQPRKASTSQ
6459	20360	A	6513	3	294	FFFSEMESLSVTQGVVWHNLGSLQPPP PEFKQFSCSLSPSSWDYRHAPPLA/NC FCIFNRDGVLPCL*LGWVSNHLGFTGMS HCTQPLLALSFLHG
6460	20361	A	6514	1	526	FRLGRKPR*GGVM*PVWSRGEPSVGAE AG/RS*SAPRRLHHHPAAGLATGLSASG RRSARWKMERASGLSPGGGLGATSRQMS PGTQLANPPDHGDKDCLGRISPGSGKQI QAAGQLPGPPTSLAPAQGRRLRSLTPWGL QTPHSEPEGIGHLQAATEAVLPHSTQN LITKRNL
6461	20362	A	6515	747	451	QAGVQW*DLGSLQPPPPGFK*FSCLSLP SGWDYRYPNPANF*FLVEAGFHHFG QAGFELLTSGGPPASASQSAGITGMSHH TPLGVHALVGENIQ
6462	20363	A	6516	444	3	PGGGGFFPPPPWGGKPGKIS*/PPGGG SNKPKLPPCLPPGGPK/GNPPQKKKKK GFPGVVAHACNPIIPALWEAEAARGLP PDAGRYGPGGRREAVRREAGPQECQDPE QGV*GDPRGCGAAHAPARGHPKA*RGAE GSSPGLPTK
6463	20364	A	6517	257	575	ASSVTWAGVRWCHLGLSLQLLPLGFK*FS CLSFPSSGWDY/GHAPPGPAKFCIYSGDG VSLC*PGWSQTPHLR
6464	20365	A	6518	337	389	SQHFV*ISCLHDMPALASQSAGITGVSL

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						RARLIFIFR\MDS CYVPQAGLE/PPELK RSSHCGLPKPWDYRHEPQAQPVCRFIRA TKCAYVSTQALSPAPVQPGMTPPAKRGL PCQPPGSPCPSLCHHQLAGTPPYE
6465	20366	A	6519	61	323	FMWDRVARKGSI EGASLEPLGGSVGGH GSCISMVVGALGHSS\THV*HTHTHTHT HTHTQTNTHTPSSDSKSSILDKEBAEG CMTF
6466	20367	A	6520	399	101	KIQIKATMKY/HNIPIRMGFFFKLSSQG /C**RCRK/IYTLKHCQ*KCETVWPLWK SVW/RVFLKLNHPLHSP EIPLLGTYPR /DMKT*TCM*MFTATLFTTYS
6467	20368	A	6521	1	276	RTRGFEGLRFFLGFFGTVLLCCPGWSAV E\QSWLIAASASCLW\VK*SFCLSLRG WDYRCIPPCLANF**R/CGSWAQVILPP QSPKALGLQT
6468	20369	A	6522	280	277	GDDPSCSMGGGHCLASRSE*GSVGVGPS KPGAG\YNLLVCYLLRPLEKRSIRVGSV QPSRCHQSWLPFDRKGNSTPCTYVWR
6469	20370	A	6523	2	327	SLFSS*D/YRHIPPHPGNFRIFCR/SAL TMLFRLVSYSWPQVILLPQPPSVGTST SHCPQPCIMPLKADLNPVRCQFRCALAP EPIYIQDPFLRDDVAFFCLGASAPWHLA
6470	20371	A	6524	298	414	PGPQSETLTKKKKGGGRLKGSNFTPAGM EGNIFF/CFFLSKSHSVAQARVQW/P*W LTAGSLQAPPFRFKLFSSLL*VAIYASP TLLSS*DYRCTPPRLANFCIFPRDGVSP CRSCKAAVFNLLDTRDWFHGRQSFHRLV AGDGFRM
6471	20372	A	6525	376	180	KCKKYPGGVAHACSPS*DYRHVPP/RPG YFLHF*QKHFGQAGLDLPTSGDPPASAS QSAGITGVSHRTQPQLNYF
6472	20373	A	6526	415	86	LYLPYDLATPFLGMYPRGKKKCAHTKIC TRIFTVVLFIARK*KRSKNPSTREW/I KMWNITVESHVSVIKRKELLIHASMILV H*/WMIFENIILSDRSQMOKITYCMVFF T
6473	20374	A	6527	391	166	FFFFFRDWFSLSHPGWNAE\S*LTVISN SWSQARLIFKFLKLRQGLNLLTRLVSNS RLQGI LSSWPAKVLGLQA
6474	20375	A	6528	544	176	TMRYLLTPVGMAI IKKAK\NT*C**GGR E/IGTL/LQCR*ECKLVLPWRTVWRFL KKLAIELPYAPPFLFSL EYGLFSLGSTN CAQLRSVYRKAVQNHQGVSGECAGFQDS SHSAPVAIPTARQ
6475	20376	A	6529	392	139	TYVKMHCK/WLGMVAHAWNPSTLGGRGG QIT*QASTKLSHSGLSRESRFWLECY SRSCSFCSRLPADCTSLTDSKQ
6476	20377	A	6530	362	87	NGPPFFFFFGEIDKLLILLLWKCK/RPK IAKTVFKKKNKVGGGLI*HYFKAYYKGTV IKLVQFWHKVRKTDQ*SRRESPETELHI YVLVNARDSA
6477	20378	A	6531	1	346	APTRPRLKKTLSKLKTTNQLPYDPAFS FLSVYPREMKT*R\FAKICV*MFMASLF MIVTTQ/NVPRCPLMGEWLNKWR*FIT *YHTGMKNT\VMHKTTWMNSQRIMLNEK SQSLTY
6478	20379	A	6532	3	294	FFFFRDRVFLYHPGWSAVV*S*LTAALS

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						PWLKRHSHLSLPGS*GHRMH/PPHLGNF FV\FCLFL* RQCLAMLPQVLRSWPQVI FLPWPPKAVLGLQV
6479	20380	A	6533	2	280	PRYLVRNPTPTLGSCVTVDK*LSLWASV LYIYIYTHTHTDIYRKIYAF/IFVCYI YIFI*KHIYYKEQAHAIMDAEKQDLPS ASWRPGKLVE
6480	20381	A	6534	96	183	DQLNVFHRKLKRYDTYTFVALLARHGG SC/LSLGSS*D*RYTPPIQTN*K*FFL* ISLPMLDWLVNSWPAQAILLPLPPKSSG LEA
6481	20382	A	6535	2	241	GPKRIDSNFESSVGKVPNT/TIFCERKS LSMHQI/SLLSYFKKLQDLQCSAATTL \IS*QPYTLKQDPPPTRLQPAEDSDGY
6482	20383	A	6536	485	97	PTTRPILLGLFYTK*LKS\NKSDSCPPM FIATLF/ILKCPSTDKWLKKMWYKHTTD YYSALKKGNHA/YM*QOMNLEGIMLSEV SQSHEGQLLHSTYVRYLK
6483	20384	A	6537	411	57	LFPSHIKFVLSWQSCFAKTSGPQTPSFF FF*LFFF/RDRVSLCHLSWSAV/VSWLT VASTSQAQACLSLPSSWDYRCPPPFPAN FSRRGFTILPRLVNSRAQEICPPWPSK VLGLQRRGI
6484	20385	A	6538	438	201	TYPKEMKT*VHTKTCI*MLIATLFTLAR KWKQTKCSSTDEWINKMWHIQ\TMEYYL AIKRNEAQLEHGEIIMLSERGQSQ
6485	20386	A	6539	466	131	SFPKKGGRAPPPPPPPPPPPPPPPPPPP VLSLCCPGGSQTLGLKRSAPHLVLPKC*D HRHKPPCLASN/SFFNRHRMMTNCLMC IKSWCLCIINPFYHLDSSLWMLSLIYR
6486	20387	A	6540	419	50	PLPFFKPGPRIF/CLGAPKKKI*VPT/L REIKLFPLKGPPLFFFLNKGPLCFPGRK GRGVLFPLATPKSWGQKIFPPSKEGASF PPFFPPFSW*RWDLTMLPRLVNSWPHV ILPSQPPRVGLQV
6487	20388	A	6541	1	341	SIKTAREKCLVTY*GTSIRLTGDF*KY I/SAKILQVRRQ*NDIFKVIK/EKNCQP RIQYPAKLSFINERKIKSFPNKQKLREF ITARPDLOEMIKGILYLETKE*YLPK*K HMKV
6488	20389	A	6542	409	290	NCKQPTCPSTNEW/IKL*YICITEYSSA IKRNKLQLHTTT
6489	20390	A	6543	32	397	AMIVPLQASLGNRSRKTLSLKKRKKKKG EKETLPGGST*KEKVRKKQNNLLV*KTH IKPG\AGAHGPNPNIWGGGGRQITRSGN KNHPG*HGKTPFLQKKKKRGALLKGTNL TARGRQSKTF
6490	20391	A	6544	402	0	LSWTQ*CKPIAPATGEGGTGGSLEPRES RLWCAMIAPVNA/NCTPAWVT
6491	20392	A	6545	1	365	RKVTSLPSTSRCLSILPHFSDGPRPVKP LQ**LRCSICSASLPHTLHTARAAGLLP \LASSTAVNQN*SRELGACVKWEHSGIK YGLF*RD/RGLTMLPRLVLSWPAQAILP GQPPKLLGLQA
6492	20393	A	6546	1	331	ISTFKSYLRNIFSKAIAAVDSNSTEGSG QG*LKTFWKGYTIIDAINKNIYDLWEEGK TSTLPGVVK\LDDFEG\FQTSVEEVTAK VVQIAKELELEMDPEDVTKWQLQSHDTN

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6493	20394	A	6547	1	417	TRPKINKTKNLLFERINKIKKP*VKLTK NKNKNKTPHITKIRNESEAFTEKLKSI LRE\YMNVCVYNLLYANRKPRQMDKFL RYKQLKLTQEETETLTD\YITSKEIKFV I*NFSTK*S*GPNGFNSEFGRVLWFTPV
6494	20395	A	6548	410	288	AHFLFFCINK\SLTMLPRLV*NMWP*VI FPPQLPKTLGLQV
6495	20396	A	6549	1	216	IDRGFTMLPQLVSNLS\LKRSSHLSLPK CWDRCCEPPCPACFHFHFLSECNTCIKNQL HVTLFFPNT*GLTSEG
6496	20397	A	6550	479	146	VPGFKQFSCSLSPNS*KYQRAPPCPANG FAFSVETGFPHVGQAGF*FPTSGDPPAS ASQSAGITGLSLHAWP\ENL*KLR LHAT GLRLHDHVLKVPNYLKVCSFKFEIADV
6497	20398	A	6551	42	484	SMRWNSMNVTIMPANTTSIPQPTDQEV SVFNS/YYYRYRYCKATAIDSNLGGG RQSKLKTFWKGLTIIYAIKNICDSWEEV KIST*TI*KKVIPTFMGDFGVKNSIK\ EITADVAETAR*L*LEVEPRVGLTPVI PALRKAIEVG
6498	20399	A	6552	304	74	HTGKAACKKEC/WRGTVAHAYNPNTLGG *NGWIT*GQ*FETSLINMVKPRFYSCIC ISGYTHKVIHRIICCKGKLE
6499	20400	A	6553	432	62	FWAGNSRMQQWCTDT/VSAHCSLDLLGS SNPPASAS*VARTTGARHARLMLITMN EKPLGARYCARIFFENKLG IYPNESVPT KTNANVSKPRSCFSHDPDPGHWIYLS SGLIVNKIGKVK
6500	20401	A	6554	2	174	YCNLCCLGPSDLPTSAS*VAGTTCMCHY TWLIFFCI\LVETGFYHVAQAAKLFIYS I
6501	20402	A	6555	3	268	DAWADNIKCR*GYGAI*TLIHCWWECK\ W*ATWWFLIILNMLLPYNPVMV\PRTC IQIFMSTLFINTKTWKQPRCHLVGEWIN CGTCR
6502	20403	A	6556	3	402	DAWTDNIQCR*RYGAI*TLIHCWRQC/K W*ATWWFLIILNMLLPYNPIIMDHK\TC LQIFMSTLFIDTKTWQPPKCHLVGEW/I KLWSMPAKEYHSLARTEL/IVP*NT*R RLSCT*LWEKSQYEKATYCVVPTV
6503	20404	A	6557	396	2	KKQNAFQSPSFLPRL*TPKITILISFHN IYIYTHYIYIHVCIFYIHTHYIFF/ RDRFLLCLPGWRAVQSQLTAASTSQAQ GIPG*FFFK/SIFCRDW/SITMLPELVS NSWAQAIPPPWPPKVLWDYRCGS
6504	20405	A	6558	393	175	FKSQGLVLLPRLFESGMLIAHCSLKLPG FSDSLNSA\SQ*LGL*GCTATPGPYLL IYAGELGLNKRSISSK
6505	20406	A	6559	401	188	SPPEPFI LGGPRVFPPFPFLKPPRI*F WGPKKKKNF/CPPPGPKNFFF*KGPPLF FFFFFFFFFFFFHRS
6506	20407	A	6560	37	343	YEPAVLLDIYPKELKT*AHRTCTRI IASPFKTVKMWQPPD/CP*ADE/WDK*T ACLQTV*CSARKRSELSTM/IEMWRKL KCVALSERGOSEQAACVVIPTL
6507	20408	A	6561	792	141	LFPPPF/YLSTSPNAGA*TTSPLPQFL YHSPRRQQSGTKPPFFSKK/PEPPSP/S PNKFYPGPWGVSFFKFPFPQKS*GPK

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						KSELPPEAP/PAPPLTQDCPPFVSNPGG KKKTPP/SAKKKKDPTPS/PSPPPRH*I GGPPGFSPPLFKTPPPKLILGPPKKKK IFPPPGGKNFFFLKGPPPPPPPPPPPP FSLLPVGVWSRWLRSEADLCGEYSS
6508	20409	A	6562	1	356	FFNFIFITYLF/NFLRWLSLSPRLNGV QWSDLGSLQAPRPRLMPFSCLSLPSSRD HRRPPRLANFLYF**RWGFTMLARMVS IS*PQ/CDPPASASQ\STGITGICHGTR LIPRNPMIA
6509	20410	A	6563	416	84	LSLPSSW/DYRRPPPCLANFLYF**RRG FTMVVIS*PHDRPTSASQSAGITGVSHH TQPIISFLKSFFFTLSNRFNRVCIDSEL LLQCKDFYLQKFNHLIAFQYETHCHGVH Y
6510	20411	A	6564	2	51	FVVREMQIKTVLRYFSLKLVKIKK*DST FFWKGC/GETGNLIHKNW/R/SI*QYL KKLYVHFLFVPVIPPLEYLKNKKILST K*LFAVFIVTEKC*KKKRCG*T
6511	20412	A	6565	2	511	VRW/SCAGL/LHTAV*TPGRITTEKCA QQVDETHRN/LQRLQPALINRKGPIILLH NNTCLYTAKPMLQKLNELGCEVLPHLSY SPDLSPNTYFFNHLDNVLQGKHSHTQQN AENAF*EFVKF*SMDFYATGINKLIS/H WQKCIACNGSYFD
6512	20413	A	6566	3	248	GDICT\SMLVPAFTVPK/TWNQPVVIS K*TDKMWYTPVEYYLAIKTKFC/SFS ATWMILEDIMLSKPGTER*ILHVLYLCG R
6513	20414	A	6567	3	258	WRDHSSLHS*PFGLKWFSHLSPLSNWDY RDVPACPANFEKVL*K*GLIMLPRL\LL SSFPEW*ILSSRLPASSFQSVGITHMNH CS
6514	20415	A	6568	392	166	GGGGPPRGGGLEPPGPPPPFFLKNKK*/R PPGGPGPLFPFPPGGGREKFFFLGGKNF H*TRVGPPPLSGGKKKKIRG
6515	20416	A	6569	234	411	PGAVWHAYNPNTLGGQGHRS*GQEFKT S/LGNIVRPHLY
6516	20417	A	6570	1	175	FLQHV*NKFPQTMSDQIIGKIDDMNTLID LEKNVKDL\LITQTEVEELEGENKIPIL PG
6517	20418	A	6571	392	140	LPSSWDYRHVPPCPANFVLLVETRFHLV SQAGLELPTSASQSAGITGVSHQARP/E **NSIRKGATTIQRDLGPVLQVRYLVRC
6518	20419	A	6572	2	228	RTCTQMSVATLFLIAKNWKQPRCPISGE WINKL*YILTMYYLVIKK\NDFSCHKK TRGNPKCILLSKRSQSEKA
6519	20420	A	6573	412	100	ALHSHPLGGPGQGVPKSRIPNPPCPQGG TFFFPKNPKLTRPGFARLPFPPLKKLP EKFPNPG/MPGVPLN*IPPPVSHPGVQP NFFSKKKKARGFCLVLNPS
6520	20421	A	6574	406	257	NKREKKTRKMLDSIVIRKRIKHSQMR SAPIQMAK\SNRQSPKFWVRQRTISL *HC**ECKIVQSMW*TLQKFLPAIVFLC IYHTEKLRFTQQP/CT*IFLAALLMIV/ RTV/KRLVCPSMGEWLSKLW*VNLSFSV
6521	20422	A	6575	370	68	EQGSVGMRPSEPGPGYNLLVCR*LRLPE KRTIWAGVS*FSRCSLSRLPLARKGKSP

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						NP\CTS*VRFSNGLS
6522	20423	A	6576	1	259	IDLIDVLRPSLTVT*AVVQWCNLSL*P*PPG\SGDPSASASRVAGTIGQHHHRWLIFVIFVEIWRHILVYFHTAIKNYLRGLNL
6523	20424	A	6577	418	218	KGKTRLGRVPPPCNPSTLG\GQGGWIT*GQAFRTSLANIVFPLM
6524	20425	A	6578	1	401	EKAGCSGSYL*P*HFGRPRQEDHLTLGI*DPGQCSENLSLQKNF/TNISWA*WPGIVAHAACNPSTLGSQGRIT
6525	20426	A	6579	3	356	HWDRHEPPFPV*MHFFIWLPGCHSLLASPNLTGCGFFSISITESLLSLFIYLETRV*DLQCSYFWERRG\SLCCPCWSRAPGLKRSCCLRLPSSWDYSRLTPHLANYCILGGECESS
6526	20427	A	6580	411	158	IGSVAQARVQWRDLSSSDPSAN*APPGLKQSSC\PASLPSRWY\NKCTPPDLANFYIFFVETGFYVARLADCFYPPPL*KMTGSY*VFTMCQIPH*AFYKF*FI*FRVGEDKNSLPAWQHRETLSLQKKYKN
6527	20428	A	6581	399	218	GGAEKLVPK*GGGPGSPPLPPLQKPRPKGFLWPGG*GPPRPPGEAPSPLKNKN*/PLEG/AGPPPVPPNWGGGFYPRG*GFG*LLPLGP*TLARGKQDPVFKKKKKN*NVNKKKAKL*KS*QFFFFFFLKTGSRCPRAKVQGPNGSYPKPQPRG
6528	20429	A	6582	392	214	GSSDPPNSTSRVAGTTDEVLPSPGWS*NSW/VSK*SACLGLPKCWDYTREPQHLAGRSNF
6529	20430	A	6583	390	257	PKRPPPPAFFC*PK\SLGMLPRMISNSWAQAIIRWPKVLEKQA
6530	20431	A	6584	65	251	HYENSFNFFLMGSSNHPTKNPG*FFFFLTFYKKN/SLTILPRLVLNSWAQGILLPWPEKGLGL*AQGILLPWPKGLGL
6531	20432	A	6585	2	143	RHMPPCLSSF/SYFL*RRGFAVLPRLFSKSWVQVILMPWPPKVLGLQA
6532	20433	A	6586	142	334	GRWLSQLLILNFTTRSVLKQMSW/MACVSETWPA/STLGGRGGRI*GLKEFKTSLQNMARPLYK
6533	20434	A	6587	485	377	RTRLSCRFFILSLIFRFGNFYCFTLKF/H**VFLLSFVFC*GHP/FEFIFVFFIIFFHFKVFCVFKYLLFFFILIAETFYFVFNIFSFKFVSVMFVLLIEMFYGRFTIPLR*F
6534	20435	A	6588	241	251	NSLFTKKKKKKGGALLKEPILRAGGGEGIIFFKGPKQSIIPGPGFKAGREKPGPSP*NWFF*KGPPFFFFFFCKE/RSFTMLPRPASNSWAQAICLPQPPKVGL
6535	20436	A	6589	429	54	YFLFLPSLPTFFPSFSSFLPSVLSFFLPSI/SSFLPSLLFYILSSPPLSSPPSSLFLSFFLSRVSFCHPG*SAVAQSRLTATSI SWAQAILP/CR/NRDFTLMSRLALNS*PQVIRPPRPKVLGLQA
6536	20437	A	6590	411	137	KCIGTITTHCSLHLLGPSDPPTSASRVVGLQAHHHIQLAC\F*LID*LID*LNVEMESRHVAQAGLELLGSSDPPTLASQNAEITEMSHCIF
6537	20438	A	6591	412	196	QPQPPGAKKTSGGGFPPIR/WGHQPPPPG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						AKKYNFFFFFFFFW*ROALAMLP RVVPNCQ T*AIILPWPPKVL*LQA
6538	20439	A	6592	28	400	IMENCFPKWL YITFFFFF*QSL/DSV AQAGVQ*HSLGSTATSAFLGFK*FSCPP AFLE*LDYRHVPTHTPTNFCVFNKD/MGF TMLARLVSNS*PQ/CNPPASASQSAGIT GMSHRAQPHLFVLKMEKPPPNFLFILLM NQSIHIYLLNFYRF
6539	20440	A	6593	414	23	QTHLFWFPDGFSPDPFFKRNPRIFFLGA LKKNFFFFFFFFPRHKNLFFLKAPPPFFFFK RSFFPPGWCALGLFSLQPPPPRFK*PFC PSLPKKWGYRPLPPRPGKF/CFFFFFFVI LVENGFFHHVQDGLDLLIS
6540	20441	A	6594	91	274	ILHWS*PLGNYHL/WLGVVAHARDLSTL GGRGGRIAGGQDFKTSLGSKQGSISARK KEKKKK
6541	20442	A	6595	391	251	HLKRCSTSSVIREVQIKTTTTCHFSE*K R/SEINMCW*ECGQTELSALLIRC*\WD SEMVQPLWERKEYLKQISTESSWAPAIP LLDI*P*ERCASLSLRKGWGYRPEPPEL ASFLGGSYI
6542	20443	A	6596	465	268	ILLCHLGCSAVAQD\LTLCSLKRSSHLT SPSSWDSRRGPSHLTKFF/C**RGLNTL PSLV*NFWAQAL
6543	20444	A	6597	3	229	CHGSPQPCPPGLK*SSHLNLPTPK*L\D YRGMPPRSANFLFL*RWGRCVAAQAGLEL PDSSSLPASASCPRQPVLYF
6544	20445	A	6598	122	418	IIVNELCHIMCFFFFFFFFKQNLGQTQAG GQGGKNNG*LKP KPPRLKGPWLTLPGG WNYGGFPP/HPS*FFFFFFLGKKGPYFCP PAGGKFFNLKGPPFFA
6545	20446	A	6599	1238	930	FETDSCSFA*AGVQWRNLSLQTTPPF\G SNNSCASAS/RIAGITGTHHARVIFAL LVETGFHHIGQGWSRTPGPQAI RPPQPP KVLGITGVTSRARAISKHFV
6546	20447	A	6600	398	78	PSSPFYLFIFRQSFPFFARVEEKGGHPG FPNPPPSGLKFFFYAPAPPGSKAPGQGP PA/RFYLFIFRQSFPF/CCPGGKRGPS GFPQPPPFVKKIFLCPSPPRK*GPRAG PFRPRKIFFFFFSSLFFFFVVRWGFTML PRLVSNSGAQAICPPQPPKVLGLQV
6547	20448	A	6601	3	473	FPKGGKKGPPPPAGG/QLKNPSKKPNKK PGAPPRGPRGPKKGGGGLGSPQPQGG EKWTLKGGPNLPPPRGGLGARPPPKIG GGPLFPKGGGPKGGT PPPPLFFFLLRRS PALSPRLECSGAI*AQTSS/SPPARVGC PSPAPTRPTGLTVSPGSN
6548	20449	A	6602	398	156	NGRKHTDVKPEELPSWVPTRDLTPTGTGA GAF/Q/RGYGYNKYVTVKKGS IAGVS TVLAA*VLFSYCLSYREIKHEQLLRAH
6549	20450	A	6603	380	77	FPFKKSPPL*NFPFFF*KKKVPPPPGK LPLSFLFFFFFFFF/RDRVLLCRPGWSAMV HGHGLSPVNFICISTRNAL/SMLPRPIS NTWTQAIRPS*PPKVLGLQM
6550	20451	A	6604	352	204	KRGPKI*NFFFG*QSLHMLPRVVPNSW AQMILPPWPP\KVQGLQA
6551	20452	A	6605	631	357	FFF*DRVLLYHPGWSAAR\SLTTTSA SWV\KQFSCSLSPSS*DYRCAPP CPASF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						CIFSRDRGFTMLARMVSN *PQVIRFP PPKVLGLQA
6552	20453	A	6606	3	397	VLHKLTRQCSAVPLRAPTAFLTEIGTQTP KRVVKCR*/RETQNNLLDKEQDFKTYQ KATVTKAVWCQHEDTIEQWDGIESTEKK FHTQRAGGRDHSVSRVKKRKESLFFF LKRGLILFPNLEGTGGISTP
6553	20454	A	6607	323	35	YLKTKIGKPGGLAALQFLGFRPSKNTQL GNRFMCETHHTHTHTVHPHTSQYLPH RSISFCSYLDSE/SP*VLTESSNSNPTP LKCC*HFPSPL
6554	20455	A	6608	439	252	LVPPLFFPRSFLLFSPPKKRGGPKPV*F GPPRAFYPFPF/V*RGPPFFFGAPKKK IFFSPPPG*KCFFF*SPPG
6555	20456	A	6609	3243	2602	FFFGRDGVLLCCPGWSQTPRLKQSSSL L\PKC*DDWH/RATSSGLQVFLSICCSI ISIFFMPSICDKSTKQFSN/PQAYILV G*R*VIYLGVVLAFLFVFLRQHL/NTVA QAGVQWCNLSLL*PPPARFKRFSCLILP RSWDHRRLLPPRPANFFVFLVETGF\TIL ARLVSN *PRDPPASASLSAGIMGVNHR TWPILVFLHPSVFFKVLQFLYL
6556	20457	A	6610	81	395	TWAALKLYSTCIFSSSETEPDVSQSQIT DTTACIMEPLFW/YRSIIWTL*FHHFF WRDGGTLTLRLVWNSWAQVISLPGPPK VLGLQASATAPNSFILIREGIS
6557	20458	A	6611	1	126	GRLRQENHLNPGGRGCSEPRHLHCSPAW AIEDRSVSKK/NKNGLRKCFHLRKKTLK GEKRIV*PGGRGCSEPRHLHCSPAWAI ERDSVSKKKMD
6558	20459	A	6612	389	67	YLFMYLF*/DRVLLCHPGWSAVAQS*LT AASNSWPQVILLSNRFKSWTVLLSSKI PVVQGSTPCPRCYSWHPKCLQLQGLGL DCSSPKYPRGPSLAARSLPKWHV
6559	20460	A	6613	1	384	RCFKVKDLKMRPFWNQVDPKSNCKPC KRLKRRGHASLPPEKRRRPGKDGGRGW NSAVTSQGT/VEATRSWKSQGSVLP*SL *RERSPV\ELAHF*QLAMLRLVLNSW PQDISPPWPKALGLQEP
6560	20461	A	6614	385	174	CLRLSALKKPKLNSWY*K*LYIMEY*SA LKT\NKGILSFAITWMNLDDILLNEISQ TQKDKYHMNSLICEI
6561	20462	A	6615	1	370	MNPRHLSFLLRRKERRILWLKALGHIM /FTV*GLTGIALANSSLYIVLHDTYGV SHFHYVLSIGAGFAIIGGFH*FPLFSG YTKKKKNIRGGTKNFLLCALVQREK VNPFFALTNLWG
6562	20463	A	6616	3	342	YRHEPPHSAIFAQLYKL*K*LIYALKTG KVYVYKLYLNKAIKSQ\SYNRASLT* *PRVKRKR*PGTGAHTCNPSTLGSQDG LIA*VQEFETNLGNIAKPC LHQKKKGA PV
6563	20464	A	6617	1179	915	FFFETESCLVTQAGVQWRDLGSLQSPPS G\SSDFQLIFVLLVHGQAGLELLIS*SF ALASQTARITGVSHHAQLVWSDFIKSIN LFCCL
6564	20465	A	6618	3	390	HASVKMELPYDAATPLPSIYPKELKARF *DLCIPI/FITALFTAKRWRQLNCPSV

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	M eth od	SEQ ID NO: in USSN 09/515,1 26	Predicted beginning nucleotide location correspond ing to first amino acid residue of peptide sequence	Predict- ed end nucle- otide location correspon ding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						VIRSWGREGVKESCLMGMEFHSAR*KSS GDTFHNTENCY*TVHLKIVSGKF**L*C VLNYVGFFVHNKNIKRLS
6565	20466	A	6619	392	49	QFLFERLFSSYSGYVSGVKMLGSTEVL FPRKCEMKSCSVMPRLCSCGGISAHCNL CLPGSRDCPASAS*VAGLIFY/IFLVEM GFHHDG/RELVLNS*PQVIRPHQPPKVL VLHV
6566	20467	A	6620	193	282	TPGLK*SSCLSLQNSWDCIWDYRRLLPLY PVNCFCC*FVCFVC/IFVEPGSCIAQYC LELLASSNSPMSASQSTGIIGMSHGACL ILT
6567	20468	A	6621	383	8	LNDTVSTFFF*DRISL/CPSWSAVARSQ LKAASTSWQAILPPQPKTNLLGSSDS TSA*DQSPGFK*SFCRLPGSWDYGCVP PFSANF*IFCRDKLSL/WAQAILSPWPP KVLGLQALWEAEEG
6568	20469	A	6622	395	42	HVSSTSFQGDHLHLRIVALPLP\PLHNL PLPLSPRSL*C/HSRGWTVLPSPRLTAT SLPD/SSCLSLLSAWDCRRAPPHLSGFC WSAVA*SW\SLQPPPPSRPLPWPPKVRRL QPLPSRHPV
6569	20470	A	6623	3	327	PSEPSRWNPKDVPNPQENLGIFFFFL*T RDLATLRLV PNS* TQVI/WPPKVLGLQ A
6570	20471	A	6624	395	47	KNRALFFFPFPRKRGFFPKPLIWGTFRF FPPPPF*NPPPYFFFGAPKKKFFFS/SP PGGKIGSFKRPPPPFFFKQNFPPVPPG GGPRGDFGSLQHPPPRVKGFSLAPIIF FSSF
6571	20472	A	6625	100	267	LSLSKKANISKFWLGT\VAHAV\DPSTL GA*GRWIT*VQGFETSLGKIVRPLYFC
6572	20473	A	6626	409	126	PSSSFSSSSSSSPSSSSSP/PFFFFFF FFFSFW*KWGVSLCGPWSQTLGLKQSS CLSLPKCWDYRNKPLHLAFLASLILFTF QEVVDITD
6573	20474	A	6627	506	323	REAPGTLIPCWQKYDMIAQLVWQFLRK PNIYLPYNPAIPL*HTCPRKINTQVT/C FITKTCTRMFIAALFIIPQNWKQPT*PF CPFTIIISHSCSPRDNWF
6574	20475	A	6628	330	117	DVCPRKIYTLVLQQLCT/RMFTAILFSI AL*FCKPMCTSI LEWIKKL*SIRTEYH LVMRRNKPLLYSMPQM
6575	20476	A	6629	396	139	FFSPPEKKGVPFSP*NLGTPGFFPPPPF KKRPP*FIFGAPKKK/HISPPPAEKFF FFKRPPPLFFFFFFFFFLFFFFFFSAFKL KV
6576	20477	A	6630	79	405	VSGRMTALESYLLASSA/RNKCSSNCKI KKMTARLDVLAHRCNPSTFGG*GGRIC* AHKFETSQGHIIIRPCLYKKKKKGRPFKR TOFSPARWQNGFFWGT/LKNSRAGF
6577	20478	A	6631	2	417	SFIFPCKFLNQFISFYKNVCHDFDCNCV ESKDQLG/WPDAVAHTCNHNTLGSQGGW IA*AQELKTNDNMAKPCLY
6578	20479	A	6632	74	417	KTVFRYNGWAL*ASENRISLADLLPSF HVLLCLPKAG/PNFPLPSSIKKFFDLPD LIRSHKTHISEGVLPFP/RRKEPRTER PRRI*TDRCWVSSLSLIVLDHAFVQS

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						QFYM
6579	20480	A	6633	740	776	CSFFLKKQTRSRAAVQAGVQWCHYSSLQ PSPFDLKQPPASASQTV/KD*GAYFWCC FFLFLKRWGL/NSVVQAGVALLPDLFVV RRLVPLSLWAVEPALWAAQL*LL/SP CPLASQSPRHQTGQSPHQKCFPDILGLH LALRSSFSPLERPTLRLPPGLASFHT* ATWLSWPLPYK/PPKRVNMYLVKADRPE PFL*GTRGRKSVQMTHAKTLQETLYSG PEAQAAASVTDEF
6580	20481	A	6634	2	296	FFFLRQSFALVVQAGVQWHDLSLQPPP PRFK*FSCLSLPSGWD*RHAPPRPAIFV FLVEMGF\TMLTMV*IS*PGDLPTSA CQSAGITGLSYRARP
6581	20482	A	6635	407	212	GRPR*TPPPLGKKKKGAPPPKTKKKKNF LGGRDSYSQKKPFFF*RNKTRPGGGGPP GIPPPPLKG*AKKKGLPRGPKFPVT*/NK PPPPPPGGNNQNPFPKKKKRKRSTR*I*K IRISRFILYFFFFFLLERGFGCSPRGGG GGAFLSYGKLWPPG
6582	20483	A	6636	20	223	PCKKLPPQLQPSAT\TLISQQPLTLRKD LLPGKRL*LAEGSDDSYQFLVAKYFKIK GLSFGRNKLANI
6583	20484	A	6637	866	647	FFLDRLV/LCHLGWSAVMRSWLTAALTS GLKQSSCLSLPKLRDYRHEPQHQAANNIS *SSWSDSNMQPRLKTTL
6584	20485	A	6638	398	26	KGAPPPNIFFFFLFNIFFFFFFFFFFFFF FFPINFLQCLLYRALHFNKVKVINNF/ PLNFCAYYHPL*NM*FSYISFQNLKFF LI/FGVFNLSGIYFNVL*IANF**G*LI LPGTIYLLKCYFTTN
6585	20486	A	6639	1	341	NWDYRHALPCSANFFILVETGFCQLPRL VLNSCPQVSHHA\KFLFFFFFFLFFLEEG GFVGPPRLEYREGSLQP*LPKLKGSTCL TLPKG*N*RGEPLPPARSSFFFISKFFI ET
6586	20487	A	6640	391	118	NANFEKSFSGMKIL*NSLAWYKKILCD/ RKNRSMQKTPLD**YYFKKLPPQL*PSA NTTLIGRPALTSRQGLPPAKTL*FABGF DEMILSLF
6587	20488	A	6641	352	285	KKKKKGGGGGAYSGIPTF/CFFFLNGVF LGPAGVQWQNRSLQPPPGVKLFFFLS LPSH*GPRHGPPRPGMFIYKNF/CFF/V RDGVLLHCPGWSQTPGLK
6588	20489	A	6642	433	64	TGNFFLDSLIFYFNPGPLGGGGILKGFFS FFFFLETKFFFFPPAGQWRYFSSL*PP PKFKQFFFLSM/WPRPGKFFFFFFGIL VEAGFHRVAQAGLKLSSGNLPTSASQS ARITAKSHRTVF
6589	20490	A	6643	424	11	PPSIFLAPPPSRGGGPPPPPKK/KQSP KKKKKGGGGGPKNPPPKKGGPPKKTGF KKNPPQKKKKKNSPPKKGGPPANK*KP PPRPQPFYFLTIFYKIFYIFLLKFLLF YILFFFFLKSSKQGRPLAI
6590	20491	A	6644	411	2	PPLRIWLASPPSKIF*PQPLHI/YFSPF PP*KFFFSKLPILFLGGFFPKFPPPKKS FFPKNPQGVF*NPP*KKKIYFSSPP*NF APPKIFLKTTPPPFFFFFFFVEMGSRY

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						IAQARTRETRGRTRGRTRG
6591	20492	A	6645	34	381	AKLGTRGAAKQEKEIKVTRI*WKEIELS QFTEYTQKNL/NVTDKLL*LVYMFSKIT GYKVNLIKINICIFHKHTNQKKILKMPF IIA*K/TIK*L*INLTQDQDLIYQ TLKAEL
6592	20493	A	6646	17	448	HFYAKLGRASLSCSGLHPV*ASQPLYL PTQASAMADAPFPARLPNSLISYCCTS NEQGSVGVGPAEPGAGYNLV*HLLRPLE KHSI*VAVSRFSHYSLRPLARKG\NP QTPCASWVRQCPTLLRLALHGLHPLSNQ SQGD
6593	20494	A	6647	462	336	SLRLPGSNDSPASAS*VA\GITGPCHHA RLVFVFLVEMEGLS
6594	20495	A	6648	447	62	KDDIWIATTHMNRWSISLAKRM*IKIT MKYPYTSIKMA/IKQTNKN*KKSSIKC W*ECRTMRTLHCW*HITG*PLWKTW KFIKLNLYLPYDPA\TCTQMFTA/ALF IILKY*KQSKYPSSGYCVA
6595	20496	A	6649	3	1492	LAYARAFDDTNTKRYPDNKVKLLKEVF RQFVEACQALAVNERLIKEDQLEYQEE MKANYREMAKELSEIMHEQI/CPGGED ERLTFEPPSHLQHQWDSNKHNGSRDDQL VFGRVITSHGPCVGTCTFVICKLRMLSKA NHWGDRAQ/ERTKGKGRERK*RTTLEFLN R/RFYRSWKVHIF
6596	20497	A	6650	495	170	GAAEFPAQSAGIAGVSHHARLEEFFSL DSGRVMRGTEVLKYLGGYTITI*SIFFF FSFF\WPGLGSLQPLPGFK\LSLLSRW DYRCPAPHLISL
6597	20498	A	6651	9	222	QTTTRPERNSGDPHTLSL*SSWDYGHVC HHAWLI*F*K/CFSGGLALLPRLV*NSWA QAVLPPWPLKVLGLQV
6598	20499	A	6652	241	833	KKTPLAMWNPWPGPPQIPHPLTKLVQMA G/QENGCLSGHDLESIRPAGLHNSARGE VLGLSSSLGKELVFLQEELDLSEIHIPE AQEVEMASGHFAFLHVPVDPGRAPYCKA SLSSASSLEPTPPEDTAISSLRPPSAPE MLTQHGAEQVEDHPG/Q*QPSPHSQSR PSPQKDPQALVIASLRSTERKQASHGG TRPG
6599	20500	A	6653	1	398	FFFDIGSHSLTQAQVQ*HDHGHGSLHPR LPGFK*SSHLSFPES*DYSRHTPPRPAN F/EVETEFLLHVPQAGLMRCNLLPAT/AT SKSARITSVSHHVQPEVSIKW*NNISNL IKCFLLFYKYKCIFINTKFVFTV
6600	20501	A	6654	489	282	PAS/WDY/RHMPPLANACAFLC*RDFFS MLPGLVSNWWARVICLPWPPRVLRIQAR ATTPG
6601	20502	A	6655	953	908	SQSCSVS\RLCSCAISADCNLCLLGSS YSSTSAS*VAGTTGARHHTQLIFVFLVE MGFHHVGGPGLLELT*VIHLRSRSPKVL GL*APSSARGQNSVSQ
6602	20503	A	6656	412	44	RISERRKSLGAVHTKDKYSSSRVRTSN PNCARSGASSKQSFLLGKKRAPHPIKS F\KDALLVVDGITGVHHA*QIFVRSRE R*IRPVIPALWEAEAGGSRAQKIETILA NTVKPRPSLLRA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6603	20504	A	6657	3	241	FFIFLEARSHSVIQVGMQWCDHSSL* TPGLKES\PASSFHRAGITGVSHHTYLF L*GH*SHSQGPHPHDLITSKRPCS
6604	20505	A	6658	467	42	FFFFFFFFKQGFGLFPQLEGKEGIPGPCNP CPPGANDSPSTPLGNGGPGGPPNPGN FGIFGI*GGEGGF*TPGSGKPSGPGSPK \IPFCWVIRERPHGPPRPFFFFLQSL CFAQAGVQWCDLGLPLQPPPRFKQFCLR NS
6605	20506	A	6659	2	286	KNLKINWT*WLMPPVVSAT/WGGSCLKPGR LRLQ*AVIAPLHSSSLGDRARPYLSVSQY LYFSLSLSLSLSLTHTHTHTHTHTHKIE LLGCVAEIIHFF
6606	20507	A	6660	3	249	LSRP*CGDTISAHCNHLGLSSSSPAS VSQVAGITGACHHAWLIFVFSVEMGFHH AGQDCLHLL/NLVIHPQPPKVLGLQA
6607	20508	A	6661	3	1507	PEAPVPFLDSNQENDLLWEEKFPERTTV TELPQTSHVSFSEPDIPSSKSTELPVDW SIKTRLLFTSSQPFTWADHLKAQEEAQQ LVQHCRATKVTLPKSIQDPKLSSELRCT FQQSLIYWLHPALSWLPLFPRIGADRK AGKTSPPWSNDATLQHVLMSDWSVSFTSL YNLLKTKLCPYFYVCTYQFTVLFRAAGL AGSDLITALISPTTTRLREAMRNEGIEF SLPLIKESGHHKETASGTSGLGYGEYVIK ITL/SSSTDWLTHEIDLHRNSL*NRDSN CSNF/LREQAISDEDEESFSWLEEMGV QDKIKKPDILSIKLRKEKHEVQMDHRPE SVVLVKGINTFTLLNFLINSKSLVATSG PQAGLPPTLLSPVAFRGATMQLKARSV NVKTQALSGYRDQFSLEITGPIMPBSLH SLTMLLKSSQSGSFSAVLYPHEPTAVFN ICLQMDKVLDMEVVHKELTNCGLHPNTL EQLSQIPLLGKSSLRNVLRDYIYNWRS
6608	20509	A	6662	326	1	IMIFLFFQTGSRFVA\RLCSGTTITHC SLNLPSSNP\PTSAS*VVTHCRTRVIL NFSVDPGSRHVVKGGLELLDAILKPWPP KVLTRTGSTPEFRSGSGSVIRIRGFN
6609	20510	A	6663	414	105	QGVKGFVGLNPLSRLHFFKQKLFVLS *KGQVKKLSLKIPFPFGGFFSPPI*NPP P*NKPQRFPKNPFMGFT/IRKKILFLAFK STKSGG*NPPSK/HKKI*FSF/CFWETE SRSVTQAGVQWHYLSLQPLPPRFK*FS FCKPKRVRVKPLGLVLWGGISNRRRKKT SGGKRNFKA
6610	20511	A	6664	1	407	GCVFVPPAAREAEAG*IA*TRET/RLRW AGIVPLHSSVGNKSETLSQKKKGAPSKK SLQGVAFSLSQLGLPPFLQKKRPORG GGRGQLAPGYNPPAGKTLVGPGLHSLFC SKKAWKELRPWKKPRGFWFLINST
6611	20512	A	6665	1	280	FFFF*HRVSLCCPGWSTDHLLPP*LAR FKRSSHLSLPSSWDYRHTPT/HPGFFVC LFVFCRDRVSFVLPRLVSNFWAQAILLC GDRKVMGLQA
6612	20513	A	6666	408	89	WLPNSLILPN*NYFVSYSLDRVVSICRP GSTAVAQ*ELTA\A*TLGLKRSASFHS HSCSLPSSWDYRCTSSHLANFFFKRWGF TILPRLIILNSWPQVILLPQSQRH

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6613	20514	A	6667	484	208	ITVVSAAGLIHYSFLNPGEPMTEKYAQ EIDDIH*NLQHLQPALVDRKGPIFLHDH A*PHAAQPK\LQKLNKLGCRVLPPLPYS PDLPLT
6614	20515	A	6668	495	227	PAFVKVPPEKDQRQNSTHAGRNHLEMET LLL*KKKLIBTESHSVT\RLCSGVITA HCNLKLLGSSDPPTSASDYRLKPWHLAP SSFSMS
6615	20516	A	6669	2	65	DGVLITLTLARLVL\NSWPQVINLPWP PKVLG*QAGLGTPLK
6616	20517	A	6670	403	224	ILL*P*PPGLK*/FLPSSWDWRASLCL ANFLFFVEMGYPRVARAGLKFLGSDPSA SQSAGVTGVSRRPGRFLIRTVL
6617	20518	A	6671	406	162	RSYAQAGTQWLDFFSLQP*PPGLIKQSS HFSFSQSASH/RHPDNYCIPCRNRVYVG QASLELLGSCDLPASASQAGITGSCL
6618	20519	A	6672	453	32	VVSATLHTSVVVCACATRCVGMCMTLGV CGCECVVV*GCVCTSVN\HTSTGWSEK V*LCVCGCV*LCVAECMAFVSRQCVCDP VCCLPEKMRLSPISVA*VCAPMKVSPCP PQLSELHLLSLNIYINKCVLSQNAWLF L
6619	20520	A	6673	378	180	NEVIRSYKVSLEFSPRIEKWINK/I/HWY IYPMEYDSAIKRNEVLHATT*RKLENI TLNERIFDIIPFI
6620	20521	A	6674	378	94	PVKNRRTKELHIKDVCTPMLIVILFMIV K/S*KQPKCP*IDWMMKMYTHMVEYC SVSKKEGSPFICYNEDITLNEISHKKTN IYNSTYIRYLE
6621	20522	A	6675	1	380	VCSL*VLCRHMSCFQNCSL*FSFSFWFF WROCLPLSPRLCEGPMASAHNLRLEGS SDSCASASLVAGIRGACHHARVIFVFPV EMG\FHCVGQAGLELLT*VICPPWPPK VLGLQVLATVPGQPHIF
6622	20523	A	6676	424	135	SHRWGVKCFKYNIFFRD\RV*LCCTGW S*TPELK*SSCLGLPKQDYRHETLRVS Y*F*NSI*QIGVLAMVSKLVLS*QAAT LLEWPPRVLGLQI
6623	20524	A	6677	408	91	HTHFVWPPVLIP**PMR*VLLLTPTNTF FLRDRVSPCHPGWSVEAQSQITAASN\Y GLKQFSSHPSVPKCDYRRELPCMVSLLI FIYVHLHMYVHARKEKPEYPL
6624	20525	A	6678	1231	217	PPYFNNPLTFPQKRFFKGDKTLKKWL*I REIILQNRGIG*KTDSIR*MGKTEAPLK EKFLLGTLQPSFLPYMLGHFKEE*GEE FPGTHSWPFPSFPVWGLGLSVNHRGIHG PRVSLQTWGPGQEAMECECGNHGTEDTG \GAVLQPG*VT*GFHTPTSEPLVAPPC TCSGLKAEA\GFLKLPKQG\SEGALPP *SPLPSACFPPELGLRRLGSSPGLMIHPG WGLFTSPLGLKILGPRHPAGPALPQIAQ RPSLKFR*RRLGWGPPELLPAQTCAQSL GPSTAPLLGQGPWGLG*HASRWGTGLA VAPGNEVPSLSR*PRGAGPLHRHRVPV RSWG
6625	20526	A	6679	1	178	RGWDYRRPLP/RPG*CFVFLVEMGFHRV GQDGLYLLTL*SSQSAGITGVSHRARLQ PPIF

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6626	20527	A	6680	3	135	KSEHLEREPTIEQLSTMFF/TAKYGWHLRGH*HRCQKKPEPPEDR
6627	20528	A	6681	425	107	KGEPTPS/PPPPSPVFPTEKILVPPFFFPFPFPFKPPPNIFWGP/KK/NFSPPRGEKNFFF*TPPKYFLGAKKKKNFSPPRGEKNFFF
6628	20529	A	6682	424	284	CFLQPGP\PGSKGASPPSFQDNWGLRQALEPP/RESFFLFLFLFFPIVQTGFHHVARACLELLTSSDLPASASQSAEITGVSH*A*PFP
6629	20530	A	6683	1290	449	PLSAPPPGDPSP*KSSPRAPNLPAP*PPNLSPPWPPKCPRRR*PASS/PP*LPVPPKSPSPPV\PVVATEASRGHQPIIT*ELGSLVLRMTEKGTWG*GIPDSIMPLPRRRSEPTCRE*GDTRWRWRRRRSTGAVSTFSGGFACGGGSGA/PAHPGEQKLGASARPE/PVCPAAWVLLPSARVVASPAAPPPLESQPVH*RFKP\SPPY*PP\ALPPLSPFEPSAPPHTGSVPY*QGVPP/SEGCPSTSKPLISVRPPVTINGCLPQSQQPKTHTVSRLYEEN
6630	20531	A	6684	425	40	EWASLKN*HPP/GANQAVEAVEAPTHCW*GCKSIEPLWKTWVQCCLDKLNICLLYDSTPE*MSEHVYQAACKKSFTAVLFMIPPNN*KQPSCPSTGWLGQAWWLTIVIPAPWEAKVGGSLERSLRPAWATG
6631	20532	A	6685	2	107	SWLTAASTSQ\VKRSSRLSLPSSGDHRCMPANFFFLKDDVSLPRLISNSWTQAILLSLPTKGLEL*AHCSLNLPGSSDPPASAYQVVGTGTGACQLIFFF
6632	20533	A	6686	12	224	TPFGSTHASGAPPCLANIKFNY\L*RLPRLFWNSWPQVILLPWPSKVLGLQVWATVPSPFLIFDRDIDREI
6633	20534	A	6687	404	2	TAARGIIYGGPIKLLPRKPADVK/SGSFKTAAPFFFLGTRTLTEFLFIIQN*KQPKRPST/DRINKLWYISTIEYYSAMKRNKLLIHTTAWMNYKGINVSKRGQSQKSI FSRTKTGFGRNHISGCFLYPLRL
6634	20535	A	6688	410	163	PRGNTPPGFSPEKENQKVFNPFPGNIV*KKGGPPPQGAQKKGPPY*GPPLSFLPPKKKKKKGPPPPPPKKNPPKGN/SFSPKKKKKFFPPPPKKKGF*GGPPLKTLFFWGGGKKFFFFFWGKKEFFLGGFFFGGGGGGGPFFFFF
6635	20536	A	6689	205	405	KSPSPGGPPLIGKLEIGGAPKPKNPPPLGPKGENPPLALGGGGAKNHPNPQFILLFLGGKNP*KSPSPGGPP/ANRKIGNRRGPKTQKLAPPLGAKGGKPPPCPRGRGGGQKPPQSPVYSPPFGGKKPL
6636	20537	A	6690	3	199	HGSLQH*PPGFKSSSSLSLPSSWDHGHVQPRPAIF/CFFLILEKRGVSPGFPGGPETPGLKGLDLL
6637	20538	A	6691	8	350	SVCLGLP/RCWDYRYEPHFLA*LAFLCQIIFHHMDWIYHVSILVVDGYLGCFYFLAIINNV\G*AGLELLTSGDPPTSASQSAGITGVSHCTHPYCYTFTLTREITTPKEVKI GLCM
6638	20539	A	6692	373	197	LPSSWDYRFMP*HMLFFK\FLFLFCRD

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						E/SLTMLSRLVSNWAQATLPPQSPKVLGLQV
6639	20540	A	6693	369	100	PMLARMVSTIS*PRDPPASASQSAGITGV SHRARPIYFFK*R*SHAGYSAPVHRHD PTTDKHNSFLFCFLQTGSCFVVQVGMQW HDHISL*PRTPGFKQYSHPSLPRH*DYK PTPP/HPS*FVVQVGMQWHDHISL
6640	20541	A	6694	12	182	FLSSWNYRCVPPHLAN*KKNFFFTDR/ SLAVLPGLVSN*TAVALPLQPPKVLGLQA
6641	20542	A	6695	402	248	SSWDYRCAPPANFYKIL*TGS/LLC* PRFVSNWDQVILPPWSEKVLRGV
6642	20543	A	6696	301	309	VQEF*DRILLSRCHPGWRAVA*SRLTA ISASRLKARPSHLSLLSSWDYR*VPGP ANFLHFFCR/DRGFAMLERLVSNWTQV ICLLRPPSVGITGVGHRARSILLD
6643	20544	A	6697	3	387	PCLANFF/VFFVETGTHYAA*CGLRLLG SSALPV*TS*SAGIIGMSHCTC/LQITL LKTESHS\VAQAGVQWHDLSLQPLPPG FM*FFCLSIQSSWDYRRTSPRANFCIF SRDEVLPWPGWS*TPDLR
6644	20545	A	6698	1	287	LWFLYQGNAGITGISHRAQPNSEVFFKD RVLLCCPGWSAVA\HSSLTVALTSQAQV IFLPQPPG*LGNFCIFSRD/RGFAMMPR LISNSWAQVIRPP
6645	20546	A	6699	412	3	FEMESCSVARLECSGTILAHCNLHLLSS SSSPVSASRVAGTTGACHTWLFFFF V/FLVETGFYHVAQMGLNNWAKAILPQP P*VLGLQARITSSPNSSTREHTSGSG VGYPKAFHSIVLLLLLYLLFHLCCGVF
6646	20547	A	6700	393	88	QKLYPYLTPYAKVN*QWIKNLSVTAKNI *FLGENTGVNLHSFRFIKGFLDM/TPKS ISTKRK*KIKWSSSKL\KNFYALKNNIK KMKRQPTKYEKIHLTLNNWV
6647	20548	A	6701	494	239	KAGSHS\VSRLCSGMISAHCTFCLLS* NNPLTSASLAAGTTGVHHHAWLI FVFSV QMGFCHVTQAWVLI FDCGFESPINIKYN LL
6648	20549	A	6702	2	379	RPTWVTWQNPASTKKKNFFFKTSPT VPQAGQGGLG*RKFLPPGLKRFSGLK RPEAPKGQSCSLMGGGLCPLLP/WSGT PPQR
6649	20550	A	6703	220	47	TGFSGSQIN*EK/IWLGTVHTCDPSTL GGAGGQVT*GQEFKTSRHEPLHLTVLCS LF
6650	20551	A	6704	80	414	ICYFIVFAIYLNQFFSNCYRSFTFFFC PFETESRSAAQAGGYNPTLTLLHPPPLG IKQFSCSLTPSS\WARS*KPPCPTWGN S VFGIYKNKLGGGGAI RRVQTCNQTSYSG
6651	20552	A	6705	69	416	NVEKRNNIHNKIKTPVYFKGFLLYCCKA EVFYVLDNPFIFYFLFYFFETHCAQAG VQWHNLRSLQPSHP\SSSDYRCAPPHLA NFCRDGVSPCWPSW/S*APGLKLIHPPW SPKVL
6652	20553	A	6706	373	75	HAQLTFKFYFRNTFCKAVASTKSNSSD RSE*SKLKTFWKGLTILDAIRNISDSL\ EEVNMSTFRGV*KKLTPIIMDDFEGFDF TRESNHRGARHGG SRL

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6653	20554	A	6707	331	379	K*KINKN*KGLTILDAIKNICDSWEEVN IST/LTGVMKKL/ITLIDGSEGFKISVE EGNAGVVEIARELEIEV/EPEYVTKLLQ SHKKT
6654	20555	A	6708	578	152	LQQHNPGSLQPLSP\GFKRFSCLSLPSS WDFRHAPPCSANFFVFLVERGYHHVG*A GLKLLASSDSPTSASQSAGITGVSHRAQ PLIGFKVNSVKKSVSVPTRRILKGNMSM YEQL
6655	20556	A	6709	392	146	FFETESLSPGLECSGTVAHCNLSGSSDS PALPS/RLGSSDSPAPAVVLYSFKL*I Y/FHKTCNYVLKINILLHVAIPYSFSWS C
6656	20557	A	6710	9	393	KSKPCN*DKSQSYRL*LFAQLFTF/SNF FYFLETFF*ESHCVIQAGIHSGTIMAHT LKLQSSNPASAPPSSWDHRCGPPPLA TFLKIFL*RQWAHYVSQARDNGLIMFPR LVFELLGLKRFLLPQS
6657	20558	A	6711	34	387	QDFGFLSFFLLFFFEKGLGGPTCRAGPE SNLME\GGPPGLKQFSGTLTPRTGNNGR ASRSRAKFWN*KGKGGPPGPPVELETFT LRGPPHLSSPKGNNGGPKPDFFKKVG KKAPNP
6658	20559	A	6712	1	188	IQAWWYTPVVPATWEA*AGGLR\EPRRS RLQ*AVIVVLHSLGDRVRPCLNNKKG SFPQPPLW
6659	20560	A	6713	377	98	SLGLKQSSHLNLPSSWDYRVPVPPCPRNW FVPVPPFF\RE*GLAMLRLVSNS*AQV ILPPQPSKVLGLQARTTAPGFFSHLLKT LVPNNVNLNI
6660	20561	A	6714	353	229	SSCLGLPKSWDYRHEPPHAYFY**RQ ALV/MLPRL*Y*FLDVNM*LPLPFHVAP SHLLNSVGMV
6661	20562	A	6715	371	64	ENHGDCPTAWATRAKLRFKKKT/CYQMF ITTLFTIAKRK*LKCPSSDK*INKMWYI HMEY/YAIKRNWTLVKLNQNPYAL*KV LLRE*KQNP*SVRNIFKTHI
6662	20563	A	6716	462	232	HFNLITIKIIPFF/C*DGGLTMLPRLVP NSWAHAILLPQPPK*LGLQARACKL
6663	20564	A	6717	425	48	GFGGPPFKARFGFLHFF*TPPVLRPRP PPVFFGGFKASPPKKKTPK/PPGGGGPP PYFHPFFLSFFFPFFFEKEPPFFFWRG LGPPPPPFKNPPFFFWVEGGKFLPQKK KKKFFQSISTRSVIHK
6664	20565	A	6718	3	413	GTFLTSTLCGTLTY*VISYMCV*FIS* \SYLVYIIYFKDICV/LLYMYIFYIYTC VHISVCMYVCMYVCMYKA*PANLKTF CTQKHLANGWVQWLISVISALWEAEARE SPEVETNLAQLGPTLSLPRKKKKKKK
6665	20566	A	6719	408	71	SSWDYRC/LPPGPANFCIFSRDGVSPYW PGWSRTPD*RSLLPGDVMPALVIRHVPE LLKKQHSSVRSSRPANPIW
6666	20567	A	6720	375	57	SVIREMQIKTMKYPFIPTGLIVIKKTE NN/RGWQRCREIKACIY*WWGCKMTQLL QKTIW*FLKKLNIEL/PYDPAIPLGM* LRELKTCPLRLGVVAHACNPSTLRG
6667	20568	A	6721	391	164	RISETCT*MFPAALFIV/DQNNPDKWTN LMWSYTHTMDDYSAIKRNEVLLHSSTWM

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						\ENLENLMLSKRGQSPKTPFG
6668	20569	A	6722	381	278	SSLQPQTPGLKQSSCLSLSNS\PPRFID *SISLYRQGLTILLRLLSNSWSQAI VLP GPPKALGL*ASKKFLYSNI
6669	20570	A	6723	2	363	QRSLEHRPCKKC/CGLVV*VS*KVQYLV YKSSSFKNLLRRIHCNLFSGIVFHF* KLLRTPRSFCLCGLHIPINFITIF*IKIE KFKKC*PGTMAHPYNPSTLGGLGGWIT* GQDGLDLLTS
6670	20571	A	6724	352	58	HGGAIGARFKVFNL I*FNLVCKDE/SF SLLARAVINSWPRVILPPWPPK\VVGFG AKTPLPRLKGFLESLPSLKKKNLAYAR TITAQIGLLVCFIDQQ
6671	20572	A	6725	383	54	KSSPFFFFEQGLLCCPGWSAVVSPLQPK CPRKQFSPSL/LPSN*EYSCTPTTFSL HVCVSIHKYI*YIDQYIFKFF/CR/DRT LAMLPRLVSNWSQAILPP*PPKVLGFG V
6672	20573	A	6726	3	343	LEV*ARATRQE*KINGT*IIKYKKVKQY SQNDMILYIQNPKDSAKKLPELVNKFSS FKVNRQNSVFL*NSNKS/EKEIKKKL /PFTIAS*RIKYLGINLTKEVKNLGRAQ WVTA
6673	20574	A	6727	3	615	HTSQGNL*IQYHTPWHPPSSSERVERMNQ TLKSHLTKLVKTRLSWTCLPIALVKV RTVPQKEVGLSPCEMLYRLPYSHFTVDI PTFETKSQFVKSIVLGLSSTFSSLKAK/ ELFSTDATLGSSPGTSAFSLGDDVLIRS WEEGKLKPAWEGPYLVLLTTKTAVQT/D NKKMQTHHTPVKKASPSKSCAIVPRPI PTKLKIKKKKA
6674	20575	A	6728	2	228	SGAI/SVHCNLHFPFG/SSSDSSASAS*V AGTTGVHTMA*LI FVFLVETGFHPISQA GLELL/NHMCPPWPPKVLGLQL
6675	20576	A	6729	98	359	KVEYTVLLP*GFKGKFPTLPLYLSFSSP LKNHLISNFFLNRLVLCYPDWSVVG*FT AHCNLSLCLSLPSTW\DSRCVPTGAWL RFI
6676	20577	A	6730	10	428	RSTRTDYAALREVLPDPRRCRPRTGAW NGRRDRPGAGHSGPKAEARETRETLEKGL LFCCPGWSAVA*PRPTATFASRAQSLTV SPRLECGGVSAH*NF\SFHFQRWGLAV LRTLVLNSWSLALLLLWPRKVLGLYALA
6677	20578	A	6731	425	158	SQTHDLR*STCLGPKCWDHRCAPPRPAL FLF/FNKCPMSIRKIENAQ*LPGI*KKN FCRDDHLPLLSRLILNSWAQGIL*CRPL KVLGL
6678	20579	A	6732	431	22	RDRVLLCHPE*SAVV*S*LTTVQNSWAQ GILSSI*DYSCVP\LPVNF*TFKSVYY YFIIFIFEIYFCNSKALGL/LGVSHRAR PPRLVLNSWPPQVILPSQPPE*LGLEAL ATAPAI PRNSNLVWHQYSEKSI PDDL
6679	20580	A	6733	44	414	AIYDLPLFLLDLIPMBELRASIRAHCT* RFVATLFTVTKRLNQPTCPSTDE*QNM WSL/YIMNYPAIKRNEILIHENIMLCK RSQSQAHT*FHICEISRISKAETED ELVVATRWGKGRE
6680	20581	A	6734	375	49	QRLTYHCRFSYNTASNKMRLS*TQMHQK

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						SACSMCPGRL*GVHAMRPKVLMLRSRSH /VARPIAATCAQ*VCDRIK/R/SLLIEE QKIVVKVLKAQTQSQTAKFKNETFFRNK N
6681	20582	A	6735	381	88	SLFPRLETPGLRPSFFFFLFSLSH\PGW SVVV*SRLTALNS*ARFSLLSWCVP LH QAHFF\FFCRDR/SLTMLPRLVLKSWAQ AIPPEPLKRSGLQV
6682	20583	A	6736	384	293	AHLSLLSGWDCRCMPCLDNCVCLC/RV FVCR*GQAMLPRLVSNSTQVILLPWH P KVLGL*AQDQEPWGRSGPGLPQAASG
6683	20584	A	6737	24	300	NILSAFLCLS*P*H*YGLVIL*NVPQFR FLPLFFPMQMYTHIFFKIRIRPGVVSHA YNPSTLVGQGR\SHEFKTSLDNIARPR LYQVQNKIR
6684	20585	A	6738	2	353	IHCW*KCKITYTLEKTIVWQFPPIQLNIVL PYIPA/IPLLGIHTREMKTHIYTK/T/C MQMFGVVLFIIAKIVFQLVNR*IKL*SI HKVDYHSE/IRNKQLYEAT*LNLKCTVL SE*S*TQKTT
6685	20586	A	6739	2	336	IHATYTNP*HRH\VHTPTHVHT/HVYTH NGTHHTARAWTPAPPTSLILPSPTESP PALQIPNLFPGLSSSPHPAGSSQGEPEE GGCQRRAKNRVGHRAEKWETELCAGDMN L
6686	20587	A	6740	3	385	KKQATLLWIHLATTFVSVEI*QSKIEVH DIFKVLKEKK*TTFPKITTNPCKIAP I HEGKIKLY/IVK*QLRDFINSGLVLKAM LKRVL*SKRKGH*QTIRNLRVQNSLVTA NTQPNTHEYCNTVIVVGN
6687	20588	A	6741	406	155	TGSCSVTQA*/CWSAVIVHCSLDLPGSS NPPASASWIAGTTGMCYHAQLPSFNLCL QFYCMGCVFSRFLRFTFGLQSYTRKQK
6688	20589	A	6742	1	215	LFYSPDLSPTD/Y/HFSKHLDNFLKGR FHNQODAENAF*KFIESQSIDFYAVRIN KLISHWQKRVDNCNGSYFD
6689	20590	A	6743	376	109	YHMEVWNLYSLKGSSYLRLPSSWDYWC P PE*QANF*K\FFCRDKDLAMLPVVLS NS *LQAILLLRPPKAEPLQLLGQFQFRRES GVVN
6690	20591	A	6744	382	148	NIPQFMFDILFQ*LITLSCPASF*SKFP LSSLYFIQ*GR/WLGTVAHACNPSTLGG RGQR/*A*DQELETSLAHKARPHL
6691	20592	A	6745	403	209	HIVINRIIRKYCA*HYANKFNNLDKLD T FLE\NTTCKNLTQEETENLNSPVSVKEI EQGKLCSDRN
6692	20593	A	6746	366	40	QGSVLSILNVKIVFWFKTGCVHFLFELN FLSLFQNYVCSHTS/YPLSLIPHESLWS FPPSFNHSS*Y*HFLKTN*MPDAMAHAC NPSTLGS*GRWIT*DEEFETSLANI
6693	20594	A	6747	392	57	APKKKGGGVYPLYPKKSGRKKKPEG/PP PKPKKKLKTTPGRKNDADIKPGGAKFFF SPKKKRGAPPGVPPRLF*KPPQATI*GG PKKKKKPPQEGGKKGAPPKAPPLFFFL YF
6694	20595	A	6748	376	140	LEDNI/GYSNQNAGAGRVS*INTPKIKV S\QSKIAKWDLIKPKRLCAAKVSMNRVN ROPPEWDRIFALASAD\RGFLNKILG

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6695	20596	A	6749	540	172	FFLRQSL/DSVAQAGVQWRHLGSLQAPP HRFMPFSCCLTLPSS*NCRCLPPCPANVL YF*QRWGFTVLARMVSI*PRDPPASAS QSAGITGMSHCAQVVNTLSLHAFSCDKV PQNDLL/WPSKSFCTLSHEKACKDNVF TTWAQWLMFVIPALWEAEAGGSRGQIE TILANTVKPHLC
6696	20597	A	6750	1	353	WFLERESTRSENSVNIVEMTT*DLEYV SKAVAGFEKIDSNIKRSFTVGKMLSTSL H/CYREIFHERKSQSMCQTSLLSYFKKL PQPPQPSASATLIVNIKAKISAKRIKLT ECSDDC
6697	20598	A	6751	404	231	SPS/PPPPYFGGPPGFFPPPVF*TPPPE YFFGAPKKKNFPPPGGKNFFFKGPPP
6698	20599	A	6752	77	371	ITCPVLYLTSRNTKTKKYLDCCCFFWP* WNNRDQTYLHLFFF/CFIKKNFFFPKR GARGGFCINETPPLGGKGNPPPPPPGRG EKRAPPKTLCCFFFF
6699	20600	A	6753	354	169	ETESHVTHAGVQWHNLSLQPPPPGFK RFSCLSLPKK/WFSVKLN/PNT*SFCYH ILKALII
6700	20601	A	6754	1	442	CTCRAFTTGRATRSEKEERKKERMYD *KKERKKEKEGILLKKDQEEEEGRKEE RKEGRRQTQDEFGGQNLSTVKQGS*PK KRK*GIQ\QTGAPTQERDKETSQNKNEE KARHDS*QQA*RTQSRLLQEGRKLWKR GLVSRRK
6701	20602	A	6755	366	262	FF*RWGLTMPRKLVLNSWAQVILLPPPL E*LG*QA
6702	20603	A	6756	3	223	GLKQSSCFCLSNEDCKHVPP\HRLFFL FVCLFCFVLEFFW*RYGGLAVLPRLVLKS WP*VIPQPWPPQMLRLQA
6703	20604	A	6757	418	244	FSLSSWDHRYMPPRMATF/SFVLFLCR EGCLTRFLRPV*NSWTQAIFPQSPKLLG LQV
6704	20605	A	6758	46	256	KLKNKTEARHSSSACL*/LPGSWDHRYL PRLANF*TFWRDRVSLLPKGVSNLWAP TILLPWPPQVLGLQV
6705	20606	A	6759	391	55	FIFFFFPHSSHGVSPCCPGWSRTP\GSS GSPASASQHAGITGRNHHTRLQDIY*LE /TGQTVTLQFSVLADTTLTKRLWSILC CYNKIPETG
6706	20607	A	6760	377	2	FGEPPGFSPPPVLKTRPRNLFLGPHKKN INFPPP/WELNLVPLKGPPFFFFFLR*G LAMLPRLVSTSWAQVILLPQHPKLELQ VHAMVLSSRTSHSPRSRSLSPRFSQRL PVSCNPAQPSMA
6707	20608	A	6761	2	259	LTIA*KNFIFLGL*QGICQIPKDYQTS R*IKDNLNK/WDTPCSWIGGLNIVEMSV LSKLMYRFRAIQMKTTSGFPFFFWKKG IFF
6708	20609	A	6762	1	169	FFETEFRSFA*AGV*WHDLSLQPPQPSG \SSDSPASAAALFFFFFLKKKIFFFPPG
6709	20610	A	6763	1	496	MATCTPKHINTQICVSFLSLKLSEFEQ MSIFKKGENELALGTGNIRPYDSCPGNR P/APFATSPAPRHPSGPSWRPPTSGGVP ARAECPASPNLPPGFCGQSPSRGRKEE *LRGESTSTLAIF**APNRYHSF*LPRQ

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						P*PHGDCPARKKKKKPNDRPRLQPTVT
6710	20611	A	6764	1	229	VLLLCFFFFVL*DRVLVGHGPGWSSRLYL KTKTKQKKQNNIFVCRVGG\LTTLPRLV NSWPQMVLSPQPLNALGLQV
6711	20612	A	6765	580	273	WRQSLTHSVAQPGVQVHDLGSLQPPPPG FKRFSCLSLPSSWDYRRAPRPTNF*Y LVQTEFHHVGGAGLELPTSSDLPTSVSQ SAGITSVSHHAQLDMIFLR
6712	20613	A	6766	220	239	AQEFKAAASTTALQETELCLKKKKKKKG GVSLGGVSSNFTGGGASVTSPSIF/CF FFFF*DRVSLSGVQWCSLQF*TPGLKRS SSLSLPSSWEYRHHVPLHPA
6713	20614	A	6767	89	387	FLSPSGSQEHLQIQLRSTFSFFFFFKR EPRFGRVGGQCPNLG*WKPPPPG*RF GLTLT/SNWERWATPPPTNFWIFKKKG NSPWWKRGAKIFGPWDF
6714	20615	A	6768	397	223	IREVGVVINWQHKDPCD/KWNCSVY*L* *WIHKPTHDKT\HRNTHTHHTHTGMHS HTQK
6715	20616	A	6769	3	367	SWKVCCKRPIPSPSLFF*KHPRVLLRAD GT**VSLATL*HMQLS*AGSVKEAEP NAPPHKATFLFLFFCTD/SSLTMLPRLV LNTWPQAILPPCPPKVLGLPARANSSSL SVFKLTSFCC
6716	20617	A	6770	490	260	FEETESCSVV*AGVQW\LELLTSSDPPA SASQSAWITGMSHCARRCGTHYHLCE LVSFVTALLSOLLELGLAHSRC
6717	20618	A	6771	418	130	PSPRDLNLFPLNGPPLFFFF*DRVLLC CLGWSAVASN\FDLK*STRIGLPLKCLDY RHEPLCPAMWDTLSSL*EIFGLFCHRP LEAPRTGPGSQ
6718	20619	A	6772	311	314	FAVGELFLLHHVGHACLPFCHDCKFPE ASPAMLPY/QPVEL*AT*TGIEVLTPGC RFQAVFGLKVGFGHGGPTFVYLG
6719	20620	A	6773	465	283	CPSLPSSWDYRHPPRPANF/*YF*YHV GQGLELPTSSAPPASASQSAGITGMSH RAWPK
6720	20621	A	6774	410	91	RDHSLQKPQTFRLKQSSCLSLPSN*DYR HMLPCLAGWLAGWLACQTDRTDRQTD QTDRTDR*TDR*IDSRDR/SLAILPRM FSDSWPQVNLPLQ\WPPKVRRLWA
6721	20622	A	6775	409	253	LIFAFF\CRDGLAILRLVNS*PQAI LPPWPPKVLGLQARAPGVRPDL
6722	20623	A	6776	3	278	FFFFSLHLWAPLAFFFGAISAHYNLPI PG\SSDSPASASQVAGTIGACHHVQLF\ VFLVEMGFHHVGGAGLELLT*VIHL PPKALELQI
6723	20624	A	6777	79	442	RDEDRGLERRCVSACSTPQLGNASTT*G CPGVSDPSLHILF/CFKEN/SCFAPQA EGGGHNLG*LEFGPPGLKQFSCSLTPQRI WNNGGAPPPPLYFFFLKKRGGSPWPGW A*TS*PRS
6724	20625	A	6778	77	417	HRGLHLSFFLF/SFLFFFLKRAALLWPR EQGRGWIVWNCTLSLRGGISKALPS*E AGTKGGRPHPTLFLVF*KKTSFSQVDQG GIDLWARGNPPPGNLKWFELQKETLCPG HIF
6725	20626	A	6779	62	235	IQELRIREGKCLAYEHTARNKGSQDLHA

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						GLSCLCCCCCCC\CNCWP*STRKFFTKPE
6726	20627	A	6780	908	566	SKMEFRSCCPGWSDLGSPQPL\PLGFKQL\SCLSLP\RAWYYRHAPTHPANF*FLVETGFFHVSQAGLELPTSGDLPTSASQSGIIGVRHHAHPECVFOKQLSEANLRRINWQED
6727	20628	A	6781	11	483	TTALLKAVRH/G*HLSLQRLLSF\VCLCPAPRGGAYRGRQAS*SCGGLHPVRASRLCLPNQAWAMAGAPPTSLPPCSLISDCCASNQRDSVGVGPSEPHAGYNLPVCRFLSPLEKRSIRVGVTFRSRLSPLSLTRKGNLTPCASRVSSASPCS
6728	20629	A	6782	225	589	SRSEPGNFRSCLGVGVTCMCLSLSLPSRSFLRPLFLSLSVCFVCLGTRVPCAPEGGFLARRPFFWSASPRVSAWVLPVGNRFPGGSGLVCEGLGNVGI\WSEPQGFSPFHPEQPLC*AGSRRALPNQGR\LPGAHRLPAGGCPQSFKKVVTVPVLCPHREM*PQLDAGTEKEAGKGMGQACLSLKGWPSWPSHPFDTPPRMPVVVAWPPRILPGLWPLL*PPAGRNARRKKPETDRRGRSAGSQPQACADGVRVSLPKSGALVMSRTGLPVC PWAALSPVARSRGDQNPATSGAAGWVLPVAVCVSLSLSLLSLALSFAISFSLCPSVCS CALGHVCPVRRRVGFLHVLSSGQPLPASLPGCCGRLAIVFPAVPAWGSVKAWATWASASEPQGFSPFPHPPEQPLC
6729	20630	A	6783	458	170	PCIVTASASQSAGITGVSHRTRLLVNFSKVGSVTISLG*EVGLRHWP/NI/GRLDKTGPGEKQHFILHAPQSAPSVYHCLGNTQELPPLSTAMISQPKR
6730	20631	A	6784	1	192	FFFFG*ILPLSPRAGVQWHDLSLQPPHPGFKQFSCLSLP\RG*DYRACATRDGLIFCNFRLGD
6731	20632	A	6785	3	246	SLCVCQYYCRCACV*VPKQVSG*VTMGI/CATGFVLIYLCG*QCLCG/C/C*EDPFYCEQLCVHVCSVCLGRGWSVCVCISRL
6732	20633	A	6786	408	128	GPVVPYKARG*SPFWPPGEEKSPFPKNPKTPGGGGGAVLFPPPPWRGRPENSPPPGKRC/QPN*IFFLPPHPGHKTQGPppppkkkkKISAEFLSVV
6733	20634	A	6787	1	418	LTILGVMKNICDSWKEVKISFTGAWKKLIPTLTD/EY*GFKASVEEGTAHVLETA RELEVEAEAVTEL/LQSHDQT
6734	20635	A	6788	3	237	FFFLT*VLTIV/PG*SAEVQS*LTAASTS*\VK*SSHLSLPSSWDYRRMPHPANF FFFFGKKSLILHPGRGGPSLPTP
6735	20636	A	6789	282	3	PHPDNF\RFLV*TGCLHVQNGLLALLSPGYPTLASPSAGITGVSHCTRPKRYF*MVLSNKSILNRFLCTVLPCLQAPRRTGP PPATVLRGT
6736	20637	A	6790	62	328	FFRDRILFCHPRWSAVIQ\SWLTEASKSW\IK*SSRLGLPKCWDCHPEPLCLDNTTY*CRQNTLPITLIGCFRVSPLPYAKYTGFWGAEG
6737	20638	A	6791	67	353	TNKHTYFLELNKREKPLQTVFFFF*REL RGLILANGNFRLRG*SNSPA*PSKVAGI

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						TGPPHQAGLLLVFLEKTGFNYVG/RRGP PPPPPKELALQA
6738	20639	A	6792	744	382	MTFFKTAHTFYFYLYLFTYLRQSL/DSVA QAGVQWHNLSSLQAPPFGFMPFSCLSLL SSWDYRRPQPRPA/NFFYF**RRGFTVL ARMVSI SRPCDPPASASQSAGITGMSPR AWPKLHIFKL
6739	20640	A	6793	372	129	RVLPC HSGWTAVVQS*LI AVSTSQA\KR SPHLSIRHVPPHPA/NFKQFFCRDGLIM LPRSVS NFQAAILPPQPPKVLGLQA
6740	20641	A	6794	395	25	QPGFLFCFTPRKKPDSFSKVFVAVLSF/FP PSL*FS/PLSL*VQEMVSI CC PGWSAV\ TPGLK*SSCLSLPKGRGYRCAPPHSANL KFFL*R*VLFMLPRLGLH\SWVQVVL CQ WPPKGPSLR ACTSKI
6741	20642	A	6795	412	176	KKS*/CLATPSENWVL*NGPPLFFFFL *RRDLAML PRLVSNWSAQVMLPPWPPK\ VLGLQAGATMDHSCVQYSHSFAPE
6742	20643	A	6796	444	95	NFVRNCQSFLQSGCTFLHSYQQFLL/PC PCQH*IMSVFQILT*TVIGVYMHV*ICS ALMTFDLFMCHVLICH LHIFFGEVSVQH FSLLLFLFESGSIYV VQAGLHLLFSSNP PASAS
6743	20644	A	6797	378	732	FFFWLNLGSSQPPP\PAFTR\FSHLGLL NSRDYRHL PPRLANF*FLVETGFRHV QAGLKL LTSGDLPALASQTGTGVTAS PSLDEGVFKALPPPVGTTLC LPPWTTGG PFLGPAL
6744	20645	A	6798	444	1	PLCFPPGGGGFLSSHQGFPPPPPKR KGS VGAKKKNIPPGFPFFFFFKNFFF*GPY PF/SEP K KARWGPPPPGPGFSPPRSLVS PLGEKKKKKIPPPETQPPSFGA*NGKK RAPPPGPRAGGRNSFLEGGRGQRTGGS VREFRAGR
6745	20646	A	6799	462	83	IEPLRPALCLS*SNPASI*KPHFLLEF/ CLPFLSFFFS/SFPFSFPFLFPFPFSPF FLIPFLSYSLCCSGWSTVA*GLTIAS\ TYGLKQSSHL/SLPASWFPCLTN*KKIF FRDGGLTMLIRLAYLFLNF
6746	20647	A	6800	433	185	PPPGGRLLVEKTRGEGQLKPGQPGRQAG LGM RGNPGKAQPRPASGAPEMQLPARPP SGGHL YGCGAKNNEGGANPLL CGGTGSG SVAAAGEVSKSAPDSGLMGNSMLVKKE/ AGGGGEPQANQETEN*EG*PMSPE SGAL LLTSPAAATLPLPVP PQRGRGFAPPSLFL APQP
6747	20648	A	6801	395	60	IEFLLFLPLSVDGRLWSHQLLPVMNEAT /MSIP*HAFATC/SSF LRGGCLGA*ST LLYGGYMF SYLRNKQTI FQSSCCIVNGE QPRMRNLFS*FIQHLVFSVFLIRAIL E GI
6748	20649	A	6802	423	98	RGVPY*PGGLQPPP V/REFFFFFTGRVS VLQAGAAAPTCRAQSILPGSWDYRHLHA NMSS*FLYFV*RQVFSMLPRLVSNWDQ AIHPSQPHALFFT CVVSVKPLATL
6749	20650	A	6803	396	194	SLMKLAHV*VLHTDGGFMHPDSATISCHD IFDSLHLTGEGSAKICRALYELIMQLME EHP\GEKQT TIA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
6750	20651	A	6804	373	192	PALNPWAQANLPHQTPALSSNFFYF/CVEMGLTVLPRLV*NSWPEAILLPPWHPKVLGLQA
6751	20652	A	6805	370	242	KKGTSKFLFFPSYSFFSKFWYQKKVKIAFFFF*DRVSLCHPEWSAVW*S*LSAALT/CPGLQGSWGYRHVLPCLANFS\FFC*DGVSMLSRLENWPFCLF*PVFPQGHCNSISTKK
6752	20653	A	6806	464	182	DGPHRFEPPISS*FLPPWPPQKLEIKG*APLAKQIFFFFFFL*RDIVLLCC*GWGTVYSVYSWVSSRLTAAS\TAVLKQSSHLGLLSSWDYKHHH
6753	20654	A	6807	3	228	YTCAGFFRRQSLCHLWGAVARSQLTVALTL/VPPGLK*SSNLGLEPKCWDYRCEPPHLACVNFNTVKDVCFCILS
6754	20655	A	6808	506	173	NLHLPGLKQFSCLSPPPSRDRYRRAPPC TANF*FLVEMGSRHVAQAGLELLNSGDSASASQSAGTTGVSHGQISLQILSTRISEVIFLTLLLRILHDLPCLELPSL
6755	20656	A	6809	676	397	VSSCPRDQPGHHGETLSVLKIQLARHGGCL*SQLLRSLR*QTRLNSGVGDHSEPRLSHCAP/AWATEQVSRSRCKKRLHQKERIPEWVRS
6756	20657	A	6810	367	31	QVFQELYSQDLFIYLETLSLCHPG*SAVARSA*VVTAASDSW\VKQSSRLSLPSSWDYR*VPPYSAHFDVNSSFLTYCTSPGLTQKIEDSWLGTVAHACNLSTLGGHSGQIT
6757	20658	A	6811	469	251	LLSSWK/YQVPPPHLVFIKIL/CRIGRETASCCI*PRLVNVSWPQVILRPQPPKMLGLLSATMPGPISVFCFCFCF
6758	20659	A	6812	16	462	EIISYCGFNLHFSNDYKKKRRERERKRRKKENIGE/HI*DIGVGS DILDIPKAWTTKLNIDKWHIKL/QKLLSS*RVAKTNKLKSFCTAEEIITRVKRQPMWEKTFASQTSKGLISNTYKELQNLSTETNKQKNNFDLLSADKG
6759	20660	A	6813	492	243	SSWDTGCTPSRPD\IFVFLVETGFPMILARMVLIS*PRDPPASASQSTLVDTSRYKVYQNIHQVNMF*NYGWCFFDIFTASVGD
6760	20661	A	6814	32	308	EYTLPHPYLITGPPVPKPEYSHS*YFLSPNTQCIQ\PAVRTLNTASSTCLSRRTARFVPIYQDPSLEPLQLPPNSLTLPTRLRHSPCWV
6761	20662	A	6815	97	274	GRFLELKVKRGSILGLGMVVHAYNLSTLGG*GGRIP\QGFKASLGNIKSLYKNKGAA
6762	20663	A	6816	74	376	DFFIVYSVFTHLVNIKDVKDVLYKSLKYFFAIYRMGENIYKLYILGGINIQISMYYTA/IKKD*ILLFAATWM/LEDIILSEISHEQKS\KRCMFSLICGS
6763	20664	A	6817	1	1127	MRVTA PRTVLLLLSGALALTETWAGSHSMRYFYTAMSRPGRGEPRIAVGYVDDTQFVRFDSDAASPRMAPRAPWIEQEGPEYWDRETRNMK\ASAQTYRENLRALRYNQSEAGSHTLQRMYGCDVGPDRLLRGYHQDAYDGKDYIALNEDLSSWTAADTAAQITQRKWEAAREAEQLRAYLEGLCWEWLRRYLENGKETLQRA\DPPTHVTHHPISDHE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						ATLRCWALGFYPAEITLT\WORDGEDQT QDTELVETRPAGDRTFQKWA AVVPSGE EQRYTCHVQHEGLPKPLTPERWEAILPS PTSPIVGHCAWAGAVLASWSSGAVVAT VDV*EGRSSGGKGG\SYSGWRPSRPVP QGFWMCLSTALKKP
6764	20665	A	6818	34	382	STAGAIHVCMCMCVHVS TCVCAKMCVRV KF* IWDIETGAAQLSCCVLVAQTEI IYL QERNSSLSERECVC AK\CVMCMCMCVHVS TCVCVCVCV*V*KRHNWPGMVAHVCNSS TLGG
6765	20666	A	6819	1061	305	FFLRWSL/DSVAQAGVQWRD LIGSLQAPP RGFTFPFSCLSLPSSWDYRRPLRPANFF YF**RRGFTMLARMVSI*PRDLPASAS QSAGITGVSHRARRRNTILY*HLNFEVIK SHKPPDIVFRDL*GPRLHLENPVL*GAK SHSSCPWLNLSPPPPHAGSHCLSSSSPR MGARQDLLFNASSHTGLFFFLQLNQ TAS RPTSQVPKSLCFPLP WVQPFALP WVRQD EGRASVNSPQDPPRPVSCAGFT HSCNLS
6766	20667	A	6820	610	248	ERRSHPVA*AVVKWCHLGS LQPLPP\GS SDPP\T*AS*VAGTTGVRHHARLIFVFF IETVSHHVAQPTGF*TPGAQAIRLPQPP ENARITDVKPLCLAHFCYSKH FIMVPAP CISHQKV FH
6767	20668	A	6821	3636	3332	TCLGSHATPHCGHSFSSCKILLF*FFVF EM*SHPVQAQAGVQCRDLRSLPPPPL*FK RFSCLSLPSSWDSRRPPRLANF\CIFS RDGILSCWPGWSRTPDLR
6768	20669	A	6822	563	146	APGLSFNCYIPPAPAFMPGELTLFEVD/ NRSIFPTEY/TIHILISSEDILHS* TIP LLGLKTD AIPRCLNQTTLTGRPGLYYG QCSEICES/N/HSFIPIVLELILLYFK T*STSTLKYHCKAIQHLPFKLKIDGVYT SLQ
6769	20670	A	6823	399	201	KAEPKPAKSWSKGGYVLP RS/IRLDHVK WALEPDDIAVLNFMKERHPQSKS*TILO KWIQPFSPIVQK
6770	20671	A	6824	323	323	LPTVIVIIILSFYNFFFSMRLIRTL SFI CMYVCICIYVCIYVCIYVCIYIIYVCIY /IYINISF*NDRISFFMLE*YVCVYIH EWIKKI
6771	20672	A	6825	396	122	LPPGGHRPAVPGGREGMGP SRGNPGNPGR F*KKGPPSPGGGPAPGGPPSP EG*ARKM G*PRGPSLP*TQIPPGSPP/WGPPGV T PETLVGFKKRGHPPRGGPPPGVLP RR AKPEKWNVPGGQAFHEPKSPPRGPPRGA KPETLSPKKKKV
6772	20673	A	6826	414	64	RGVEGGAACIFKGLSVAGKPG/YLSAMR SCFRRMLLFKS*G/QVIATKHM LPTVLR MVGDPVANVRFNVAKSLQKIGPI LDNST WQSEVKPILEKLTQAQD VDKCFAQEAL TVLSLA
6773	20674	A	6827	2	519	KTKTCLVEEIS*ITGRFLERINKIDKPL VNL* RKK\VQVLNIRNEKVDVTTDRT*K \IIKEHYGQLYANKFN/IDEMDKFLKRD KLAKLTQEEIENLNIPVSI*KFLI*NIP KMKTP/GPDGISREL

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6774	20675	A	6828	413	114	GGKRGPGPTPHPPARGPQ*GPGHPAVQV PEPPGLSFPFHRGGFPSSGGCQRGEGRK ERRPSWTGPSWMAQEGRTPAARLEGAVL PG/APGPEAPGTGTTMSAPTWPPEP/G/ GRQVQDVPAFPEGSARQAR*HEE*LHWK EILL
6775	20676	A	6829	479	261	PCFSFSLNEDCRHAPP/RPV*F/LVERG FRHVARAGLEFLT*SGLPASASQGAGIA GVSHCAWPLQVGIEASLQY
6776	20677	A	6830	492	313	HPIGWPVNWGRASAVGEFRDWKLFYPEC EIRTMGGREHGQSPGAQRTFFQLLSFX VESK
6777	20678	A	6831	378	1	SNGICLQASSASPKNKIVPSTSLKVCNS\ VRVDGSRNPSVAFPPLT*PNLFAVAPSIS SGMGIETIPIQGYRVDEKTKKCIPIF\ V*ANRHSPSGVYNINVAHVSGPPLSDDS GVNKPQMKHQHCSA
6778	20679	A	6832	374	76	QLVEKWTGNVKSMTDRVLTMRCELRL *ALRTPGTWNLINDQIGMF\KFSGLSPK QVECLVNEKHIYLMPSGRINVSGLTAKT LGYYAASIQEAVTIIQ
6779	20680	A	6833	369	56	LKYLGTSVENRYADQAKWLSPVISALW* FE/CGWIARSEDREDHFG*QSEIIPS/PAN FLFLVEMGFYHVDQAGLDLMTSGNPPAC NTGMSHCTRPGRTDVLAILCSDP
6780	20681	A	6834	457	142	DCLALSSRLDLQWCDLGLSQAPPPGFKQ FLCLSLPSSWDYRCLPPRPANF*FLVE TGFHHVGGAGLKLTTSSDLPASASQSAG ITGLSHRAWPDSSFEGLSSSS
6781	20682	A	6835	407	35	TAPAIRGVHLRGRGWTVVGAV*AVPPAS IPAYPGVVYQYGFYAGADLYG\DMQHS DMLVMSQHSMPHT\LQQS\SVTVMAGC TQPSHTMPLPLPLVY\ELALWRVYAEVA TSYLPPAEVMLAPCK
6782	20683	A	6836	1	428	GKTLNPPSLGKSFGILGLPPENDWPPDV SVPRAAFPLRGPRSVQSVVREMEQVQA LLL*MLTFTPHKRISAFRAL\QHSYLHK DEGDPE
6783	20684	A	6837	3	612	FKGSGVFNRKKLEEHPLWQDVALGTAL CPQLPSLPGWGVIEWPRAACLPNPLQ CPHCCGPQEAQYPL*AGGQ*GQHKEKPG A\GPHPPSGQVPSAPGEAMTAMEGRKL SPAVAQNPQPKNTLPRGPLPRGAPTTT P*SLRPR*TPVGAGLAAPIRSHHPGCSG QEALALCPDRPHKDRGVRGAGGPRGRR VQLGGIPP
6784	20685	A	6838	3	412	YRWGFTMLTRLVLSS*PR/CDPPASASQ SVGITGVNHRVRLFFFFGTGPHS\MAQ AEGQGHNLG*LQPQPPGAKGTLPRGNF KGGPHTPPNF/CIFFGKNGVSPYCPGWD FGAKAILPPGPPKELELEGSPPAPGKVF
6785	20686	A	6839	419	26	EETSLWSIGQCPLLIQTAQVLSFTSGH GRHREHRKPTDSPLPSACPAP/RLTFPP SMCPASHSLPSSQCMPTLTPTTACAR PDTHSPPPSVCPAPLP/CRPVCPPPRSL PTPA*TKPRTQLPSSMYCGRSS
6786	20687	A	6840	365	66	LLERQIGRSVYGPSSKSSIFDVPSLPHR GIKLVFCLCHTSSWDTGWHYAPPA*SWH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						TVVHPRPRQVGQ/AGFELLTSCHPSPLT SQTARIAGVSHRARPKEFM
6787	20688	A	6841	445	188	GFQ*FSCFGLIGGWDTRHVPPRLADFCI F/M*RWGFAMSARLSSNS*SAPSASQSA GITGMSHCARPATLNSPICGTSLPLGSF FF
6788	20689	A	6842	3	412	PQOSPQLTTVTAPRPRALLMGTTMANLQ TRVSTSHLQGPRLTSALTYQMAQVAVAT PPVSVLAVVVLARSARVTVLP/LN/VNGI SVVIRQLQKAAGRQPPSPHQTRNNSLE* VASNLSKFLILEVAELFCHVLTFFSYQ
6789	20690	A	6843	113	410	NHKCNVNFYNGPRSLERLITLPLHYF LNFILCKSSYLTLNLKLQTNLFCK/YE M/ESHFVTQAGVQWHDLSLHPKQSSYL SLLSS*DYRGMPPHLAN
6790	20691	A	6844	2	357	FCPLARILQSGRFVLPWNSSGLVRGRRO EGPHGAFREHT/SLRAPQPRSENERR/ RIACALRAAHQASGWRLTPRAPRSPSGC HCPPEPTSR*EAWGARRKKGHGCCPAPH QPAPQDIS
6791	20692	A	6845	392	279	HFFFFPCRD/KSLAMLTRLILNSWA*VIL LPQPSKVLGLQV
6792	20693	A	6846	3	275	VNLVDKAAAGFERMDSNF\ETSSVTGKM LSSSIARYREIFYERKSPSMQQTFLSH FRKLP*PF*PLATTTLIY*QPSTSRQDP LPAKRAR
6793	20694	A	6847	1	454	FFFFETQFHSPLRLECSGAISAHCNFCL LGSSSSPASASQVVGITGMHHHAWIIF/ VLFLVETGFHHVGHAGFELLTTCGPPTL ASIMCILVYLLVFQHLVSLKNLKGQNAS FYFSPFGQHLSGFVKCSIWCCGSLSGLE GHFLPPHSPPLH
6794	20695	A	6848	13	148	GSAWRHTPAG\ELLKKLRHRYGLNPEGG GCTEP IWCYRTPPWTTD
6795	20696	A	6850	204	30	TIFSRQVLRIONVLSEKLRVSTVYANNG S\VLQGT LWASVYHGKILIGTVFHKITLY CEL
6796	20697	A	6851	2	429	EVWASGITGKAIMAMPVIVQPKNPSSYP CRRQFPPLQLEAKEGFQLLTEKFQKHGLL IPYN/TPILPVKKSNEKYRLVQDLRIIN EAVVPIHPMIPNSYVILPQPPDAQWFPV LDLKDSFFCISP/VDPSQFLFAFE
6797	20698	A	6852	3	160	SGWDHRRHTQLIFMYSFLFFCRDR/SLP MLPKLVLSWAQVILLQPPKVLGL
6798	20699	A	6853	2	243	ACMILAAATIILRVV\PLRYIILWGIN KFTKKLRNPYSIDNNELDLFLSRVPSDV QKVQYAECLKCSSHSPLRKKRSAL
6799	20700	A	6854	24	458	SRAARRAAGTTRRSSHTGCRPRPADPGA RCLPRGSPHPRMDPPESP/PSETSPGPP PMGPPPPSSKAPRSPVSGSPASGVEPT SFPVESEAVMEDVLRPLEQALED CRGHT RKQVCDDISRRLALLQEQWAGGKLSIPC KEENG
6800	20701	A	6855	3	183	CCDPFVSASQRAGITSVTY/Q/WPSLGS LQPPSPFEKRFSCLSLLSSWDHRHPPLR PACKVFC
6801	20702	A	6856	2	242	GNHPYARKLA\AQRRASTVSSVTQVEVD ENAYRCGSGMQMAKDSKSLKTHQTQPGI

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						RRARDKAL\LVANGKRLWCIEGSVC
6802	20703	A	6857	54	401	EGERLQKFMHVLKTHTHTH/AHTHERAH THTHTRTHTPRSGMHRSGNNRNLAKNLFK IFFFLSSSPPSLFFLIIFPFLSLSLSSL SLSLYKHTPLCILSLRTEHLHRMGALLG GHILE
6803	20704	A	6858	1374	579	CENPSRSTRPGQGPLLLPHQLPFH/RPA PSQSSPPEQPQSMEMRSVLRKAGSPRKA RRARLNPLVLLLDAAITGELEVQQAVK EMNDPSQPNEEGITALHNAICGANYSIV DFLITAGANVNSPDSHGWTPLHCAASCN DTVICMALVQHGAAIFATTLSDGATAFE KCDPYREGYADCATYLADVEQSMGLMNS GAVYALWDYSAEFGDELSFREGESVTVL RRDGPETDWWAALHGQEGYVPRNYFG LFPVRVKPQRSKV
6804	20705	A	6859	36	269	IALGSMVDVLTILMFNEHSKNEIKRTIPL KIATR/IKYLGINLT\RGKKDLDTENYT TLIEEIEDDTNKWKDIPCSWTGV
6805	20706	A	6860	47	888	TLRARALQARPTGSSCTAATWTS/SGA SQHSLRALSWRRLYLSRAKLKASRTSA LLSGFAMVAMVEVQLESDHEYPPGLLVA FSACTTVLVAVHLFALMVSTCLLPHIEA VSNIHNLNSVHQSPHQRLHRYVELAWGF STALGTFLFLAEVVLVGWVKFVPIGAPL DTPTPMVPTSRVPGTLAPVATSLSPASN LPRSSASAAPSQAEPACPPRQACGGGGA HGPGWQAAMASTAIMVPVGLVFVAFALH FYRSLVAHKTDTRYKQLEELNRLQGELQ AV
6806	20707	A	6861	3	391	NKISFFCRDWGLPMLPRLVLNSWAQVIL /LISTCQPPKVLGLQA
6807	20708	A	6862	322	175	GCRCVPPPRASFKEGRV/RGLDILPKL VSNWPQAILPPWPLESILVLQA
6808	20709	A	6863	700	294	YVLRQGLTLLPRL/ECSAIIAHCSLKL LGLRNPPTSASRVAGTIGACHHTRVIFI VFVIESCLLAQAGPKLLGSSDPPALAS QSAGIAGISHHAWPPYFYWVLSSTIPS VLSLHSHLILATILRGDVTSTQDK
6809	20710	A	6864	371	77	RSMFAN\NLVYDTSDDYHLLKVL EEG IQTLMGRLVGSRRTGQILKQTYSKFDT NSLNHVALLKNYGLLYCFRKMMDKVETF LRMVQCRSVEGSCGF
6810	20711	A	6865	273	34	DYLPPTYLKLFRLLFF/CLIIETESHYVA QAILELLSSSNSPTSASRSAGITGISHH TQPNFSNNTLLKPYLRLSYALLFA
6811	20712	A	6866	1	190	GAKGMHHTWLVRYF/CCVEMRSHYVTW VGLE/PPALKHSSCLSLPKCRDYPHEPP HLALFCFSF
6812	20713	A	6867	506	293	EKPSNGHKKPYTWISAILFIIAKTWKQ S\PRCPSAGEWINC/WYTQTMEYYSMLK RNELSNCEKT
6813	20714	A	6868	2	116	LFPFCRDR/SLTMLPRLISNSRAQGILL PWPPKLLGLQT
6814	20715	A	6869	10	141	GSAWLFFIFCR/DRGLALLPQLVSNPWL QAILLWPPRVLQLQA
6815	20716	A	6870	2	603	APTFINFPAKGKPKRGDTYHLQVRGFS EQIARWIADRTDVNIRVIRPPNYAGPLM

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						LGLLLAVIGGLVYLRRSNMEFLFNKTGW AFAALCF\VLAMTSGQMWDHIRG\PPYG PKDPHKGHVNYIHGSSQAQFVAETHIVL LFNGGVTLGMVLLCEAATSDMDIGKRKI MCVAGIGLVVLFSSWMLSIFRSKYHGYP YSFLMS
6816	20717	A	6871	375	1	GFPGFPPVKFGIPAPVAPQNPFPFPPSF/ PQGPFPSPGGPNPNNGKNPFPKTPFFLK NSPQKKKIIFLKKFKRGPP\GPNQKPPFK DFKKRGLKPPKGGPPLKKKKKKKRSN YSLKKIYSPFGFHFF
6817	20718	A	6872	255	23	GRVDPTSTSQNAGITGVSHR/GVQWRDL GSL/QPLSPGFKRFSCLSLSSSRDYRLV /FCIFSRDRILPFWPGWSQTPHLK
6818	20719	A	6873	5	157	YLLFTSYTHAHTHTHTHTQFLLWTS GLS\SCCYIFSLSGPNTKCNMIF
6819	20720	A	6874	351	132	SPRRC SAYVA/IYLFYFLINLLSLYS IFYGFAPNSFLCEVQEPGLG\SGWEPLS GNHFSSIKMKIAHREVN
6820	20721	A	6875	99	337	AGSFFQKKGKKKISRVRNQPIQLEKIFM NCASDKGLVPRIYKELESAR\KYQSIPS KVG
6821	20722	A	6876	69	306	YVSHLSFFF/CFFGGGEKALFFCPRTG IKWPQFGLLEBSPSPGLKQFGLNPPETL EYRVFFPPPGKFFFFFFFFFFFFFFF
6822	20723	A	6877	335	169	WHDLGLLQPPPPG\SSDSCASASQVAGI TGMHHSFSNFIYLFICYFEKVFLTFITLD
6823	20724	A	6878	2	237	ELGYKVLPHPPYSPDLSPTDYHFLKHLN NFL\FHNQQCAENAFQVFIQSQSTDLYA TGINKLISHWQKCVDSNCSYLN
6824	20725	A	6879	2	199	RGRVGRQFQKEIEELKKLEECEE/VAP SSSSSSSDPLISEPDISGSEEDDDEGE VGEDGEKKKKK
6825	20726	A	6880	1	206	FFFFETESCVAQAGLELLGLGDPPASA SQVVGTTGARHHAQLIF/VFVFLVEMGF HHVSQDGFLLTS
6826	20727	A	6881	1	123	WYIHTMEYYSALKRRKFLSFATTWMNLE \EIMLSKISRREG
6827	20728	A	6882	15	105	SQLL/WRLRQKNRLNRGGGGCSFPLWCH CTL
6828	20729	A	6883	223	1	AASTFLFPNLKNSLRG\SLRTFSSVTNV RKTALTWLNQDIQFFSRRSLTLVARL ECVVRSWPAASRRLGCL
6829	20730	A	6884	193	3	QGEQDFLPPCLPNFFNF\FFCRDTVSML PRLISNSWPQAVILPEPHKVLELQARAT TPSHVFIF
6830	20731	A	6885	2	355	RLLTSSDLPASASQSAGVTGMSHRARPR NF/CILPNLSPCNTHSPSLPQPLAPTI LLSLWICL/SLDIS/WDYRHMPPLAKV FFFGDGVSQ\YRPGWSAVVPFAASTSGV EAILPPQPPK
6831	20732	A	6886	1	151	HSVAQAGVQWWDHGSRLRPGTPGLKQ/FL PPLKQSSCLSLSSWDHRCATLY
6832	20733	A	6887	314	203	FLFFCGDKVLLCP\RLVNSNWTQVILQP WPPKVLGLQE
6833	20734	A	6888	334	86	QNRSTFKRGM/MGAWNLMFVIPATWEA EVAAKIAPLHYSGLDRARLSKGGMKCTS IFCSKSAKDCQTLPVKKKISLPTLPSI

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6834	20735	A	6889	345	152	QHARIMSVFIVETGFHHIGQSGLELMT/S/GNMHASASQSARITGVSPHARPSLPY YKCSKKQLCNE
6835	20736	A	6890	2	169	ARECSGATTAHCSLDLMGSSDTFTSASQ VAGTVGVTIMPRYIFK\FFVEMESHCIA
6836	20737	A	6891	361	184	NQSSCFSLSSWEHRLMPPHLANF/SFF DRDE/SLTVLSRLVSNWTQAILPPRI FENS
6837	20738	A	6892	3	330	HESAAITGVSHCTQTFFFF/CETGPRFV PQVKGGHDLSSGEFGPPRLRNWPGTL QNAGNTGTLPPTHRTNFGDFRRGSFSPCG PGGFGTRDLGGFPHLTGKRDTGLDPP
6838	20739	A	6893	2	348	ARAFFFWNFFCK/NRGLSMLPRLALNSG AQGILPPWPPKKLGLRALPTWPKTGSSG LEGHSSLYPHHSLIFPHHCSKFCFKQW RLFILRITENQGLTPLNAKPAEPMNE ARTQA
6839	20740	A	6894	340	240	CRD/RSLRMLLTVLNLSWIQAILLSWPP KVLGLQA
6840	20741	A	6895	155	1	HLCFWAG\PVAHSCHPGTGGGRGRITR GQEFETSLLGPGTQDVLAKCSRA
6841	20742	A	6896	454	294	PSSWDYRHA/PPMHNVPDFFCRDE/SL PMLPRLVWNFWAQLILLEPWTPKALQLQA
6842	20743	A	6897	49	333	IYICLSFYQSIYYLYDKQHDVLETVSHS VSLDLPGLRFSHLSLWDRILPWLASS NNFF\CRNRGLLVLPRLVSNWSVQAILP PWLPVIVLGLPA
6843	20744	A	6898	434	324	FFFFCRD/RSFAVLPRVLHLSWTQAIRP PWPLKVLGLQA
6844	20745	A	6899	127	365	LPERRRYVSIISGYRYHLPQSLLFFYAQH ATFNNELW\LGVIHACNPSTLGGDRGR MALGQEFEGLDLSIVRLHLCNKIK
6845	20746	A	6900	208	1	FFFFFWILVETRFHHVA/RAGLELLSAG NPPTSPSQSARITGIWFFVWFSSNLSQF CYAHSFFTCWYSRA
6846	20747	A	6901	1	162	GTSGTRLFTIGKRWQPKCPMAELINK MW\YTMHYSVLKRKEIFCTNLTLQLL
6847	20748	A	6902	120	313	DKVL/WRLRQENPLNPGGGGCSEPRSHH CTPAWATRAKLYLKKKNFKGTLSNWYS FRRVANTNLQMQSGSNYMQI
6848	20749	A	6903	340	234	IFFCRER\SILPRLVSTWFPQAILLRP PKVLGLQV
6849	20750	A	6904	1	327	GTSGTSRILPWGPGCIRTFELKQSAHLS LPKCWDCWNRYRHEPPVYSFAMLI IKLFF ELHLSVILWFLLLANPQTQTESKTF SKT /PRLVLNSWPQAVLPWSLKALASQA
6850	20751	A	6905	532	359	RDG/DLVVWPRMVSMGFKQSSHLGHPK CWDYRCEPLCQDFSYSIITVVFPPSREL RR
6851	20752	A	6906	270	3	GGTTVYPRKTKT/WPGAVAHACNPNILG GRGGWITRSGLPVSTKNTKISRACCAA VVLATPEAEQENRLKPGDGRDHHGQHG ETPSLSC
6852	20753	A	6907	1	312	GTSWKKMLPTLMDDFRG\KTLVEELIPD VVEIAREVELE\MEHEDVTELLQPHDKT WTDEELLTDEQRVVLEVGSVPVEDAV NIVEMKTKDLEYYISLLIKY
6853	20754	A	6908	331	61	FRHVQGAG/LQKLLTSSDLPAPASQSAG

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						ITGMSHHIRPKLILRKSMRAKLDSRQTRLQPPVVEQGLLEEQHEVYNVMAHVS KSSSRKLS
6854	20755	A	6909	419	199	SAVQDGV\SWCDLGS L\QPPLSRLKQFPCLSF PSTWDYKCAPHPATFCIFIRDGVSPCWS DWSQTPGLK
6855	20756	A	6910	341	69	EAEVGGLLKARSLRPAWAIQODPISILKKSFTLG GQGWI TRSGDRDLRASASQSA GTTGVS HRAQ\ LIFAFLVERRFHHAGQGGLDLLTL
6856	20757	A	6911	174	356	KTYLMP LRSSLRPGMVAHACNPSTLG GQGGWITRSG/ESRPSVLVNRLTRCQANTVKPCLY
6857	20758	A	6912	391	3	SDPPPPFPSPFPFPFPQNFPPPGASSFFGPPPP/YFP PPPKKSPPPNPPPPFFFP PPLGKQFFSPPPPFPFPFGFPFPFPFF FFFFFFFF FFFFFFFFCDDKKYFICLMICMLFFCKYILNFCRYS
6858	20759	A	6913	43	331	IRDTYSFSL SAPALAPMLGTGVL LAVA SLGSRGASLCVFCVCLCVRIH\IGVQASGCVCVCAC/CVCVCVRVCVCVCPHWPASLLTKDLQCLPFTV
6859	20760	A	6914	250	11	TPNLWGLFLVFCFEM/EVHYIAQAGLE/PPGLKPSSSL SLLSSWDYRHVM PHAAQICISVFS LAQKGVPPSNWILITHYSIKS
6860	20761	A	6915	532	53	SQMALHEGFL LLLFLKEKELHGKFSHPPPSAPNSSMSKVVFYFSE TESHVQAQVQWCNLSLQPPPPGFKQFSRLSLTSSWDYTYLPPHLANFLFLVEMGFLHVGQAGLKLPTSGDL PALGSQSVGITGVSHHTR\PRFLFKIGPLFLFSKMSQDEARI
6861	20762	A	6916	2	373	WHTPVVLATHEAEAGSLEPRRAKLQLA MIVA/NCTPAWVT
6862	20763	A	6917	1	270	GTRQSPRLS LSSSCDHRRVSPHPADF/SFFYFYFFCR/DRGFTMLPRQVLIWAQV MLLSQPPKLLGLQVGVSHGARPPHCLGYSWVYNKP
6863	20764	A	6918	2	367	RCAPHCPDNSSFFK/RVKTGLTIFPRQTSNSWPQVILLPWPP/KVLGLQA
6864	20765	A	6919	3	354	HEVNIVETTA KDLEYSINLVDKTGF EKI DSSFKR RSTVSKMPSDSITCYREIFCERKSQSM LQTSLLSYFKKLPPQPQPSA/TTTVISQQPSTLRQGP PAKRLRCAGLND FQHFWL
6865	20766	A	6920	366	41	STSGEDAVHIVEMTTKGLEP/YTAVPGFHPSSERRSVVGNMLSNSVTCYRGIFGERKSQC/RQTSLLPYFN/KPQQPQSATITLI\SOQPSTSR RDLPPKRLQLTESSNDH
6866	20767	A	6921	3	368	QLLMGLHLEPATL DDLQLKT\TIQGGSHSHHITAIP\PS\FTRENTLMFIHLSPI LLSLNPDIITGFFLLKKKNKPKNHKNRGPSYKRTPEGPLLLLVVAQKTLPPKGGLYKIAPLRLFGEDS
6867	20768	A	6922	3	91	FSVLPRLV\QNSWPQVICLPWHPKVLGLQV
6868	20769	A	6923	334	91	ERCCKCAHISEIFLSSLDYIYIFVY\FFFL FFFFFFFFFFFFFFFFFFFFFFFFFF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						QKFNFKSKSEKMFNKTMKKVQVTF
6869	20770	A	6924	375	37	TKAGVQWHDHGSLSQPQPPRLKPSSCSFSL PSSWDYRHAPP/RP/ALFLFLFGLVWFG LVFLVEIGSCYIAQAGLKLGGSSDPPTL VSQSARIIGPTHHAWPTLTTSIQCTIRG PG
6870	20771	A	6925	647	1054	CFWKAHIQAGETNNIQEGSERFHFPCPAD EVYVHSGPAVEDQPQRSEFAL/SAQAGV QWCNLSLLQPLPPRFKQFSCL/SLPSSW D\HRHVPACLAKFICIFSRDEVCHVGQAR LELLTSGDPPASASQSAGITGMNHHV
6871	20772	A	6926	3	204	DAWETTFGFMIDSLDYAKKNEPKHR/L ARHGLYEKKKTSRKQRKERKNRMKKVRG TAKANVGAGKKK
6872	20773	A	6927	1	112	PTRPRTRGVASVLYFTTILILIPT\ISL IENKILKWA
6873	20774	A	6928	1811	478	DRARSPRSERA\RRSSSRLRQRDPSLGR RRLRREIRPGLPESEPRPPPAALTD QPPPRRLSESRGGGGMSE\AGE\ATTTT TTTLQAPTEAAAAAPQDPAPKSPVGS APQAAAPAPAAHVAGNPGGDAAPATGT AAAASLATAAGS\EDAEEKVLATKVLGT VKWFNVRNGYGFINRNDTKEDVFHQTA IKKNNPRKYLRVSGDGETVEFDVVEGEK GAEAAANVTGPDGVPVEGSRYAADRRRYR RGYYGRRRGPPRNYAGEEEEEEGSGSSE G FDPPATDRQFSGARNQLRRPQYRQYRQ RRFPYPYHVGQTFDRRSRLVPHPNRIQAG EIGEMKDVPEGAQLQGPVHRNPYRPR YRSRGPPRPRPAPAVGEAEDKENQQATS GPNQPSVRRGYRRPYNYRRRPRPPNAPS QDGKEAKAGEAPTENPAPPTQOSSAE
6874	20775	A	6929	324	203	LIFVFLVETGFHHVQDGLDLL/NLVIR PPRPPKVLKLENP
6875	20776	A	6930	3	364	HEASLTQTRTMTTHCSRTTGCSTASGRT WTSRHS CAWCSAALWRAAVASRCPS / IPVTPPQCLSWP/WKVPLQCPPALS
6876	20777	A	6931	2	165	GRVGFCVAQAGLQWHDLSLKLPLPP/G SSDCPASASRIVGITSIAFHFLNNVF
6877	20778	A	6932	1	370	TELSYSFSPNGAIISSQCNLCFLGSGYS/ RSSTSQVAGITGA/R/HHTQLIFVFLVE TEFHHV\AKAGLELLTSGDPPASASQSV GIAGVSHCAWPHVYILKEIMLGNLVRCL MSICHHHTESICLFL
6878	20779	A	6933	1	441	RRANTPNNPEAPPN/QKKKKKKKKKKKG KNPPGGPPPFKTPPPFKNGGSPPGKK KGGEKKRGKIFFPFPGGKPPQKKKK GGGGKKIFFFLFGPGGGGNFFKKKKGPP PFPPRKKKIFPTGGGPKKKKKKAPPK KPRGFYFP
6879	20780	A	6934	518	340	PKPKNFPS/PSPPKIPPKKKVFSKKPP GGFNNPPHKRKKYNFPPEKLGPPEFL KRPL
6880	20781	A	6935	396	299	VVEVC/GVCVCVCVCVCVCIHSLCKSTL HRTGV
6881	20782	A	6936	486	272	PTRAPTRPAPPHLADFLIFCSDR/SLIM LPRLVLNSQPQMILPLWHPKVGLQA
6882	20783	A	6937	1	264	YSNLRDRARSCLSLPSSWDYTCSDYKC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						ASLRLANF/SNFCRERGLAMLLRLVSNS WAQVILLPQPSKVLRLCLAVSVFFGEKQ GQCS
6883	20784	A	6938	2	407	TTGTCRSVWLTFFVFLVVTGFHHVGQAGL ELL/RPPQPPKVLGLQA
6884	20785	A	6939	422	65	LKGPPPSFFFFFFFFFFFFFSP\LP YILYFDCASNACLFKKNTWRYIKRIF SPTPFIPFFHEVENVTSLSYVMVFQYCF FF
6885	20786	A	6940	462	209	LSEFWDYRREPPLPAKFAIFMLCRDRGL DTLPSLVSS/SWHQAILAPQPPIMGLQ VHSAYKGFCLPVLTFEEVIGNRPLGLLP P
6886	20787	A	6941	491	299	CAEYSPESGPTHASAHAS/SNVQMVS ISCKEELLGRTSPSKNYNMMTVSG
6887	20788	A	6942	429	256	FSHLSLPSSWDYKHLSSCPANFCIFVQT GFHHVGQA\GDPPASASQSVGVGTGMSH S
6888	20789	A	6943	932	661	FKTGSYSV\TRLEGSGEISAHCNLRFLS SSDFFHLSSQVARITGSSQYARLIFVFF VEMGFAMLRVGLKFLGFKPLHPP\RT P RVLGLQE
6889	20790	A	6944	381	55	PASLPCCSLISDCCASNQRDSVGVGPSE PGVGYSLVRRFSLRSEKRNIRVGVT SRCV/LSPLSLTQKGNLTPCASQVRQC LALLRLAHGACTHWPAPTVMHSLVR
6890	20791	A	6945	816	513	FFIFIYFFEMESLLPRLECSRMISSA HCK VCLPRSSSY/PASASQVAKITGA/TRHS RLIFCVCVLVERRFHHLAQAGLELL/NL VIHPSRPPKVLRLQGVTRTA
6891	20792	A	6946	383	234	LTPSLMDNSEGLKTSVEVTVADVVKIVR ELELKVKE/NVTDLLQS\YDKT
6892	20793	A	6947	423	60	LNPPPPPF\YKPPPKKKKFFSPPLKFG PPTKFFKRPPPPPPPPPPPPPPFWHGT F PLNSLVGPPKVEGWVSWAQLPRAVGPP L PNPKWGLNKPPAGGLNKP\HFP SLNGSG EATPPLIPWC
6893	20794	A	6948	1	327	MRLLAAALLLLLLALYTARVDGSKCKC\ SRKEPKIRYSDVKKL\EMKPK\YPHCEE KMVIITTKSVSRYRGQEHCLHPKLQSTK RFIKWYNANNEKRRVYEEAQGLRRRIG
6894	20795	A	6949	952	796	FFLHFLVEMG\FLLVGQAGLELPTSGDP PALASQSAGITGMSHRARPSVSS
6895	20796	A	6950	364	6	ITTHKNYFLSRTATPPKEGLPQRKKIFL FFTPIFIFVVGFI FWSGGRGFLVFFV FFFFFFFFFFFFFFFFFFFFF\RVK TFIGFKVLFKINVFFFLIRAVPLDYMN HALTIFQW
6896	20797	A	6951	418	266	ISFFFFXXXXFFFFXXFFLLFFFPFFFF FFFFFFFFFFFFFFFFFFFFFN
6897	20798	A	6952	459	7	PSYLYKPGSPQPNRRRHSVP/HIRSNKD PPPPEVMKKWGPPTPQKKKYFP PRKKKL GGGGGPIYPPKKKVFFKKKPGGFKKPPK KKKKIFFSPPEKRGPPPSILKNPPHPI FFFFFFFFFFFFFFFFFFFFFLIGEKA MLLDMGA
6898	20799	A	6953	325	143	LPSSWDYRRVPPHSAHFKFFCRN/RGLA MLPRLAKPRFPSISIFLNHPQVSEILGA

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						TRLAR
6899	20800	A	6954	585	306	KTESHSAIRSQCS\GEISAHCNRLRLPGS SNSPASASRVAGIKGTHQVQLIFVFLV EMGFHRAGQDGLRSPALVICPPWPPKVL GLEAWPALHC
6900	20801	A	6955	2	155	FLVETGFHHAGQAGLELLISGDPPTLAK S\DSQDVRITGLSHRAWFLDIY
6901	20802	A	6956	3	346	DAWPDAGWK\RNWPPHQANFYTFVE/TG FT/HVGQAGLELLGLSDVPTSSSLDAGI TGMSHCSRPRPEISSRDVHTIPGALQET WHTPDLASSIRSLRCLDCPHNHCPDLK DGVTL
6902	20803	A	6957	1	224	QCGRIRSRKDARKGNVQIIPREGRRRTS PRYLFPPVTGQETDGWG\MGLPAWLLKTR STSPPRSPLHRRRGATSW
6903	20804	A	6958	102	344	GLLKPKSLKLQCTIITPVN\NHCTAAWA T
6904	20805	A	6959	3	296	KEEEEEGEGEGGGGGG\EEEEEEEEEEEE EEEEEEEEEEHAEFTGHVESITQCKLLL CHLSLRVEAGITHLLCFTVRAVTRSQRL LTKRRNGSVGHTSE
6905	20806	A	6960	3	172	RLGLPKCWDYKREPP/RPGLELLTSSDL PALVSQSDGIKDVGHDTPEQDFYTLGQD P
6906	20807	A	6961	2	224	LALLPRLARSGTIIAHCSI\NRSRLRGL SDPPASASESTGTTGMSHCSQPAKLLST CIRNSVAETKYLLMFKCK
6907	20808	A	6962	2	330	KGTLRRQVITYKGTLLIR\LVADTLAETFH ARKEWDDIFKVLKHCQPRILYLAKPSF KNEGESFSQRKCIITRVARSKMAKGVHLH LEVKDISTIIKQMKIRSSLEVIQHKW
6908	20809	A	6963	1242	929	ETGSCSVVQAVVQWCGHGYLKPQPSHAH /DDPPTASSIAGTTEAHYHAQLIFKKFF NSLCCPGWSQVSWRILGSSDPPASASQN AGITGMSHGAWPQLSIYRKN
6909	20810	A	6964	1	378	KFFLQFLHLSFIYEHFLFFSFLFFFFFL RPSFAFVAQAGVQWRDLGSPQPLPPRFK QFSCLSLLSRWDYRHAPQSANF\EFLV ETGFLHVGQAGLELPTSGDPPTSASQSA GITGVSHRTRLAFY
6910	20811	A	6965	393	43	VSPFFPLKNFYFSFTPKTFVGGGGPSGPP PQKRFFHTPNSPFFFPFPF/YKSGPRP GFFFTPPPEKGKNFP\PLRLGPPPVFF TRPPPPFFFFFQRTCSFLHFLVVR PLRFYFL
6911	20812	A	6966	225	2	TRVECHGVFFGSCNPLLPGLKEFSAPAP RSGNSGPFPPPR/RNSFFFFSVLLE MGFHHGQADLEILTSSDPP
6912	20813	A	6967	8	341	FVSVPPIHLHLFKIFFFLRRSLCLPPR LECRGTISAHGSLGLPGSSDSPS/STKN TKLPLRGGTCGLPQLLGLLRHEKTWTLG GGSGSYPKSGKRAMALQGGVQNKTCVPH
6913	20814	A	6968	29	362	DYTCKHPHSELKKKKKKKKKKKKKKK KKKKGGPPKKKP/HGGQFPFPGRQKKIF PFKGGFKKPPRGFFEKNPFFGGGNLGGP PPPKNKPGEKKNFLGGRGQKNSFLSAW
6914	20815	A	6969	391	17	VFFFFFLKKFFPPPKLFFPPFPLKIF F/SPPNPFFFLGGFSQISPPPKKGFPPK

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						IPPGV/YFSPFFKKKNFFPPPLNFGPP RVFFKGPPPPPPPPPPPPPPPPPPFLGL RGNAGDCNGYGDVSYK
6915	20816	A	6970	374	268	IMLPRLVLNSWPPQVILEWP\PKVFRLO VRAPVPG
6916	20817	A	6971	614	315	FFFGDALSPGLECGGAVLARLQA/CLLG SHRSPASASRVAGTCKRPPPRPSGFFVF LVEAGLHRVGGDGLNLL/NLVIRPSRPP IVLGLQGMSSHARLFYFL
6917	20818	A	6972	861	528	FETESRSVTQAVVQWCNLSLQ/LPPG FKRFFCLSLPSSWDYRTPPCPANFCIF SRDGVLPWWPGWSRTSDLVIRLPRPQC WDYKREPLRLAKSRHPWNHLPEQEVEHF K
6918	20819	A	6973	274	119	PPN\FVFLVETGFLQGGVKLSTPGDPPP PASRRAGITGVSHPCPGKEYIFKN
6919	20820	A	6974	370	194	KITNFAKLFYILPYSHYFWCLEKNRNR /SLTLLPRLVSNWAQAFLLWPPKVLRL LQA
6920	20821	A	6975	2	239	ARGPCSSI/SDCCASGEQGSVGVGPAEP G/MGYNLLACCLLRPLEKCSIKAGVSRF SWYLSRLPLT\RKGNPPTPCISQVR
6921	20822	A	6976	361	270	POWLVPVIPA/LLETEVGGSLERSSRP AWAR
6922	20823	A	6977	363	48	GPPKEMCPYPN\PRPYECNLFGRVFAD VIKFKILRW\IILDYTVQDPKSNDCEPY KKQKRRGHRQIKRKSQADQGGRDWSGAT ARNAKMITSVGEDVRKRKPLAYC
6923	20824	A	6978	9	163	AGYNFLVCC\LPRLLEKCSIRMGVSRFS RYHLSWLFPARKGNSPTCTSWVR
6924	20825	A	6979	408	212	IETGFCHVAQDG/LELLASDDPPASASQ SAEITDVSHRAQPHSAFLPWFSKIFAY GSVWLVPFHS
6925	20826	A	6980	395	254	LIFVFLVETRFHVRVGQAGLELLTSSDLP SLASG\ITGVSHHSRPSAF
6926	20827	A	6981	408	2	KVSFFFPKGPGRGKKNGAGGFSPPFPF LGGGTKNFFYPPIFSQGGGKK/QKPPPP EKKNPPNPAFWGPPPLVLKNWGGRPGGP LDPKVSNFMGAPPFLFGAKKKTFFSPPP PKKKKPQKKGGGRSRRTSRTRG
6927	20828	A	6982	2	302	RKHLPPH\PVIFVFLEQATLRHVQAGL ELLTSSDHRASASQSAGITGVSHCSLPA TSFSTPPFSVAKMLRGTQKMKVPLIGPL PQIRLVAGHYFIYIT
6928	20829	A	6983	2	375	RGRVGGPVGGPVGRTFIFFQAGSDSARI LVLFPHYCTLPHPPLGLFFFFFTGIKSW VLLNPSPRFVIFLEKKIFLPQPPFF/HI LSPPHPGGAGGNPTARKIKGLSYRDPK EGHKRGVVAHTPTP
6929	20830	A	6984	1	146	PRPANFC/DFLVETRFHAGQAGLKLST SSDLP TLVSQSAGTTGMSHRA
6930	20831	A	6985	2	95	LTMLPRLECNDTIPAHCSLNS/SGSSHS LTSTSKVAGTTGVHHHFWLMF/PLFIIQ
6931	20832	A	6986	340	169	VCSSGLSSPLLEQHKTNLIFYASGDICT /ANGKSGFNQPPFLKTFCTHRIMSCT YL
6932	20833	A	6987	346	218	PCLTNF/SIFCRDE/SLTML/PRLVLNS WAQAILLPRPPRLRLQA

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6933	20834	A	6988	345	141	NRPKCPSTIEWIKMWHIDTMEYYAAIK KDKFMSF\ETITLGEVTQEWKTKHRLLS LIRGS
6934	20835	A	6989	154	236	ELISFSRSVERCISSEFIKLVFVETDLFT LSLSPFFSVLFFFC/RRWGFTMLPTLV NSWPQVILLPLPKVLRPT
6935	20836	A	6990	2	156	FLVE/TGFVHVGVQVLELLTSGDLPSA SQSVGIIGVSHRVRPCFLFVCICLV
6936	20837	A	6991	310	96	KNFFFLVKKSP/LNVAQGLKLLGSND PEASVSQSGGITGVSPRARPLNFYKAT DPNTSVLKGLNIKKKK
6937	20838	A	6992	15	279	NLLCFPSISPLIGIFFFERGFHHVGOA GLKLLTSGD/LRASPSQARITAMTRHP HPLVCGLLNSTHCDWRGRIPHWGFDLRF REGPS
6938	20839	A	6993	127	352	KLADTPQSRFVLVCV/LIETKYSLCCPG GLQLLASSNPPTSVSQSATITDVNHAE SQVFLNLVVPKSSKPTNTGL
6939	20840	A	6994	323	119	SSSEDHKHVPPHSAMFCFF/CLRQSLTM LPRLVLNSWAQVILPPSPKPFDLALKK KSSKWMSSLLIT
6940	20841	A	6995	230	1	FFFETESCSVTQAGVQWCDLGSLOPLPP GFKQFSCLS/LPNSWDYRHALPCPANFC IFSRDGVSPGWSGWSRIPDLG
6941	20842	A	6996	346	121	RDICTPMFVTALLIAKTRSPHKCPSVDT WIRKMW\IYTMYYKAIKKNILGMSH HASLPVFVNHMCKLKYLIS
6942	20843	A	6997	2	198	SNNTVVAFREPGITGMCHHAQLIVLLYM QFHHVDQDGLDVR/NLVICPPWPPKLG IQALNQPSPI
6943	20844	A	6998	183	31	MRHLKSSQIQQGTVGHCNPSTLGDHGE RITQEQEFKT\GNIVRPLYKD
6944	20845	A	6999	3	471	LALSCSGTILAHCNLHLLGPSLPPTSAP RAAGTTGVHHHAWLIFFVFGKDGVAPG LKLSFK/VIRPPQLPKVLGLQA
6945	20846	A	7000	483	239	GNNNILFLFFFIETGSHFVT/RLEQW VQSSAHSQSPAPRAQVLIFFVLLQTGFH YVG\QAGLQLTSSDPHSALLKVRD
6946	20847	A	7001	132	353	YAKLGTGRFARGPVVPGFLTVAVWMSF AQAGINPFCIFSNRELRRCFSTTL/PL LQKIQVTKGTLCLCYMREHL
6947	20848	A	7002	2	399	EDAQLEVELQEGKVHSESDKAITPHSQEE FQKQERESAE\SELTES
6948	20849	A	7003	2	135	IFQFLVEMGFHHVGOAGLELL/NLMIHP PRPSKVLGLQAYWHSTRP
6949	20850	A	7004	2	114	IFQFLVEMGFHHVGOAGLELL/NLMIHP PRPSKVLGLQA
6950	20851	A	7005	455	1	ALFPAPWLWLPSSSKGGLKLSHGTTTLF LLPSSTLKDLWPQEQWL/GTCNSQHFGFR PRKADRLAPGVQNRPGQRGETPSRKKGG EGNWGGGELHIYTYTHTYVHTYIHA NWTWVCVPVLAFAQETEVGGPLEPEVAP AWVTVRPCLKKK
6951	20852	A	7006	371	172	QVILCLSLPGSWDHRHTPPHPA/NFLVE TRFQHVDELLASNDPPASASQSVGITG VSHCARPCYDL
6952	20853	A	7007	486	252	PQTVFFFFFFFFFQALFSTFYILHVF FFFFFFFFPKFQFFPF/LSLIKQKGF

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						FFFFFCYLCNSLFIIVVTQYFFVNE
6953	20854	A	7008	1	113	KNFCR/DRSLDTLRLISNSWPQVTLTP QPPKVLGLQA
6954	20855	A	7009	105	383	SLHRPAHPGLLKFGKKAIHSFIHLCDK GDLAILPRLVSNWPQVILLPWST/NVL RLQA
6955	20856	A	7010	609	348	ESHSVTQAGVQWYDLSLQPLPPGS\SD SPASASHVAGITGMRHHTQL\IFVLLVE TRSHHVSQTKFVLFDTTKFVVIFYSGKR TRIRL
6956	20857	A	7011	382	233	DLEIFRGKTFLLHHIFPFFFFFFFC/RRRG LAMLPLKLVLSNWPQVILPKCWD
6957	20858	A	7012	359	199	DLPLSLPPFLPSFL\FFLFETESHSSPR LECSGAIPAHCSLGDRLRRLKINK
6958	20859	A	7014	3	274	CFFFFFFETGSHSVTQAGVQWRHLSLQPL PPPGCKRFSCLS/LPSSWDYRHV/PSSP LLVRNSSICLLSCFEMTPELFDGVLAIY CCVTNDLKA
6959	20860	A	7015	372	54	LPSAWEAEMRGPLEPKGLRSQRAETAP\ CTPAWVTEQAYVSNKNTNTERPFQKIEHV EGLSCTTQKFSSND
6960	20861	A	7016	548	158	KEDT/GATLFDGRPAVFDEA/DFPSVAV YLTGAEYTGELDSDTWQAEHLHIEVFLP AQVPDSELDAMESRIYVMSDIPALSD LITSMVASGYDYRRDDAGLWSSADLTY VITYEM
6961	20862	A	7018	396	34	QKNEIKPTMQLHLTPARMAI IKKILKNG GWHGCGE/METLLHCWQECKLVQPLWKT MWRFLKEPKVELPFDPAIPVLGIQQSQH WESSNPSTGDPAIPPLGIQQSQPRRKVI KKRYLHTRL
6962	20863	A	7020	2	241	FPGPTAARRRQKEDRYEYDKVLSDKLK EAETRAEFAERSLRLKSIDDLQDEL\ YAHKLKYQAISEELDHALNDMTSI
6963	20864	A	7021	347	3	NDLKSLTHSVAQARVQW\NISSLQRP PQFKRFSCFSLPSSWDYSLNCKFYHLH FADEEIEITLTSQRAQLECKSNMYKDIHN TVRSYKLKYKVPQKLESRNRTKSSTRE VRS
6964	20865	A	7022	2	160	LRDDRRGRGFHHFGQAGLELLTSSD/L PTSASQSAGITGVTHRAPDWSFCQF
6965	20866	A	7023	3	248	DRVSSVAQSSLELLSSSNPHLGFPCWD YRNPPLPFSSRSLFLPSFLIFCRDRV SMLPKLASSFW\VRPPWPSKVLGLQA
6966	20867	A	7024	483	143	PLNPLKFFFFPKAFKFWGGVGPICSPPK RRVLSQKSQVGFYFPQKEKGYTFPSPG KFGPPKEILKRAPPFFFFFFFLRRDK/ SLTMLPGLVLNPWPQAVLPLQPPKALGL QA
6967	20868	A	7025	414	81	PHPLKFFFFPETFYFWNGVSPFSPGGR KVPPQKSPGGFLLAPPKGKSFPFCPFK IGPPRGIFKRAPPYFFFFFFFNRRDK/S LTMLPGLVLNPWPQAVLPLQPPKALGLQ A
6968	20869	A	7026	16	218	KFAPRCRNSARENTQNQPRKHSDDTFLK K/HKINNKKLAGRGTHLWSQLLGRLRW EDHLSPRQSRLQ
6969	20870	A	7027	28	272	EFVGVGPSEPGAGYNLL\CAFLSPSEKC

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						SIRVGVTFRSRCHLSPLTLTKKGNLSLTP CASRVQRCLTLRLAHGALHPLSSSTP
6970	20871	A	7028	277	480	LGIFHMLSDFLLLLFLFVFKIFFGI FCRD\RSCYEVWAMPLPRLVSNWAQVIL PEWPLKVLGLQA
6971	20872	A	7029	24	153	SVWWNSP/RSSGEFRKTGVHDADFEAHI IDMLAKASKIEVYRGN
6972	20873	A	7030	2	470	IETPRPLWWHSAYRGRQASLSCGGLHPV R/ASWLLCLPNQAWAMAGAPPPASLLPC SLISDCCASNQRDSVGVGPSEPGVYNL LVRRFLSQSEKRNIRVGVTFRSRCV/LL PLSLTRKGNLSLTPWASQVWQCLALLRFA HGARTHWPAPT VWHSLVR
6973	20874	A	7031	487	107	SPPAPGVAPAPPPPTRVFSKKKKKFFFF FLKKIFFFKPGDPPGGIFFPGPPPPGP KKFSPPLFPKGGYRVFPFPPGKISIFT FFFFFFFF/CRDR/SLAMLPRVLNLF WAQVILLWSPKVLGLQA
6974	20875	A	7032	576	36	GYTSQMGRPGRGAPHFPDRAAGQRRSSL PRWGGWAEALLTSQMGRWPGRGAPHIPD DQPPGRGAPHLPEEQLGRGAPHLPEE RPGRGAPHFPGAAGQRCASHPTRGGRA EVLPTSQTGQPPRGAPHLPDGPRGRGT PHLPDG/GPGRGAPHIPDGAARQRLSP PRRGNCTTRIVDQ
6975	20876	A	7033	2	129	YGPTHASGAMLRSCAARLRTLGALCLPP VGRRLP\EASRDPS
6976	20877	A	7034	1	287	RLSLALVARDGVQWCDLGSPPPPPTGFK RFSCLSLPSSWDYRHVSPRPANFVFLVD TGFLHFGQAGLELPTSGDPPALASQSAG I\TGVSHRAWPK
6977	20878	A	7035	3	315	HASAHASALFYFIFFETRSRVAQAEVQ WRKLGSLQPPRFKQFSCLSHPYRHAPPH FANLVFLVETGFA\HVGQAGLELPTSSN LASQSGGITGVSRARPLNLF
6978	20879	A	7036	430	304	VIFYLIFFCKDGV/LTMLPRLVLNSWLH AILPPQPPKVLGLQA
6979	20880	A	7037	3	256	FFFFNRQKDLFGNFQTCQKWHSPSPRPT /APHQAPKGNTSPPSLPPIHLTLASTCTY PIPQAMLENWSVPSPAQAAGEAALWHPR R
6980	20881	A	7038	13	481	FARLHEFGTSRVIYLLARLVSNWPQVI CLPWPPKL/LGLQA
6981	20882	A	7039	455	255	SCLSLPSSWDYRRAPRHPANFR\FLVET GFRHVALAGLKYPALASQNAGITGVSH HARPEQFILTN
6982	20883	A	7040	490	172	KCWQG/C/GETGLVHC/WIGRNCTMMR POWQQAQVFKKLHRELPSDPAMPLLG VQPGGLKIDTQT/RMYMALLTVKRWKQP ECPPVDK/LDKLWYIHTTEYRVTIKKK
6983	20884	A	7041	438	37	IFPNLPPLHYFPQFSPPEKLPKPLLIK MAKRQSQGVFETPKEK/SRAGPPPKFT TGFSAEKNGGPKPGYISQRVQKKKNNC HSRILHSAKLSFKNRSEIKTFLNKQKLK /DFTASRPALQKILQAEFHRDT
6984	20885	A	7042	292	463	IEAISFLPFFFGDSLTAQWRDLGSLQP LPPGLKRFSCLSLPSELPCSGRCQS
6985	20886	A	7043	59	257	LASLVSQSWMKMMWYITMKYYAATK\G

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						NEIMSSAGTWMKLEAIIILSKVTQEQRKTHHMLSLRSGS
6986	20887	A	7044	279	14	RTADTEIGRGSSSLCWRYGSLQIQVSKSH NFFFETGSHSATQYGVQWHNLGSPQPQT YGLQQSSHCGLPKCWDYRE/LPPSMECS GTISAHLSLKLGMSSNPLTVASQSAGIT GNSSSRLHDINYGLQ
6987	20888	A	7045	578	253	AAASTFSCFFVFFETEPNSVA\RLECSG ATSAHHKLCLPGSSNSPVSAPOVAGITD AHNHIQLIFVLVETGFHHVGQAGLELQ/ NLVISLPPWPKVLGLQAWSHHAQPFV
6988	20889	A	7046	3	229	FFKTGSLSVSQAGVQW/PNLSSLQLPPP RFKQFSCLSFPSSWDYRHPHPHPANFCS FSRDRVPPCWSGWSQTPDLR
6989	20890	A	7047	367	151	LSLLSSWHYGHVPTSPANFFYF/CVDTG PRCVSNWTOAVCLPQLPRLVGLQA
6990	20891	A	7048	370	141	CQPPHPANFCIFVEIVFCHVQGTGFKLL TSNDLPWASQSAGIWD/TGVSHHAWPS RFNSEVQFDYVSNKNVDFSL
6991	20892	A	7049	104	361	VTAPGLEAAFKERVWPGAVARTCGPSTL GGRGRI\RGQEIKTILANTLKPCLY
6992	20893	A	7050	2	325	RFSCSLPSSWDYRHEPRLAIFFFFFF GIIRKGGFTH\VGRGGFKPWTSGNMPAL PSQGVGFPLFSPPRPVRGFFYPPLPKWG GLFLQNGVKFKKGGSGDLFKMEKK
6993	20894	A	7051	14	208	AHEILSEIENPLEPGWDHRCVSSCPAHF FVF/CYRDGGLPMLPKRVLNSWAQAILP WAPKVLGLQV
6994	20895	A	7052	103	368	GNRVHTYMLTALFMTAKWNKPKC/PVS DEQIRQIWSVHAMEYYSAIKRNEALICV TTWVNLENIMLSESSQKTMGCMRLRSIY MKGPE
6995	20896	A	7053	421	2	LFLPPEVARGFPKGRGRASPSPGGFFFG PRGGPIFFPP\SFFPTREWSKGEVFPSP TPGKGFGRGFFPPPPKGGGVPLPFKK YLGEGAPQNKGGPVFLWPPHSGPFGP PKNFFFFFFFETESCYVPGCSAVVQS Q
6996	20897	A	7054	489	40	IPEAPGGPGFKREDSPGANKSGPKALYP PKTFHPPWEGRFRSFQKGAFFFFVFFPP FFPLPFFFLRQSHSIPQAGVQWRDLGSL QPPPPPGFKQFSCVSLPCPP\QMGFRH VGQAGLELLTSGHPDSSASQSTGITGVS HCAEFHRTD
6997	20898	A	7055	3	261	TGSGSVTQAEVQAEVMAHCSLNLGSSD LSALASRAAGAAGTCHHAWLIFVFFIEM GFHYVPRL/GLELWARVIHPPQPPRVLG LQV
6998	20899	A	7056	1198	1040	FLWKIALLFYFKKLPQSLQPLVATTLSS QQPSTSRQDPLPAKRL\RLAEGSDDR
6999	20900	A	7057	271	33	LFFFFKMESSRSVARLECSGAILAQCNLA RLFLVE\QGFHHVGQDGLGLLIHPPWPP EVLGLQAQATPPSPKITYEATVM
7000	20901	A	7058	2	194	CYRRQPPHLMNFYFLNFFCLFFC\KA LSLLARLLLSQLQASLPPQPPKVLGLQ ACGTTPCP
7001	20902	A	7059	3	272	NMWKLNNILLNNQWVNGEIKMKIFKNCK E\NGNTTYQNLRDAEAFLLKGFIAVNT

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						YIKKDYRKTCRLRLFYSYHFFNKEKEYTLKTMIKV
7002	20903	A	7060	397	129	FWGPHKKNFPLPARGRKLGSKFTA/LPLFFFFFSFSLSLFFFSGSCSVS\RLKCSGTITAYCSLEFLGSSNPASFSQAAGTTF TFFLFIG
7003	20904	A	7061	3	351	SCFRLLCLPKAWAMAGAPPPASLPPCS LISDCCASNQCDS/VGVGPSEPGAGYNL VVRRFLSGSEKRNIRVGVTFRSRRPSP LSLTRKGNLTPCSSQVRQCLALLRLAH GARTH
7004	20905	A	7062	60	324	DDFVSVVQTVGHWCGRGLKPPRLSS TSRLSSPSSWDYGRVPF\NIFCRDRVSL CFPGWPRTPDLRGSSCPSPKVVKLHTRV TAPGQ
7005	20906	A	7063	481	160	RPGAPG/PDDFARMGPRPKGGAFTLVHP MPGSAAFPGLLSEP\PHRGPRSFARSP TLRYPGRAPSKSGEDPARPPATGPGPN LIQDGLVLSLTENV
7006	20907	A	7064	65	481	CLCPAPRGGAYRGRQASLSCGGLHPVRA SRIILCLPKQAWAMAGAPPPASLPCCSLI SDCCASNQRDSVGVGPSEPGVGYSLVVR RFLSRSEKRNIRVGVTFRSVC/LSPLS LTRKGNCLTPCASQVRQCLALLRLAHGA
7007	20908	A	7065	392	183	GGLKP/IPGNPNSLFSQKKKKQPGAGG SPRGSPPPGGLGGGIFFGPKGLGSINPN FGPAPPPGGQKKKSLF
7008	20909	A	7066	538	248	FFLKQSCSVAQAGVHWGLSSLQTLHPR F\KFSCHSLSSWDYRCAPPRLAN\FVL LAEMGFHFHIAQAGLELPTSNLPTSA SQNAGITGVSHHT
7009	20910	A	7067	2	127	VTGQAVVHACSPGTLGARAG/WIVWAQQ FRTSLGIMVRPCLYL
7010	20911	A	7068	379	217	KKMFCKNE/SFTIFPRLVLNSWAQTILP PWPPKVLGLQVQTTVPGSYSPLSLYKE
7011	20912	A	7069	386	176	KRDKVDKWLKMMWCIIHMEYYLAIKKET LPFATWVNLQ\TFILSEISQEQDKYHMI SLICGKMLIYRIE
7012	20913	A	7070	30	408	NSSELGSVGVGPTEPGTGNNLLVCWLLR LWEKCSVWAGVSRFFQ/CTDYDGPWVG KGNPPTPCASQVRRHPALLRRTLHGLHP CASHEKNQVPQLEMOKSSVFCIDLTGSC RVELFPFGHLGSKNP
7013	20914	A	7071	310	414	HVPWRSFAPAHCNLGSLOPPPPGFKRFS CLSLPSSWDYRCPPRLAN\FCSGSLQS WLTATSASWVQAILLSQPPE
7014	20915	A	7072	353	243	IFIFCRV/RGLTILSRLVWNFWQVILL PEPPKVLGLQV
7015	20916	A	7073	1	276	ELWDNFKEPNITLYLKSLEKKECVCEGR RDRNKTLEDIMAKNFSNWMKIINPQIQE AQOTPN\QETGRKLALRHITIKLLKTND KKKILKAV
7016	20917	A	7074	362	133	GGGGGGGRYSPOKKGTPLTPPSNWGPK GAPPPRGNEFFFFFS\RDGCLAMLRL VLDSWAQVMLLPQPLKVLKL
7017	20918	A	7075	3	177	KWSPHHSLENN\WLYRHMPPCPANVEFF CSLAVLPRMVSNSWPGAILSPWPTRMLG LQT

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7018	20919	A	7076	1	169	PQLPSSRNRYRHVPPCWANFCIFS/RRRCFTMLARLFLNSWPQVTRPHWPPKVLGLQA
7019	20920	A	7077	402	231	PSCLSLRSSWDYRCMPPHLTNYYYYYYY YFVEMGSHSVTRPQDILPPWP\PKVLGLQV
7020	20921	A	7078	422	316	FCKDK/SLPMLPKLILNSWVQTTHLPQP PKVLGLQA
7021	20922	A	7079	58	293	DPICTKSKKLKKTQ\TDKEDEITTKKAK KAKSKIKIEEDGEEGKVVVVEEVSVKK KKDKKKPWLGMAHTCNPTNLGG
7022	20923	A	7080	363	123	GVFFRDHARAFSLHTGVCVHISRCF/H VLTHFKEFLPHWFLTITHHTHTHTHTHT HTSPFPELGKAVPMHRIVIVPTNYQH
7023	20924	A	7081	3	181	YFL\FFWDRVLPCHPGWSKGWSQTPGL GQSAHLSLPKHVWCRRPPHPALFLFK NTIS
7024	20925	A	7082	453	142	FFXXFXFXXXXXFFFFFFFFFFXPPFFFF FFFLKNSFPYFFLFFFFYPLFLPLFFFF FPPNFFFFFFLFS*NFFFFFFPPPLFFF FFFFLFFFFFFFFFFFFFSF
7025	20926	A	7083	268	92	KNNLPSSWG\YKCSPPHKGNRFFFYIKD GGGLIMLLRLISNSWAQVILLSWPSKVL ERQA
7026	20927	A	7084	413	0	SCSVAQDGVQWDDLGLSLQLRPPKNKFFF CLSSTPAA\FPSDWDIR
7027	20928	A	7085	400	125	KTRSFVSVRGGVQL/CI/GSLKPRTPGV KSSSPSASPVGRNTGMCPPQIIFFLV ETGSHYAAQASLKQSSCLGLILFLSQP LGEKEGPTICT
7028	20929	A	7086	377	38	NPCPGFYFWGPKKKIKPFPFPGVKLVSF KRAPPFFF/CFFFTGSPFVAQTSLELL DSHNPPTSASQSAGITDSHHARPMHSI CMIQLWKS YHRFHFI SQSRDCSSSREE T
7029	20930	A	7087	1	151	SFCRD/KRLIMLPRLVLNSQAQVMLLPQ PPKVLSHHTWPIIKFSFMHFNLF
7030	20931	A	7088	405	111	PRILVN\SELRRSAHLSLPKCWDYGPFP PCPAQMHLVLSGTAAHKVHDFLASHSL PTHSPFPVLCSKTQISVAFFIQNLRAGQ RSGQRHFGKQCGSIH
7031	20932	A	7089	1	309	KQINKSSLRISGKPPNCBVLHLGKSVN KSLLEPHKLASDP/HLCDFLESS\EQVK SVKELNCHV\TSLYTLGALES DMAEYF\ NKYTLGPGMLAHAYNSSILGG
7032	20933	A	7090	414	240	FSLF/CKNLKKGLTMLPKLVSNFWPQAI LLPQPPKVLGL
7033	20934	A	7091	460	328	RHPPPYLGK/FFCRDR/SLTMLPRLVSN SWPVILSPWPPKVLVL
7034	20935	A	7092	388	199	KQFSCSLSPSRWDY/SALPPRPAHFCIF NRDGFSPYWSGWSLGLPKCSDYRRRIFL RAKAHVRE
7035	20936	A	7093	18	271	MHSFATYLLVNLHLLVLCRLCPLSMYSG EKSYILLTKRPMWLF/SSGPPPSWSFSS ITLRIFLTCLTLKLSCCSCCCCYCCCC C
7036	20937	A	7094	415	291	GDLGSPQAPPPG\SRHSPASASRIDGTT GARHIMNFKNLAIK

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7037	20938	A	7095	21	428	DKGLTVTQARVQW/HDPSRQPPSPGLK RFFRLSLPSNWDHRCAPPRVANYFFYR WGSYHVAQAGLELLASNTPTSASHSAG ITALFLRDTLVRFFMGSEFCFPQSFGAFF TAQIPQGRTEELFIFLFLNDYLF
7038	20939	A	7096	320	134	LPL\PKTTFYLFLNRDRVLLCCPGWSR\ ILSSKQSTLLGLPKCWDHRHEPPQQAVID HTLDFS
7039	20940	A	7097	402	221	DYRHVPPFPANF/LVEMGFVHVSQAGLE LLGSSDPNTSQAAGITETSHQAQAYTF IFIIY
7040	20941	A	7098	427	259	PEPRFKRFGSLSLRRWDYRPPSPCPGN FFFFF\CIFVQMGFHLVGQAKMLKLHD
7041	20942	A	7099	422	275	VQWYNLDSLQPASSGFKRFSHLRLSTW DYRH\PRPANFCIFSNTKDTFI
7042	20943	A	7100	3	404	HASGATWRNPVSTRVWHITIVPATQEG EMGGSLEPRK/LKAAVSHCTPVWVT
7043	20944	A	7101	539	336	FETESRSFTEAGVQWRDLGSLQPPPGF KR/DSPALASRVGTGTGAHHAGLIFVF LVEAGVSPHWPGWS
7044	20945	A	7102	408	287	WLILFFIFICRD/RGLTMLPTLVNSWAQ AILLPQPPKVLGL
7045	20946	A	7103	1074	705	SFLRWSFTLVAQAGVRWRGLGSLQPLPP WFKQFSCSLSSWD\YGRPPRLANYF F\VILVETGFHRYWPRMVSNSQPQ/CDL PAVGRPNASAGI\TGVSHCAWPKMFLNNC TCTHSPYLQGIVSLG
7046	20947	A	7104	227	55	FSQHKINIQFYISLSPTHITMSFFLCRD /RGLAMLHRL/VLNSWPHVILPPWPPKV LRL
7047	20948	A	7105	479	314	PRLLLIFFFTIERGL/LCSPGWSQTFGLQ ESSCFGLPKSWGPRKEPQPCALKWTLQ
7048	20949	A	7106	37	143	NSFF/CKRRCLTMSRLVNSWPPQVILT PQPPKLEL
7049	20950	A	7107	441	106	GAPSPASLPPCSLISDCCASNQRDSVGV GPSEPGVGYSLVRRFLSRSEKRNIRVG VTRFSRCV/LSPLSLTRKGNLTPCASQ VRQCLALLRLAHGAHTHPAPTIVHSLV R
7050	20951	A	7108	413	207	CCIQAGPAFFGGPPPPRWGGVPPPGFY /MSPPPVFRVGLLVFRGPPPNWFLPMGL QPDGPGGLGDPKKFAK
7051	20952	A	7109	92	409	PHLPDGAAGQRCPPPGRGGCVRAGPQL PPGRGGWPGGLPPPPSRTGWLPGGGAP HFSDGAVARQVRVSSLLRRGGRAETLLTS QTGSRPGRGTPHISDDGRPRGD
7052	20953	A	7110	408	13	EPWGPFGGPEARGSNPPGPPWGTPLS PKKPKNYSQGQGGPLNPPPEG/SGPGI PFSPEGKGSNLPGGQKIGAPSPPGG PKKKPPSQKKKKGKEKKEKVIKGESSQI LLFKVSKILSVNFLHLSLI
7053	20954	A	7111	290	175	LKKNCR/DRSHTMLPRLVLNSWPQTILP SQPPKVLGLQI
7054	20955	A	7112	1136	552	ILFKEMGCEAGQRCSCPVIPTILGRPRR ADHLRCGVRDQPGPTWLKPRLYSNTKIS WAWWRVPA\IPA\IRREATRFTFNPRR WRLPLNLRSHPLHSHPGRQSKIPIKKER KKGQDRKGKCGQNWQKQKRRKEGKKE

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						MGMGRIGGKKNKKEGRKERKEGRKEGNKW VWAEALGAFPEQKGKGLRRGPSEEAVGVSP L
7055	20956	A	7113	570	199	LCLLKQANLMAGAPPPASLPCCGLISDC CASNQQDSVGVGPSEPQVYSLVVRFL SRSDKRNIRVGVTRFSRCV/LSPLSLTR KENS LTPCASQVRQCLALLRLVHGATH WPAPT VWHSLMR
7056	20957	A	7114	466	284	RTRGIGWTANRRMKATQPLTFFHLIHK QEGGNVGSQKQQRD/VNSAFHWRLHDQ TANCLS
7057	20958	A	7115	474	224	DSNFEKSSSTLGKMLSNSIKCYREIFCER KSQLMQQTSM L\FKKLPQSPQPSATTTL ISQLPPTSRQNPPPAK\RLQLAEGSDGC
7058	20959	A	7116	377	111	FXXNFXSFLFFSLSLTRKNWVAHITFFF FFFFLPTPPFFYFIFLLIFCFFFLFYIF FFFFFFSF FFFFFFFF FFFFFFFF FFFFL
7059	20960	A	7117	417	148	VPPCLANF\NFFVETGSPYVAQAGLELL GSSHPPTLASQSSQITRVSHCSLLYFLM HSNTSISFFSFVALVSFLEMPSSCQDGI TVLAR
7060	20961	A	7118	2	196	RVPPPCPA\NFVFFVQTAFC HVAQAGPK LLASSNP PASASQSARI AVL SYCPLPSL RLRSHLDFF
7061	20962	A	7119	2	417	EAGGSLEPRNLRHLCA/LVAPMNSRCIP AWAT
7062	20963	A	7120	801	450	GPKFLGPPGVRIN/RRPGGGGLPRVYKK NNYPEDRPIVLPAFFSGGGR/GPGPHDK HPLPRKKQKNSPGRGGEPPFPFPFPFP GGERKNPLTPQKR RVHWGQGLAPFPFPS LSAKPKLF
7063	20964	A	7121	3	199	DAWG FALVVOAGVQCCDLSLQSP/RL ANFVFLAETGFLHVGQAGLKLLTSGNLP ALTSQRLRLQ
7064	20965	A	7122	407	164	NVAGLTGAYLDSFFGRDRV/LTMLRLV LNSWAQAILPPWPKVMGLQACTIEVSS LVAQIASKRLSGVQESDEAAWIRDC
7065	20966	A	7123	33	192	RWDFTMLPRLVLGSKRSAHLGLPKCWDY KHEP/PCCPGWSWAQRDLPTLASQSAGI TSM SHLHQAIPLKFLEQFIRFSILVF
7066	20967	A	7124	3	399	SIPVDWPSRAPTPRGRESAAHQGN/YPV GQRN\RMAGLSPRSFCWREVVSFR/SHS C/ICWVQLGKSAVLPQQRGPGAHEGSR RRGSSPPCPPLQTQLVFSPQELMSAP IHRLSVTLQGDCISTGGAPFRCLA
7067	20968	A	7125	1901	1574	FFEMESCSVAQAGVQWHDGRSLQPLPPG FKQFSCSLSPSSWDYRHLPPHRANFFVF LVETGLHHVGQ\SGLELLTLGD/LLPAS ASQSAGITGVSHHAWAKNPCFLTSTDT
7068	20969	A	7126	408	234	LPSSWDYRSPPPQANFYIFSR/MGFTM LARLLTSSDPPALASQSARIAGVSHHAQ PVYF
7069	20970	A	7127	88	277	KLSTEYKKQRPEDSFFLFL/VEIGFRYV AQAGLELLSSDPPTLASQSAGITGVSH HIQPPFKK
7070	20971	A	7128	3	140	QRWWCV PATRKA EAGESLETESRLQGA MITP\CSPA WATEQDIAS

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7071	20972	A	7129	1	212	PLLFVSPPLLSVSPPLLPFP/EPAASPP PSTHSLLPVQSESLGQFLHPPDPPLLA FPAPLKHQDLHISHL
7072	20973	A	7130	361	3	RNNISQDIAVIGNDSSNRSGQSKLKIFW KGFTILHAIKDFCDS/WEBVKISRLPGV WKKLIPTLMDDF/EGFKTSVEEVTADMV ETETELERLELEVKEPYGTGLLQSRDKT LTDEKLLMLD
7073	20974	A	7131	421	201	NFCILVD/TGFHHVGQVSELLLTSPNPP ASASQSSGITGLSDHSQRKSELVLSFNF FALFHILLCVMLAIDRND
7074	20975	A	7132	221	529	LIKFTIHSFYFIYLFIFFSGDGCFALSP RLESSGVISAHCNIRLPSSDSPDSASS VAGII/CMRHHTQLILY/CLVET/EFHH VGQGGVDLLTSGDPPASASQSV
7075	20976	A	7133	1	227	KGIFHSSANDVKKKTVLTLNLSQDPQLF RDGLDGWYHRLQKCL/ELDEVYVEK
7076	20977	A	7134	1242	300	DFVLPDGRVIP/KGIVCLINIG/THYN PN/LWPTPLEVYDPFRFP/ENIKERSP LAFIPFSAGPRNCIGQAFAMAEMKVLA ITLLHFRIPLTHTEPRRKPELILRAEGG LWLRVEPLAGTSRGNPRASSRPSLSDPW VLRRLPLPPPIFLFLLLLTPLLFVSMAR EPPSPRLRVEAPGPPEMRTPAIEATPKG TLQPAAGRLRFLSGCVPIHQVAGHRYG KDKMGILQHPDGTVLKQLQPPPRGPREL EFYNMVYAADCTDGVLLLELRQYLPKYG IWPPPAAPNDLYLKLENVTHKFNKPCIM DVKIGQKKL
7077	20978	A	7135	1	259	GTSCILASMLTRHRLRFSF/CLFETEFC SVAQSGVQWYDHSSSLQPPGLKLFSPV NFPSSWDYRHMPPCLASASILKLLFTID LGFYS
7078	20979	A	7136	1132	900	CSGVISAHCKPRLPGSRHSPASASRVAG TTGTRRHARLNFCIFFLVEMGFHRVSQD GLHLL/NLVVCPPRPPKVLELHA
7079	20980	A	7137	1	501	FFLRWSLTVTRLECSDVISAHCNHLPG SSDSPASAFREAGTT/GHDAQLIFVFLV ETG/FHHVVKGVDLLTS
7080	20981	A	7138	2	229	WHSGLLWSQPPL/YLSLSSWDYSHVS PCPAGLCLFLVETGSPYVAQAGLSLRGS ASQSTGIIIGMSQPAGFWKQL
7081	20982	A	7139	255	58	IFGKGFPFPFCQNGFGVPPPPRAFFFF FF/CPAKYYTMLPRLVVSNSWAQAIHPP WPLKVLGLQA
7082	20983	A	7140	422	274	TMLPRLVNS/GLKQSSRLSLPKWWDYR YKPPCLVYTFINRPEVPKE
7083	20984	A	7141	417	60	VWRFLEELETLPDPAIPLIGIHLKEH KLLYHKDTC/WNQPKWPSMVDWIKEMWY INTMEYYTAIKKINAIIRDPLTSPWDPF SWRKFCPLLEIWPASYFLPGINTRSLDE PLHIKGER
7084	20985	A	7142	391	70	SPPPHPPRKG DYRG GP/RPGKKREIFF FFFFLVDTGFC HVAQAGLKLASSN/LP TSASQSAGITSVRHYIQPTLLKIIPQFL DILLFLKIFHSFLKSFNFNLSGFY
7085	20986	A	7143	405	304	FCRDR/SLLMLPRLDLNSWAQGILLPWP PKVLGL

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7086	20987	A	7144	3	159	HASEKIWMYMTMEHYA\SQKKNKIMSFV ATWMRLVNLISKLMKNEMMSVNGR
7087	20988	A	7145	343	115	CEFYFLSCTIVFTYFCR/DKGLSLLLRH VSNSWPQVILLPWPPKVSHQAQPEFYFR NKQTKIDLSFEETAADLAYYS
7088	20989	A	7146	453	119	RCWKGCGLWISLRTT/WREWQLVQPFWK TVWRCLRLKLVPEPPYEPATPLPGIHLKK TKAVAQRDMCTPLFIVAFQHLLKRLFF SRCVFLAPLLKIA
7089	20990	A	7147	3	105	TIEWGEVIS/SSYSSTMANNEGLFSLVA RKLSRPL
7090	20991	A	7148	295	23	FANIFSHSAETLQTRREWGPIFNIL/EK NFQPRISHPAKLSFISEGEIKSFDPKQM LRNFITTRPALQEFLLKKEFMSFPGTWMK LETIIIS
7091	20992	A	7149	1	161	RTRGFFYLDGVRSLAMLF/RLVLNSWPQ AILLPWLPKVLGSQTLAMVAAYTVFV
7092	20993	A	7150	1	219	DYRCTPPHPAHF/SIFIFCRQR/SLTMF LSVLNSWTQAILLPWPKLLGLQACTA MPIPGVELLWVSGCFVKES
7093	20994	A	7151	177	34	ELVSFLSFLSLSLFFPSFLPSFLPFLSF LPSFNPSF\LPSFLPSFL
7094	20995	A	7152	398	40	MNDRVLLFHPGWNVAQSWFTGASN\FG LKQSSHLSELLCSWNYRHTPQCPASLLAY VCMYVCMYVCMYVCRD/RGLTMLPWLVS NSRPQAILPPQPSKIMGPELLGAVAHAYN TSPKGSQRR
7095	20996	A	7153	418	179	RNSCTQMRNEALPNSGYFPKLYYYDF/ CORQDLAILPRLVYNSWVQAILLPWPPK VLGLQHEPPCLAVIQFLKGNLKIIV
7096	20997	A	7154	767	537	QALLCLPGWS\AVAQSWLTAASNSSDPP ACLSSWDYRHVPPRQAEWSFRVSVSSP VKRDPGSPWRRMRPCSE
7097	20998	A	7155	421	301	HAQLFFCRHW/SFTMLPWLVSNSWAQAI LLPWPPKVLGLQV
7098	20999	A	7156	410	269	AGGPQTGSFFFF/CYERGVSLPRLVSD TWSHVILQPQHPKVLGLQA
7099	21000	A	7157	3	237	MQIKA/TMLYHFTPTNMTVLGFKKNSRG WQARGEIGTLVHCWCGCIMMQLWETVW HFLKRLNKLGVVVHACSPNYSGG
7100	21001	A	7158	435	211	LFLVEMG\FAVLASLVLTLE\PRDSPTS ASQRARMTGMSHHTQPLFCFLVSKFHLLA KKLSLIWQNLRRAGICRLS
7101	21002	A	7159	3	220	SSASQSGGITGVSHHARPSEQR\SCSV AQAVVQWCNYSSLITPTPLKRSSRLSL LSSWDY\GALPHPSVAS
7102	21003	A	7160	1	172	FRKVLGRTGSNGLCTQVRVEFMDDTSR IMRNVK\SPVREGDVLTLLELELETLRL R
7103	21004	A	7161	1	180	DAAPVLKATARPTRPDWK/IDIDSLDI HGETPSLQKNTNTFRAWWCIPVPATRE ADMF
7104	21005	A	7162	3	108	KKKKTGRFKLV\MQYNRRFVNVPVTFGK KKGPNANS
7105	21006	A	7163	409	110	GQHGLTQSLPLSAPPRGAVPRWAPRPD/ SGLSLSPLLPTAFATTGASSANRFVSI PRDGNFLNIPQQSQSWFL
7106	21007	A	7164	35	371	YFHHLSLLKFLASMMVFLTVVVRLL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						LLFFFLGETEPAFVAQPGR\QGPNLGSLRPHFPSVKHFPGLTTPRAGTSGLDPPSP AIFGFFKKKRGSPCGPRAWTPGPRGGP P
7107	21008	A	7165	3	382	YTGPAWWSMLVVLATEEAEVGGSLFPRS SKLQ\QPPLRHCTPAWAT
7108	21009	A	7166	1	305	TAVTVDPYHSVYIEVNARPGACMNGGGL LNGEQNSLKRKQLVQTLNKRHGEEALAMV DSLTLGPKLEEA/ASPAPAFARVRLRARQ ACRRKGSRLCWEHLVSKV
7109	21010	A	7167	383	55	RDLMSVMRKSMLAIALCFTALMGMFNSI FYGRVVAKLFPFPLSYIQGLSHRNMMGD DTTDCSFIFLYIFCTMSIR\QNIQKIVG LAPSRAATKQAGGFLGPFPCCGKFS
7110	21011	A	7168	465	166	SPQGAQIKGVGFQKLRPWGP\PGFPRGK PFFWFKKKLPPQGGGGLCSRFSGGLSQK N\SGPWGEIFPWQNGPFPSPPGGKET FSKKKKKKAVDYLS
7111	21012	A	7169	2	323	IQGFKTLSEEVSADEVIVRELGLQAET EDVTELLHFNSTACCREIFHERKRQMQ QTSLSVSH\RKLLQSPQSSAIATINQSQ PSTLRQDMPATRLHLTGGLDNH
7112	21013	A	7170	3	509	FGTIPLVLCADLNSLPDSGVVEYLSTGG VETNHKDFKELRYNESLTNFSCHGXNGT TNGRITHGFKLQSAYESGLMPY\NYTFD FKGIIIDYIFYSKPQLNTLGILGPLDHHW LVENNISGCPHPLIPSDHFSLFAQLEL/ YTAFPAPSQRHPPSQEVVKHLQRTALI HL
7113	21014	A	7171	1121	320	SSCFQTSSHACFVTEFVPGGDPMQIHE DVFPEPQARFYVACVVLGLQFLHEKKII YRDLKLDNLLDAQGFLKIADFLGCKEG IGFGDRTSTFCGTPEFLAPEVLTQAYT RAVDWWGLGVLLYEMLVGECFPFGDTEE EVFDCIRLHGRPPTPAFLSVQG\VKFIQ KLLQKCPEKPLGAGDQNAEEIKVQPFPR PTNWQALLARTIQPFVPTLCGPADLRY FEGEFHRAA\PALTPAPHSLLTARQQA AFRDFFVSERFLEP
7114	21015	A	7172	355	3	GPLLSMLGMNIFLTLFLLPLSLMEGG VCGNF/ITNCCLEIDDNRKVIEDITAKI QKLAHVVPQIWKWSPDTLFGWFFSSLG RFKTLVGIVLVILGVCLTLPCLLPLLVK NIQSANV
7115	21016	A	7173	184	2	EKKVEDDDDDDFEMESRSVIPAGVQWR NL\LHPLPSGFKPPSCLSLPRSWEHRCA PLHQCI
7116	21017	A	7174	1190	407	SLKRRPSARGSRPMSMYETGSGQKPYLP MGEASRPESRMRLQFPFAHIGRSALVT SSSSLPSFPSTLSWSRDESARRASRLK QNSTPESDYDNTPNDEPDGMGSSRKGR QRSVMWPGDGLVPDTAEPHVAPSPTLPS TEDVIRKTEQITKNIQELLRAAQENKHD SYIPCSERIHVAVTEMAALFPKPKSDM VRTSLRLLTSSAYRLQSECKTLPGDPG SPTDVQLVTQQ\VIPVCVRPFAKAAKQL VTITTKENNN
7117	21018	A	7175	3	136	AIHLASLKVFYRYRVLSL/LKRLVSNWS

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						PQVILLPWPKVLGLQV
7118	21019	A	7176	3	316	GIVKFFFFFFLTKCRTVTQAGVEWCSLG SLQLPPPRFKQFTCLSPVSWDYRHLPI CLANFCIF\ VETGFHHVQGMLLELLTSG YPPTSAPPDAEITGVIHRTQP
7119	21020	A	7177	529	217	LLPRLEYSGMVI AHCGQLQLGSSQAILG ACYCAW/HNFKAFFVETKSHYVTQAGLK LLASSNPALASQSVGITGVSHCAQATL PFKTVDKGPSFNLFSTPPLL
7120	21021	A	7178	3	150	YTLCKSKKDIKSIYHIMT/HLKTHTHTH THTHTHHKPSTTFSTYETFIM
7121	21022	A	7179	540	69	ACRGAHVQVGDGSALTYVVDGTACGPTM LSLDHLCPLALAFNFSTCTDSGERRICS HHGVTAWSLGWREKLTRGDRPLLTSPGP ALPIG\CSNEGKCICQPDWTGKDCSIHN PLPTSPPTGETERYKGPSGTNIIDSTIA GAVLVAAIVLDETGWGYK
7122	21023	A	7180	452	279	CIDSIYQEIYHLSISILSVYLSIYRSIY LSIYLPFW\SLYLGPRFLRTRDPQLLS LT
7123	21024	A	7181	501	183	HVRCLAFICALIGFPPSGYFSIMPVVT/V DLVGIEHLPNAYGIIICVNGISALLGPP FAGWIYDITQKYDFSFYICGLLYMIGIL FLLIQPCIRIEQSRRKYM DGAHV
7124	21025	A	7182	446	245	LRVRSALNQVSSASRYWDTG VATKLAT F/SLFWKDRNLDILPSMVFN SWPQVIFP SWPPKVLGLQM
7125	21026	A	7183	420	73	DSSDDSGQSKLKP/FWKGFTILDAIKNI CDSLEDFKISLTGAWKNLIPPLMDYBG FKTRVEEVTADVVEIARELEVEHGLG AVAHAYNPNTLRRLSLKPRSLRPGQHSK TLSL
7126	21027	A	7184	567	174	FFLRDRVPSLTQAGVQWDHSSSLQPRPP RLKQSSH\ PALLSSWD/YRHRPLCLAKF LIFLQRRGLAI/FARGVVSNSWSQ/CNL PASVSPSAGITGESHYSPFLSDSQT VYKTHRSTISSTITEMGCERKD
7127	21028	A	7185	345	59	RNGSSCLWQVIQSLTLRLECSGVITA QCSLGLVGSSNPPTSASC\ VESHCAQD GLELMGSSNPPTLAGITGMSHCAQPLYD LFLYEYGLSVHY
7128	21029	A	7186	1	209	LSVVLEIGSHSVTQAGVQVHSSSLQP* MLGLKPSSRFSLPKCWDYRHEPWCLPGL LRLKFDP SVGGVA
7129	21030	A	7187	3	225	EKTPVSDRGAKGCTESLVNRRPCFSALE VDETYVP*EFNAETFTFHADICTLSDKV RHFLKPIALVILNHHIF
7130	21031	A	7188	1	377	ES*RNHNGDEDDSHVRAQGACIEAKHDK YMA DMELFSQADDNRKKRDI PDYLRGK ISFELMRQPCITPSGITYDRKDIEEHLH RVGHFDPVTRSPLTHEQLIPNLAMKEVI DAFISENGCVEDY
7131	21032	A	7189	1	359	SRATDHVQRQGHG*GIHNYSDWENTDWF RETKNQSVPLSCCIETVSNNGSLAHPY DLYAEGCEALVGKKLEFMMHVIWAE LA FAAIQLLSMLSACTVMCRKSTDPAYELL ITVGTYA
7132	21033	A	7190	496	118	QNQKFFFEPGTS*LGLYPKKYKLIYHKD

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
						PKTCMFTAALLTIEKPPWNHKKHLSMADWIKKVWYGTGVGHACNQSTFLWFFFFEMESHAVAQGGVQWLNLCSLQAPAWATERDSSQKRPKIDPHKYIVN
7133	21034	A	7192	1337	342	ISEATRTTFRESIWQFQSSPREDDNRQLSASGSRQSHPGPRSTPGPGQGHRSSHQGCAPVSSAARPGGPSFRLSEGALSRSQFSVLVYIP*VAAGQFVKACLGASSPPSRL*GGLGTGHRTPGKEARSWPETSAPPAAWHLRLSLCLPSRGEKLAQARSQKHLGWKWLSKLCPKTKYSWSPDDSPSVLRDPEAGTTRWAPSGNPEEEVVLQKAKYLQNISEVLVLHLLHIKALQLHSTNFFVNARHLLVGQISSALTNLNLSQILFLLLRFPFLSQVERHSPLQKTGTETNLVLFQDTPVMNFPSSILLPSKYSKCPALDKEASHFYQ
7134	21035	A	7193	469	130	SASWDYRRPPRPSNPLY**RRGFTILARMVSVS*PRDPPASASQAGCAYSILYQERFARLHPACLAPRYMASDPLSSLHHSVPPGLHLEHEHHLWHCLLPQICRPGKLWY
7135	21036	A	7194	430	149	TVWQFLKQLNIELSCDPVILLGLICPRELKYVHTKTRT*AFIVALCTIVPKQKQLKYPSVDEWVIKMWYVHTMDYFSVIKKNKLAKHRGSHL
7136	21037	A	7195	257	412	TATSNKEPLKKVRCLIWKKDCWARGFTACNPSTLGC*GRWIMRSRDRDHPG
7137	21038	A	7196	1	124	PLISGVVHPCNPSTLGGRGWRIA*VQEFETSLGELAEPLY
7138	21039	A	7197	2	120	YGIILFITSEVFVFAGFF*AFYHSSLGKKISKKESVIIY
7139	21040	A	7198	234	416	GVHAEVLISPGPQDRRLRALVVIPIIFGILEFAILLVLFVKKVAKKPTNKVGHP*EPGTEF
7140	21041	A	7199	372	3	VHYVPVQTGSPCCVPHPRGLSTIHPLHSRYTGLGMVAHACNCSTLGGQSGKIA*ALEMEISLGNMVRPCLYERTNKQSKPRHMGITFGLTFSLTLTDKYSLLISGFYLPQVLISLHPLGPY
7141	21042	A	7200	396	21	GLKESHKCCAIPACLQDRDLVRVLGKAGF*RKSLSISTELQSLFSDPFSKITGKPIKLTQVEHRAGFEWNEDGAGTTPSPGLQPAHLTFPLDYHLNQPFIFVLRDSDTGALLFIGKILDPRGP
7142	21043	A	7201	2	148	REPPHHSANF*KFFVDKGFTLLPRIVSSWPQVVLPPRPPRELGLQA
7143	21044	A	7202	1	291	AEGFRMHALVSQAACGTSYKLSVGYMVQGPLTHMLGLLISLIFLSRGSGRTWAFSHS*YKTSDLLPCRNREVIEWEFLHYRNLHSHICLSVTKTFL
7144	21045	A	7203	262	406	ILARMTSVNSIKHLILFLK*SSHLSIPSSWNYRCVLPHQANFLFLFL*R*SFTLMPRLVETVLLIQNSPTKIDSSPDDFSGKFYQTLNIVFENIRRGNTSNLLHKNSRILIPNLTKTLHD
7145	21046	A	7204	2	247	DTVLEERSGGTAALPRSTSLDRDWAITFEQILASLLTEPALVKYFDKPECMARITSAKNIRMMGKPLT*ASDYEISAMTG

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7146	21047	A	7205	2	168	FFFLVETGFTVLARMVSVS*PRGLPASA SQSAGIAGVSHRAQPALRFLMLENRM
7147	21048	A	7206	1	237	GKCAHTHTHTTRDTHRHAAHATHACTH THTYVQGCSLSQWSQDCVRMWACHIFGV PRE*ASRYTSSLVYKPGCTGVCG
7148	21049	A	7207	2	239	KVDSEHKLERSSGGVLGRFGKSGSGLN LGNNFFASRKGYSRGTGFDRLNTEGSDQDK EDDGSESE*EYS*PMPALEPCSS
7149	21050	A	7208	1	405	GSRDMNMVILICFPNAPKVS AESVKND QLDKYLECTAQEI I*NHWDVDPDLFHV RTLPSDNMPSLP PGELASMRVTIEAVY YRLNPYINDDDTSTDDMWFCSSSHG VYLDLHRRVQVNFDETFSMHP
7150	21051	A	7209	2	761	QDFGTRFATVLLFYGYFKCTRTLLKGTCL YNAILYKVCSPRNDQPDVCYNPSFFLLP IKTGELLGFLVYASREKRSIAIGD*KDD KWPPERIIQYGPAT*AQDSSWGYRIP YMLN*IIRLQAVLEIITNKTGRALT LQEIQMRNAIYKSRLALDYLLAEGGIC GKENMTNCCLEHIDDQGQIVEDIIKITKL AHVPMQIPDIVWKNIVKIPVLFCSVLIT GTCSPQSGTPCWLRSRPSHVDPFRVVS P
7151	21052	A	7210	147	390	KTGLSDQMPRAIQLSYSYLSPLLY**SY KKKKKKKKKKKKKKKNFFKKGPGN*SF WGGEKKSGPGAGLKNPGGKNTFY
7152	21053	A	7211	433	214	WGRGNALTTHPPWVPFQSESTTPSPL*G ITLLDNPFSPIPKQPPPH*SITVPYLL SSPQPGFPHPFQAPGLA
7153	21054	A	7212	532	253	KVVINVFHKAAIMSDFSDRSRHSTLKAS E*GFTMIDAIKNICDL*KEAKISILGTGI *KKS IPTLMDDF*GFKTPML*VTANVGF QRFSSKKFYW
7154	21055	A	7213	456	24	DAQAFSWYSQGYFNSSQGFSSISLPGDTS PVKIKRMGGPLFFS*LLKSTCWACSKTS RVPGKVLKTGLPRPR*PVYKDPLGGFY RF
7155	21056	A	7214	2	445	ILRDLQCRVPTWSGFPSWAMELLVEKAI SSASSPQSPGDALRTVFECISSGIILKG SPGLLDPCCKDPFDTLATMTDQHREDIT SSAQFALRLLAFRQIHKVLGMDPLPQMI QRSNIHNNRKRRRSDSGVDGFEAEGK*D *KDYDTF
7156	21057	A	7215	203	3	VRPGVVAHACNPSTLGG*GGRIA*SQEF ETNLGNTVRPCRNSEVLNRKTVSIRRA LRVFSPLHTA
7157	21058	A	7216	1	285	GKCAHTHTHTHTHTHTHMHTRTHAHT HTHMCRAV*VRGARTVCTCGSAPFLES PGKEPKDTRLPLFVSQAARAFLEGEKAF SVYRQREPPPI
7158	21059	A	7217	1	386	GDSNCEWSVLYV IATFGIGVALGILSW TVICMLKRQNGKPKMSKYKNLDATDQE SL*LKPASRAGIKQKGLLLSSSLMHSES KLDSDDAIFTWPDREKGLLHGQNGSVL NGQTPLKATSPREEIL
7159	21060	A	7218	70	379	NILYFNIFFFFK*FLKFLWVFFVFFVFF* VFFFYNNFFVFFFLCVFFVFFVFKLKI WGPFLLFRFFFFCLGFFGTQSWRFFFA

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						LFPWGLMFLFPLLFLLVFF*LVFF
7160	21061	A	7219	1	208	PRLAASVSPGDMGLGMQVLGLGTVASACN CSTLGGGRMGIT*G*EFETSLVKKARTC FYKRLKRQKSANL
7161	21062	A	7220	455	96	HYLYGSQGLSRFYFVTQGRVQWHDHGS LQPPTPGVKQSSSLSLPKWDYKCEPPCL ARPCPFFFL*TSVDTGLLLNQQPIL* IMTFPYPLLRKSLSFHHQIYEPTSI CSHLLSFCYT
7162	21063	A	7221	201	319	IYELWPGPVAHACNFSILGG*GEQIAQV QEFKTSLGHLG
7163	21064	A	7222	307	3	NRRQAGPFAKLGPRSPKGGFPNFFKLF FFKSSF*KNPKQGQWGFPLIPGFGGPQ VGSLGAPGLKPPWGTQNPFSKKKKKK RSNCTDTGTTIAHRRQM
7164	21065	A	7223	331	141	SETITANVSPNL*DANVPIQCEISPLI SYAGEGLERYVADKEFHAPVIIDENG VHEVVKNGI
7165	21066	A	7224	157	314	WLPGFRDGGEDGVCHVAQAGPKLRT*GD PSIKASQRAGITGLTHRTGPK*KF
7166	21067	A	7225	2	392	RDVRSLOPLPPSLK*FSCLSLLSSWDYR CAPPTT*LIFILLVEMGFHHIGQAGLEL LTSGDPPASASQSAGVTGVSHRTRPPSF VLVNPPIPLLPVPSPDGPNISSSTTSW RGYPEVLRWGLCSFWGCG
7167	21068	A	7226	84	204	FIFFFFKR*SLTMLPRLVNSWARVALP PQRPKVLGLHV
7168	21069	A	7227	3	307	DRAAPRGAGRAGAVGPHRTGDWGLAGTP AGRGHARHIGRGPKQGRAAGQRGHLHPG GLLGRGGNSEP*RKQRTPGSMRRAAPLL STGQVWEGPASVGDVRP
7169	21070	A	7228	52	1176	GSQQPLHLHISEAQGDTLKKAPAEAAWP PLIAFSSGRLPCSHES*SAAGYKRLDD TAAGGPPSPGGSPRSPTAFGLHPVWGG QLRPRGGRGLPATGSGEAFQALTQLSRG RACTGPPAPGSEDAAPSGCSAARWSP*M AGSSSCAIPDSAASCIPOGPPWRW*SR APARNRCSASSGRSRC*QLRRRYIPGL LHPVLHEALPDSWGCETQLGPPLASEAA PPRSRRREEG*RGSGRC**KPSLPRWS LCRNQAEAGFVSILVLSGLAGAPSRPA AAAPQIAPNQHRSPPLAPVPAASGSP WPWERDLGVLETNLVGNFAQDPNPSACS GPQSTPDITYPVQPKPTGLRLHFHSRPN TIVKSVGNMCL
7170	21071	A	7229	3	112	ASNLSRGCSSEPRPCHCTPAWV*E*DSI SKTNKQKN
7171	21072	A	7230	103	299	AMSQIRNAIPFTIAT*RL*YLEIQLTKE AKDIYENYKIPLKEIRDVTNKWKNI PC S*IGAQLCK
7172	21073	A	7231	2	137	SLTSLSLICFCL*RWGLSVLPRLISNSW PQAIFPPWPPKVLELQV
7173	21074	A	7232	3	273	LTHIVDGNFLTMTYQCLMCVC*QELGY QPVTTERCHNVNCDLQRSFKAQVFSCH ACRHDLGQNYIMIPNEIMQTLDDLAFPG YSLGR
7174	21075	A	7233	338	136	RPRWEDCLSPGVQNVCGHSESFPLOEI *KISQTWCKPVVPSYQVEGELLEIRG

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						STCFGLPKCWD
7175	21076	A	7234	437	261	HLGFPECWDYRHEPQHPT*FLEHFM*RRGLTTFPRLVWNSWPQAI*PRWSPKVLLELQT
7176	21077	A	7235	41	264	VTVMEIKGKINLVLDI*IKDIYVEGFSTY YF*RGGLTMLPRLDLD*SWAQAILPPQPP E*MGLQECNHHAQLSRYF
7177	21078	A	7236	1	154	GTRDFS*VKTL*ARREWHDI*FTGMKEKNF YPKKVYALKIPFKNEAETKKVEV
7178	21079	A	7237	1	179	SCLSLSSS*DCR*PPPCPANFVKSF*FRN GVLTMPLPRLVSNFLPQANLLAQPLSGFI LLL
7179	21080	A	7238	340	140	KINWVWVPVPI*PVTPEA*AQKLP*PGK LKFP*LT*IPPLPSRLGHQSQTSPFKKKK KFYILSSDSV
7180	21081	A	7239	2	175	QFESKPSPAWATEQDPVSKKKKKKKKKKK KKKMKKKNS*SKFKMIP*TKRQY*EGNWK N
7181	21082	A	7240	336	192	QSETPSQSNQKFIF*GQGIALLPRLVLN SWAQAILPPWPPKMLGLQA
7182	21083	A	7241	1	186	DRPGQHGEMLSL*IFCFFCRDGG*LTMLP RLV*LS*AQVILPSRPPKALGLQD*TVHC SKF*DAV
7183	21084	A	7242	2	111	VKTLNKL*GIDGTWLRIT*RAIF*KPTANI ILNMC*SF
7184	21085	A	7243	360	217	LPSRGDYKRKP*PCLVNFYFL*R*GLTLL PRLISNFWAQMILLPQSPKC
7185	21086	A	7244	35	276	VQOORVKQGRKYYSIVLKNKKKLCN*YLR VGE*MG*RNIGWVQ*VAHTCNPSTL*GGR GGR*II*PWEFETSLCNIG*TCISG
7186	21087	A	7245	1	356	IQHTFSL*ITFGIKYSYV*LVKIVSWLAAV AHACNLSTLGGRG*GWIT*GHELETN*LEF AVKPWVYDKNSFP*PTLNLRFAKSGHLWE PRGKNHGP*PETPPLSRVSP*PQRF*FGGT RPLKKE
7187	21088	A	7246	3	293	CKCGKAFHN*FYSFQNHESHTGEMLYDI RNVGK*SIF*HHCQHK*THRAEKLCEC KICREAF*SHFGNLKVHEAGRSGSRL*SQ HLGWANC*LTSGI
7188	21089	A	7247	6	387	ASIPCLTYPSWEFL*FI*QAGHFSFSKK KLFICAFFSNRDEVSLMLPRLGLNSWAQ VVLLPWPPKVLGLQVRATTPAKLGIFWG FMSVSLGQGVCLCRSLCPLPLGPGQVH SGCSQS*FVEKM*KNEL
7189	21090	A	7248	373	146	HLGKKVLI*FWPQYLALLNPPNGGVSRVY PRCRPLMV*FFFFFFC*GRGLAMLTRLV SNSWSQVIFQLQLPKVLGL
7190	21091	A	7249	2	184	AILRGI*KKFISTLMDDFEGIKTSLEEV TADVVEIAREVELEVEVEPKDVT*ELLQS HDTT
7191	21092	A	7250	795	544	EMKSCSCCPGWVQWRDLGSLQPPPPRFK RSPASASLVAGITAACHARLIFVFLID TGFHYVG*AGLKTPEA*ATAPGP*IFLYF
7192	21093	A	7251	34	242	KNTSLKKKFFWCQKLRNVSLVEEFAFWP GAVAHACNPSTLGDGRGVA*GQEFQTS LSNIGRPRLYRKI
7193	21094	A	7252	216	57	NIQVLKYVLT*SYLKKKKCA*FRLGPVAHT CNPGILGAQGRRI*SQEFETSL

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Method	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7194	21095	A	7253	126	366	INLTECQQYLDKAIFFFFLKKGLFAP*AEWQGGSFASLQPKPPRLKKSSHLTLLSTWDYGGALPCRFNGIFFFFWKKGG
7195	21096	A	7254	2	213	RPTWATWQNPASTKKKKNSFFFEFETFRTPVAQAEVQGGNLG*LQSLPPGLKRFSCLKMPEAPKGQSCSLIG
7196	21097	A	7255	150	263	EGVSLLPRLACNGAILAHCNLRLPSTSSDLCAFS*TTTRYKYSGYCFSHPNMLLICSREFTLLSSHSSSLGHLTLFLLIVCFEKESHSCPGWRAMVLSWLTATFASRRQATFAPSLELSR
7197	21098	A	7256	386	93	PPGGLPPQSIPSPRAQLKPKSPRGKKRGGPKPGGSQPGFWGFFFGPGPPFKRGGGLNWLGAKN*KGVKKNQKKKGKMPQETKRGNRSIDMKFGGS
7198	21099	A	7257	153	369	KENSRLQGYGPLFSHS*FTNSCPGQVQWLTPVILALWEAEVGGSKDQPGQHGKTPLLKIQKFARCGGRL
7199	21100	A	7258	180	3	CSTLI*IRKVLGAVAHAYNPNTLRGRGRIA*GQVFKTSLGNVKTCLFLPSPHNQ
7200	21101	A	7259	22	265	QLRAIPDLKLDPLMEGKEILSRTLLGSGTVAPICDPSTLRGQGGWIA*VQEFKTSLGNNMAKPHLYRKKLLGQVTKLEYKW
7201	21102	A	7260	326	2	KSAMQICIVDPLNAFCLEICCHANLHCRPSNAFCFLKVDNVRVAFVSPSIPQVSLILKNFSWPGVVAHTCNSNTVRGQGERIA*AQEFETILGNTGRPCLYFLKNRKS
7202	21103	A	7261	1	68	VNLCFILWLGPVVAHACNPST*GGRGGRIA*P*ELETCLSNTP*PGVVAHACNPST
7203	21104	A	7262	282	176	GLKKTFFFLVREVRLLCYPGWSAVV*SQLTAN*TPGLKLFSCLSLPCSWNHRHVALHVAENIC*CHMPVVPATWEAEAGEQLEPRSSVCSEL
7204	21105	A	7263	588	351	NNTVCLLESISSVNLCLPHLQHSVPKLEIFLFFFSSDNFPSTHHTVTRPLSPS*AIIFPVCTYTSRWPEATKDPQKK
7205	21106	A	7264	327	2	KIKERINNFIFICRDRVSICCPGWNAVVTLNWAQAIRFCLSLMSS*NYRCAPTHQVVTIIFCRDQIEIHMVPKYHLGNTLNYFFVLFCFVFLRHPFSAHRNFRLLP
7206	21107	A	7265	121	270	AQEAGFELLTSGDLPTSASQSAEITGMSHRALPSCY*FYVTLHGLTVACA
7207	21108	A	7266	3	227	SSQVSLPNNWDYRREPCLRFVFLFFVETRSCYVASLELLGSGDPTVLAS*SARVIDMGHCDWPNLSEILLHVR
7208	21109	A	7267	300	1	KMLLNTIMCNREILCKRKSPRVQQTSTFVSFVKKLPPQPPSATTLISQQPSTSKQDPFAAK*L*FAEGRLLAFPSNNVLYQLRYIMCFLPHTGIVHLVN
7209	21110	A	7268	29	344	ASLLALKKKKSGLGAVAHNAHNASTSGGRGGRIT*AQEFATSLGNMARTCLYKKKKKKKKKGKNTGVGGPQRGAPIFGPWGGKSPAPGKPGGPNPFPGKGAPTLLF
7210	21111	A	7269	3	209	LHPLSPGPPAPVAAGIPGPQASR*GPCRPDPSPDSSASVDASLPGPALSLWSWGSNRGEYGTTPASQIH

SEQ ID NO: of nucleotide sequence	SEQ ID NO: of peptide sequence	Meth od	SEQ ID NO: in USSN 09/515,126	Predicted beginning nucleotide location corresponding to first amino acid residue of peptide sequence	Predicted end nucleotide location corresponding to last amino acid residue of peptide sequence	Amino acid sequence (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
7211	21112	A	7270	86	206	CQPGVVAHAYNPSTWGGRRGRQIT*GQEF ETSLGNTARPPL
7212	21113	A	7271	45	274	GLGTVAQACDNPSTLGG*GGWIA*GQEF KTINNDKSNKWQYLAIEQINNRM LICK NKKELTDICNNTDEFQKHRE
7213	21114	A	7272	1	122	VLVETGYLRVQAGLKLTPGDPPALAS QSAGITGISHRA*SYMHE*LVETGYLRV QAGLKLTPGDPPALASQSAGITGISH RA
7214	21115	A	7273	3	242	LLKQLDYRPPHPAKFFFFLEFLVKKGPH LVVKGKFKTQTSGGLPG*ASKGVGIPGV SHCPGLIGVFNLTLKVAVSLMDL
7215	21116	A	7274	2	169	LALVAQAGGQWHDLSLQPLSPSPQFF YLSLPSS*DYRHEPPHSAWFSFFSNYR
7216	21117	A	7275	353	76	FAHLGLPQCWDYRREPLCAT*KLFLKGG *PSKFQVIFSSSLGTGHFSNACFSCVMWT IVLLIINFVWTGIDRTSGSSSVKCGNH SIYPMVLL
7217	21118	A	7276	6	87	RRGLTLLPRLGSNSWPPQAILLPWPPKVL KL*AQTPGLRQSSCLGLPKC
7218	21119	A	7277	1	203	FQVKMLCSGWMWLTPVIQALGAVAH TGN PSTVGGRGQII*S**FYTSLDSGNPPA SASQSAGITLA
7219	21120	A	7278	272	51	IFFFPVN*CGGHDVQHHEFNPS*NNLSSWS SWFMPITLPLWEA*AGK*LEPRSLRPAW ATKLDSNSKKKIIIEIHA
7220	21121	A	7279	1	131	SRDYRHGPHLPTDFVFFVEMRFHHVAQA GLKLLGLSDLPALTS*SRDYRHGPHLPT DFVFFVEMRFHHVAQAGLKLGLSDLPA LTS
7221	21122	A	7280	411	36	FLECVPNFFPPKKKFFFKKNTGQVFFPV TFL*KGPALEFFFIFFPYGKKFFFLSSAK DFPPRVFF*KGPLFFFTTTTTTTTTTTTT TTTTTTTTTTTTTTTTCFKHFIYKKVHF *SSVHFQPIIFF
7222	21123	A	7282	395	181	RKHESIHDSDVISVTNMQSLRLFFFIFF FILSL*LFRFIFFFSFLVFFFTTTCFF TTTTTTTTTTTTTTTT
7223	21124	A	7283	392	2	IKFFGYNV*FNYILKNGLF*QLLI*LIN LFILRQGLIFVVQVCNVLVFFFTTTFIF FFLFTTTTTTTTTTTTTTTTTTTTTTTTT TTTTTTTTTTTTTTTTFTQNM LFI VN FCKDTFKQQNIHLRTRGR
7224	21125	A	7284	113	291	YVCVCVCVCVCVCVMEY*SAIKRDKIVA FTVTWMELETIILSEVSQEWETTHMLS LIN
7225	21126	A	7285	327	44	LKVSSENFSPKKKVLPPKPPCTIFPPS PF*KTPPEPIFIKPPHKKKNFNSPPPQK *GPPQGFTKSPPPFTTTTTTTTTTTTT LGFSKLLIR
7226	21127	A	7286	3	215	VILITFMI*EAFWKRVLVIVEEPSINL E*LYDGGYYDGLVLTSGLGPY
7227	21128	A	7287	367	119	LKKAPAPPFLNPPFWGKNFILSPPEKMG PPRGFFKRGPPFTTTTTTTTTTTTTT TTTTTTTTTTTTLQYNNMYFH*ILIIINQ
7228	21129	A	7288	73	259	INKYLQN*KKKKKKKKKKKKKKKKGGP FKKTPRGAQISPGVKKNFPPKGGFKKK QAPGPF

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7229	21130	A	7289	337	53	LRSFAPFHLPIINNLLTDIHMVPIPLPPSS LCSHYLFNEVTVTTLFKTTTHLQLGTMA HTCNPNTLGG*GGRSA*AQESSETSPGNM AKPRLYLLNF
7230	21131	A	7290	1	96	KHHFGFEAAA*YWHFVDVV*LFLYVSIY **GS
7231	21132	A	7291	288	2	SRVEFKGPFMAHCSVTIPGSSSYVFTSAS *VAGPHGARHHAC*FLF*FLV*MLLEMG SRHVQAGL*RVSSDPPARACQSGGIP GVKPHAQSVSV
7232	21133	A	7292	121	233	YFPKKKKKKKKKKKKKKKKKKKKRKKK* KGGGRSRKSYLG
7233	21134	A	7293	3	346	NPLNPLVNLTVSPKRNSSLDTRKKPCRE RHREKETLRKKRNQHTEARGRQRENHPE TE*ETGQRDRDKQTKKQKDTDIQAYTYT DREKRDKKRHRQIR*ABERIRDTERQR DI
7234	21135	A	7294	46	346	ETGLKKWGDLSNGTVRAVLNLAQADFCV SIPSYHIKHGNTKNNCGEGKKILVVT AKKSEPGVVTHACNPNTLGG*GGRVT*G QWFKTGLGNIVRPCST
7235	21136	A	7295	254	12	RKDAENNGSRAB*IKRVKDLVQSKLKFF QELEKEGILPNPFYEASITLIPKPKDGT SKEDYRPISLMNIDAKILNKILAN
7236	21137	A	7296	258	1	CIGQCVLVAVGRELLCVSRSWCGLLHVD EVGGEALGRLLVVYPWTQRFSESFGDLS TRDAVMGNPKVKAHGK*VLGAFSGLAL LD
7237	21138	A	7297	191	263	VCSKCEPFIYIMDYAAIKRNMKIMSFVA RWVQLEVVSLELTQEQTENNMFS*VVFG FLLLC
7238	21139	A	7298	2	164	SRVAGITGAHHHAQLIFVFLVETGFHHV GQAFAKLLTSNNHARPQ*LHFFYFFK
7239	21140	A	7299	307	8	VMIITFWLPHLSGYIEKSTPYECGFDPI SADRVFPSIKFFLVAITFLLCDLEKALL LPLP*ALQTFNPLPLVMSSLLLIILAL SMAYE*LLKGLDCSE
7240	21141	A	7300	205	317	KSSPACTPSTLGG*GGWFA*VQEFETSL DNMVKPQLY
7241	21142	A	7301	140	22	FNFLFLYP*NYFFFFFFFVFVFVFVFVF FFFAMNINVFY
7242	21143	A	7302	382	151	SIHRSEFRPRRSHSVSRPESRGITLVYC SLYFLGSGDSAPVVS*VAGTTGVC PWAS LIFGFFFFFFFNRDGVLLSCPG
7243	21144	A	7303	318	17	LVPTKRPQVENYYPVHTYIWIYCTKGKRR WAGIGGSCLSQHFRPSWDPLSLGV* DQPGQHRETPSLQK*KNWQEPVPATQ EAEAGEWCEPGRQSLQ
7244	21145	A	7304	310	132	QWCDLGATPANFCIFFVRNGVSPCWGS WS*PPDLKLSARLHFQSVFFNPISIGL FFL
7245	21146	A	7305	338	168	REPPLPAANFVFFVEMRSHHVRQAGPEP PSSDDLPAASQASAGITGVHCHAWP**T YK
7246	21147	A	7306	276	161	IINAAIKKNEFMSFAGTWMKLEAILSK LTQELKVK*KLRKFNTDTILLLLIFKI F
7247	21148	A	7307	310	61	ITLVYCNFFYFINFNFLKLFDSFVILS

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3						LKQIYSCTAIVYILIL*AFVQFKFLCFY FLYFKNIFYKNIIFYKIKYV*NMIFYF
7248	21149	A	7308	257	1	CGRVDLH*AVFFFFKRWSLTVLPSSLDD SWAQVILLP*PPE*LGQSQCTTPPSSLS TFLYAFHLHPVNKMSCFVGKDRGMFFSY H
7249	21150	A	7309	2	181	RDGFCHTGTGL*LLTSGDPPASASQSA GITGVSHHARPCHLHSLTAFKKNMWWPG QQE
7250	21151	A	7310	25	340	FCVFNTMDVKNI*IFLIFVPDVHLG*QK NLLLDTI*KKKSIRIQE**QYKSISKRN YNTVSDKSWLGTVAHACNPSTLGGQGG TA*TQEFQTSLDNTVRPCVYY
7251	21152	A	7311	2	193	FVDFSMHILDMLSLYLSIVICYITLFLS IIDNIYVNGPHKIIIPYFCIKYIFYIY IWFCFWFFETVLLCCFSVFTFNDYCSYL HYFLLLGVFGLFHHF*FLYLYMVLFVLF
7252	21153	A	7312	1	245	RTEGLKQSSHFSLLSSWDYRHPVLPAN AFFFFKGP*SEPLTLASSLHWYFPGGHF LQGPAKIDDFNSPILGKLKKKSPF
7253	21154	A	7313	167	2	GKPCLLVVMCRDSQKCGEKTGLKREAL RMGK*GQARWLTPIPALWELEAGGSP
7254	21155	A	7314	334	152	CHVAQAGVQWYNHSSLQP*PPGLR*FSH LSLPSGWNHSWTPHPANFFIMGSCHLP LINK
7255	21156	A	7315	2	164	PHVQDGLELLTSGDPPASAFQSAETG VSHHARPTFYLS*QVGLTVTSFRNPQ
7256	21157	A	7316	155	9	QRIKH*FHWLGAVILTCNPSTLGGQGGW ITGGQKFETSLAYMATPRLY
7257	21158	A	7317	1	293	GIPSTWDYWCTSPQPHF*FFFFFF**KR DLAMPLPGVNLNSWIPAILQPKGPKVLGL QAWTILYKGYGKEMWHEICKGTHDVL SKLLTTKRFRLL
7258	21159	A	7318	262	73	SNSLVYLIKPDVYIFLLFVETVSSHVA QVGLLELVASSSTPI*ASQSVETGVSHH ARPKKVT
7259	21160	A	7319	169	265	GGRMALSPGRGCSEP*GCHCTPAWETE QNPA
7260	21161	A	7320	169	260	KPQKIPVACDQOFTDKRNC SHGDYECNM VDFFFFFFFRERVSLCHPGWSAVV*SGDH TTALQPG
7261	21162	A	7321	580	400	FFFFERESRSVARQPGVQWRDLSSLKSP PPGFKRFPCLSLPSSWDYRRAQPCPANV FEFW*RWGFTTLARIVLLS*PCDPPTSA SQSAGITGVSHCAQP*FFFFERESRSVA RQPGVQWRDLSSLKSPPGFKRFPCLSL PSSWDYRRAQPCPANVFEFW
7262	21163	A	7322	130	26	SPGPLFGLIEPLPSRFKGFVWNLNLP*TW EYRLALTAPIKFFKFLKTGFPH*GIKL RG
7263	21164	A	7323	17	303	KSSGTIKGRAQSPFLQLVAIEQCQDCFH FRSQF*YLLKQLQPGMMHAYNPSYSKG *SRRIT*AQEFKSRNLNITKLCCCKINN SLIFKITENIE
7264	21165	A	7324	194	8	DWVEVLKKSTYRPDTVAHACNPSTLGG* GGSIT*GQKFEIRLGNVVGPCCLKNLTN QLGVGG
7265	21166	A	7325	413	72	GVPIFLKTLTGKTISSERESKVPLEK GK

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						ANFRDKRGIPPHHKRVIPAEKKL*KGRS PFDDGFQKKLTQPRVSAFKGHPPLQPLY AFIKSFREGTTHQDCPFWHLTLLSARRQ Q
7266	21167	A	7326	394	177	NVNHTHTHTHTHTHTHTHTGWCSDTGYS SDS*CITPRCIHDPTWPSSSQTVNLMAG LTLAKEVLANMTQTEV
7267	21168	A	7327	232	22	SRPSGSKKGAPALQQSSCLSLSSWDYR HKPPYLTNFCIFL*SQSPMLPRLLSNS QPHSNLPKVVELQV
7268	21169	A	7328	232	3	YHRSSGSLISLIQIRLRSKI*APSIPII KEWLSSVAHVYNPNTLGGQGRLT*GQE FETSLGNIARPCLENCLKN
7269	21170	A	7329	364	3	PKARRATVRRTRVSKAPSNRQCLGVNTH VLGHRPVPKGNAKTRWSASESQAHTCNI TTLGGQGGLIT*DREFESSLATMQNPVS VSGWLQKMFSSKQKLYSKFPNPVAYKA FR IWLLCARA
7270	21171	A	7330	177	2	DPHLHKKFKARCGGMTL*SOLLRLR*K DQLSLGVGGCFELLWCYCTPAWTERDP SC
7271	21172	A	7331	413	40	RHMYLMFYTYIYVLDIYTYTVFFMYIYI P*CVCKYISCLHIMYRFISMYPVYVYV CMVCNVIVHIVENAGSCLALSALIE ME GMARDSKMWTFNPDCKMRLSYKKQLEKL NFMILCPTWKEF
7272	21173	A	7332	147	49	KNYIYFCRRGLPMLPRLGLNSRAQEILL PQPPM*LGLNSRAQEILLPQPPM
7273	21174	A	7333	148	361	SWLGTVAHAYNPSTLGGRRGRQIT*VQEF ETSQSNIARPLLYSVLAYAVQPPLPMVA MRKLWLIPTSRITAL
7274	21175	A	7334	305	2	CPGGFVTRVHR*YVRLSQPDLRVFTSGA MPASAAQAGITGMSHRARPVCIIIFL NIFKVTCIFVELTIPNQNKQNTFLSSTV ASCRILASRPPIVVVL
7275	21176	A	7335	1415	1164	FFLRQSLLYCPGWSVVAQSQLIASSITQ A*AILPPCSWDYSSQHTWLKFFFC*DGF SMLPRLVSGSWAQMVLLPQLPKAQAKL
7276	21177	A	7336	1	206	GTRADHLSGFGDQPGGHTETLSLLKIQ RSQAWWHVPVMLPTR*IDARESLERLMT IALLKVRNRYIF
7277	21178	A	7337	65	302	KSSLFYFLKIETGFHYVAQTGL*LLSSD DPPASVFQSAGITSMSSHQTQPKELLKST RNTLEENPREWAKAREWAHRRNT
7278	21179	A	7338	208	38	NPVSAKNEEYPRGTFDLGTQAEVQWHD L GSLQPTPPGLK*FS*LSPRV
7279	21180	A	7339	2	198	ARADHPRSGVRNHPGQHGETPVSTKNTK N*AWWRVPLVPECWDYILFYMTNCMDN KLPKWLTLC
7280	21181	A	7340	2	227	ARGEIMSFATWMOLEANILSKLTQE*K AKYCMFSLLSGAKHWVLMNIKVGTDTR DYLGCSTQAVLKNLGTAE
7281	21182	A	7341	3	300	HEGRNYTLTGRDSCTLAASAEKACGACP LWGKCAESSKVCVCREASDCBEEGISIC VDVNCKEQTMPEC*AVAL*CTVHLIYVT INNALCLPQLTLFL
7282	21183	A	7342	210	351	RGLGTVAHACNLNTFGG*GRWII*AH EF ETSLRNITKPSLRENPDML